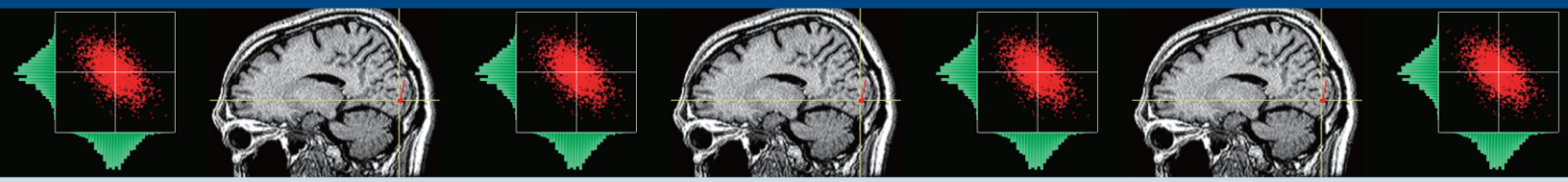
Advances in Neuroinformatics V

5th INCF Japan Node International Workshop

Advances in Neuroinformatics

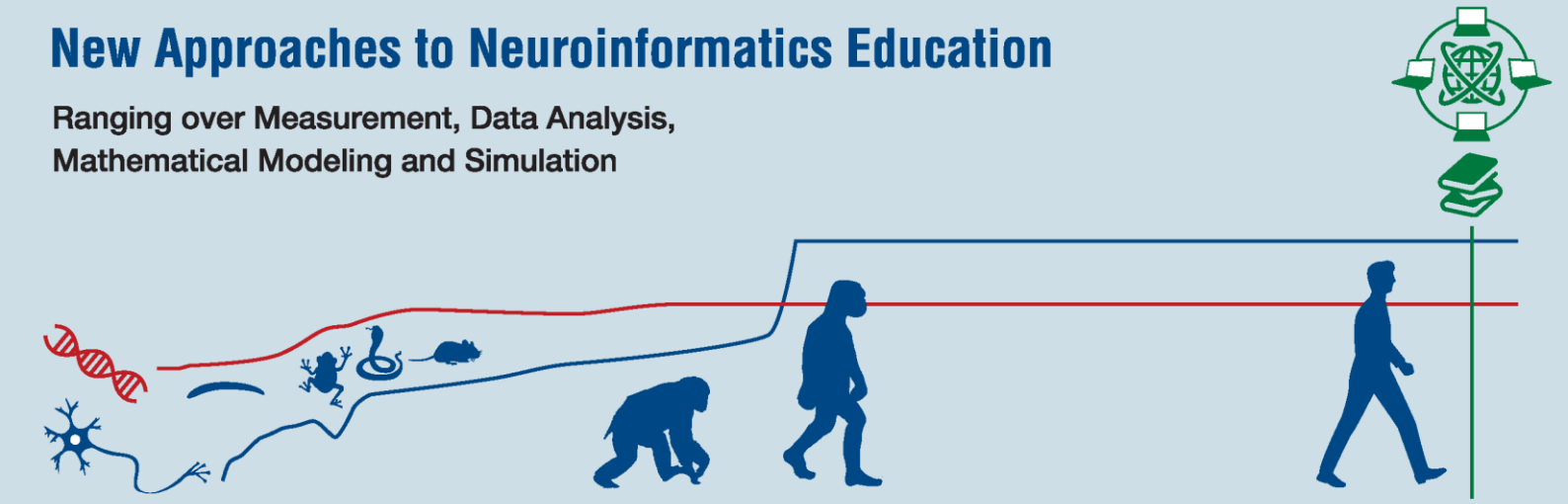
AINI 2017

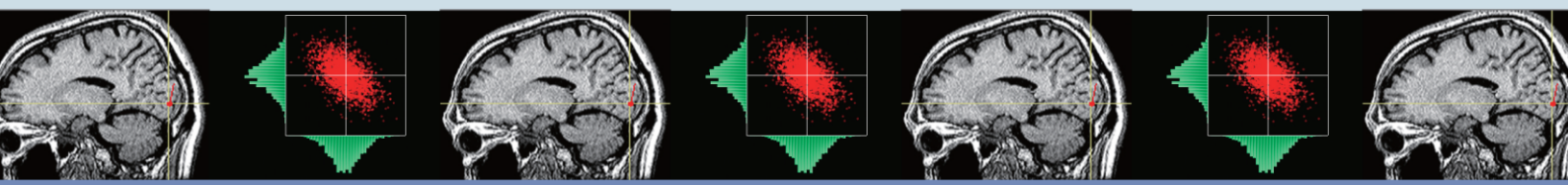
Abstracts



New Approaches to Neuroinformatics Education

Ranging over Measurement, Data Analysis,
Mathematical Modeling and Simulation





November 20-21, 2017

Okochi Hall, RIKEN
Wako, Saitama, Japan

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Date

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Place

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Chair

Ryoji Suzuki, Dr.Eng
Emeritus Professor of Kanazawa Institute of Technology;
Advisor of Office of Research Development, Kanazawa Institute of Technology;
Emeritus Professor of Osaka University

Co-Chair

Yoko Yamaguchi, Ph.D
Neuroinformatics Japan Center Director, RIKEN Brain Science Institute

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The Institute of Statistical Mathematics
Japanese Neural Network Society
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* This Workshop is a part of the RIKEN Symposium Series

Table of Contents

Message from Workshop Chairs

Ryoji Suzuki [1], Yoko Yamaguchi [2]

[1] Emeritus Professor of Kanazawa Institute of Technology; Advisor of Office of Research Development, Kanazawa Institute of Technology; Emeritus Professor of Osaka University

[2] Neuroinformatics Japan Center Director, RIKEN Brain Science Institute

Neuroinformatics has been recognized as a research field of information or data science, operating on the data obtained in neuroscience. Recently, as the scale of data being produced in neuroscience has increased, there is an emerging need for a highly trained workforce. Several efforts, including INCF's, have been initiated for educating neuroinformaticians.

They are required to become somewhat conversant in both neuroscience and computer science and have the skills to manage the big data produced in neuroscience. All of these efforts are important and valuable, however, neuroinformatics as a discipline should not stay as one field of information or data science. It is expected that a transdisciplinary approach between information science and neuroscience will create a new paradigm for the understanding of brain function. The neuroinformatician should not just wait for the data from traditional neuroscience, but should join the process of data acquisition; what kind of data should be measured, how to acquire it and how to analyze it. And they should reconsider whether the approaches for big-data in other fields can be applicable or not to neuroscience.

Since 1970 we have some experience concerning these matters at Osaka University, where we have established the department of biophysical engineering for undergraduate students, aiming to develop new types of scientists and engineers. The curriculum was designed so that they can learn quantitative literacy, hands-on research experience, and become somewhat conversant in neuroscience, physics and engineering. However, how to organize a transdisciplinary approach that will create a new research paradigm for understanding brain function is still an essential issue for us. We are expecting this workshop will provide us advancement toward the solution of the above-mentioned issue.

Keynote Lectures

Decoded neurofeedback as a causal and computational tool for neuroscience

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One of the most important hypotheses in neuroscience is that human mind is caused by a specific spatiotemporal activity pattern in the brain. Here, human mind includes perception, emotion, movement control, action plan, attention, memory, metacognition and consciousness. This is a central hypothesis for computational and system neuroscience, but has never been experimentally examined. A major reason for this failure is that most neuroscientists including us, from the beginning, gave up the possibility to experimentally control spatiotemporal brain activity in humans. Sophisticated manipulation of firing patterns of many neurons across a whole brain is a very ambitious but essential experimental tool to make a neuroscience causal. Decoded neurofeedback (DecNef) is a novel method to fulfill this requirement by combining real-time fMRI neurofeedback, decoding of multi-voxel patterns by sparse machine learning algorithms, and reinforcement learning by human participants while avoiding "curse of dimensionality". We demonstrated that V1/V2 activity patterns can be controlled for specific orientation information [1]. Not at a neuronal level but for humans at fMRI level, DecNef enables manipulation of spatial activity patterns that correspond to specific information represented in a specific area of the brain. They include orientation in V1/V2 [1], associative memory between color and orientation in V1/V2 [2], facial preference in the cingulated cortex [3], fear memory in V1/V2 [4], and confidence for perceptual decision-making in DLPFC and intraparietal sulcus [5,6]. Furthermore, DecNef was shown to be capable of changing brain dynamics for therapeutic purposes [7]. DecNef induces changes at neuron and synapse levels via reinforcement learning mechanisms while crossing gaps between voxel level and cellular level and avoiding curse of dimensionality in learning [8].

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Citation: Kawato M (2017) Decoded neurofeedback as a causal and computational tool for neuroscience. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.kl.1

Responses to the (life) science reproducibility crisis: evolution of training and publishing in neuroinformatics for a more efficient research.

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Lack of reproducibility has been shown to be a major phenomenon in many scientific fields [1-5,11], including neuroscience and neuroimaging, leading the scientific community at large and funding agencies such as the NIH [6] to explore ways to solve for the so-called reproducibility crisis.

Solving for this requires a clear view of the causes, both on the technical and sociological levels. In the first part of this talk, I will review the most likely causes, including the publication-focused research incentive system [7]. I will then review the cultural changes required for more effective research using the specific example of neuroimaging, and how funding collaborative research may play a central role in initiating these changes. I will then review what technical tools can foster this cultural changes with a focus on datasharing and linked data technologies, and take examples of preliminary solutions developed by the International Neuroinformatics Coordinating Facility [8,9,10] as well as by the NIH funded ReproNim project (ReproNim: A Center for Reproducible Neuroimaging Computation, NIH-NIBIB P41 EB019936). Last I will argue that a new type of teaching is now necessary for life scientists, one that will move from short term and often superficial teaching of tools and propose teaching material on more fundamental aspects at the computation, statistical (see ReproNim training curriculum, figure 1, see http://www.reproducibleimaging.org/) as well as cultural levels [12].

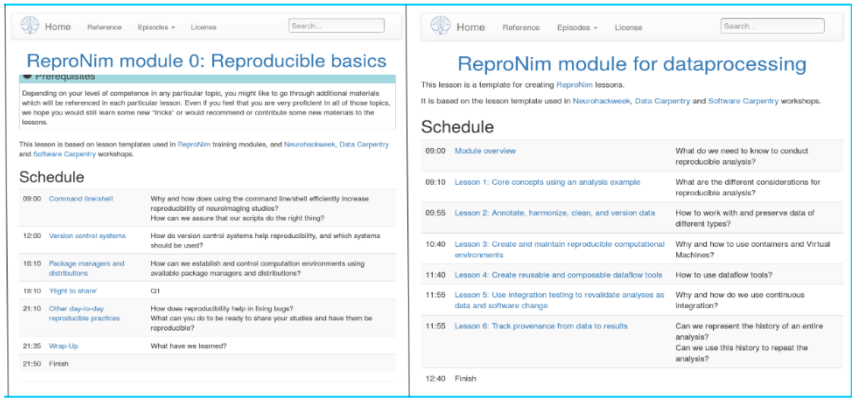

Figure1: Two modules (from 4) of the "ReproNim Online Training"

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Citation: Poline J (2017) Responses to the (life) science reproducibility crisis: evolution of training and publishing in neuroinformatics for a more efficient research.. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.kl.2

Computational theory for constrained self-organization in neural systems and its applications

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Studies of self-organization have a long history in various fields, in particular, in biology, chemistry and physics. Among others, the cybernetics researches extended the concept of self-organization to control theory and neural systems, too (von Claus Pias 2003). Since the 1970s, Nicolis and Prigogine (1977), Haken (1977), and their colleagues developed theories of self-organization to elucidate the mechanisms of pattern formations in far-from-equilibrium systems, with key concepts of dissipative structure, entropy production and slaving principle. These theories have also been applied to large-scale neural systems in the brain (for example, see Wilson and Cowan 1972; Freeman 2005). However, the theories seem to fail to elucidate a neural mechanism of functional differentiation of cortical modules and even neuronal differentiation in embryos. In such systems, functional elements are produced by a certain global constraint operating on the whole system (Tsuda 1984, 2001; Rosen 1991). We studied how functional elements emerge, adopting a certain variational principle, and treated such an optimum principle in important but not yet solved problems of neural systems such as the organization of neuronal units, the organization of functional modules, the existence of propagating waves in non-synaptic couplings (Tsuda, Yamaguti and Watanabe 2015; Yamaguti and Tsuda 2015), and neural mechanism of complex visual hallucinations that the patients of dementia with Lewy bodies can see (Collerton et al 2016).

Acknowledgements

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Citation: Tsuda I (2017) Computational theory for constrained self-organization in neural systems and its applications. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.kl.3

Translational Neuroscience: from bifurcations to personalized medicine

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Over the past decade we have demonstrated that the fusion of subject-specific structural information of the human brain with mathematical dynamic models allows building biologically realistic brain network models, which have a predictive value, beyond the explanatory power of each approach independently. The network nodes hold neural population models, which are derived using mean field techniques from statistical physics expressing ensemble activity via collective variables. This approach has been successfully applied to the modeling of the resting state dynamics of individual human brains, as well as clinical situations including stroke and epilepsy research. Here I will illustrate the workflow along the example of epilepsy: we reconstruct personalized connectivity matrices of human epileptic patients using Diffusion Tensor weighted Imaging (DTI). Subsets of brain regions generating seizures in patients with refractory partial epilepsy are referred to as the epileptogenic zone (EZ). During a seizure, paroxysmal activity is not restricted to the EZ, but may recruit other brain regions and propagate activity through large brain networks, which comprise brain regions that are not necessarily epileptogenic. The identification of the EZ is crucial for candidates for neurosurgery and requires unambiguous criteria that evaluate the degree of epileptogenicity of brain regions. Stability analyses of propagating waves provide a set of indices quantifying the degree of epileptogenicity and predict conditions, under which seizures propagate to nonepileptogenic brain regions, explaining the responses to intracerebral electric stimulation in epileptogenic and nonepileptogenic areas. These results provide guidance in the presurgical evaluation of epileptogenicity based on electrographic signatures in intracerebral electroencephalograms and have been validated in small-scale clinical trials.

Citation: Jirsa V (2017) Translational Neuroscience: from bifurcations to personalized medicine. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.kl.4

Organized Session I

The future of neuroinformatics education

'what is information?'-in relation to the modern history of life sciences

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It must be worthwhile for the study of neuroinformatics to look back upon the modern history of life sciences, especially the heated controversy between vitalism and physicalism (materialism) which lasted for 3 centuries since the 16th century (Fig.1). After the time of Descartes and Scientific Revolution, physicalists or mechanists claimed that living organisms were not really different at all from inanimate matter, whereas vitalists claimed instead that living organisms had properties such as 'vital force' that could not be found in inert matter and that therefore biological theories and concepts could not be reduced to the laws of physics and chemistry, although the vitalist view was more often metaphysical and then disappeared by 1920. In this century, however, it has become clear that both theories were partly right and partly wrong. Physicalists had been right in insisting that there is no metaphysical life component and that at the molecular level life can be explained according to the principles of physics and chemistry. At the same time, the vitalists had been right in asserting that, nevertheless, living organisms are not the same as inert matter that have numerous autonomous characteristics such as genetic programs which are not found in inanimate matter. It is interesting to note, even in vitalist view that almost all the life phenomena could be well explained without contradiction, if the 'vital force' is replaced with the word 'information'. The incorporation of physicalism and vitalism introduced the new concept of 'organicism' in which 'information' and 'emergence' play an important role for interpreting life of living organisms.

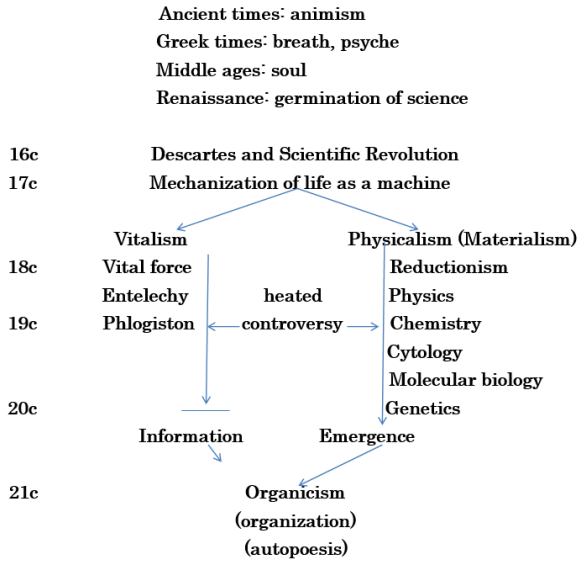

Figure1: Outline of philosophical background of life sciences

Citation: Okada Y (2017) 'what is information?'-in relation to the modern history of life sciences. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osi.1

Materials Informatics: An Emerging Interdisciplinary Field of Materials Science

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With state-of-the-art technologies in data science, we aim to discover novel functional materials. Target materials include drugs, dyes, solvents, polymers, polymeric composites and nanostructured materials. With the comprehensive technologies of machine learning, such as Bayesian inference, experimental design methods, natural language processing and optimization theory, we are developing the fundamental scientific methodology and research infrastructures for materials informatics which is an emerging interdisciplinary field of materials science and data science. This talk introduces our efforts to make successful such an interdisciplinary research project with x-informatics, in which diverse researchers from many different disciplines take in part, for example, synthetic chemistry, material engineering, theoretical physics, computer science, and data science.

The design space of materials development is considerably high-dimensional. For instance, the chemical space of small-sized organic compounds consists of more than 10^{60} potential candidates. The challenge is to discover novel materials in the considerably huge material space that exhibit desirable properties yet to be achieved. In the traditional procedure, computational chemistry methods, such as the first principle calculation, have been put at the central analytic tool. Scientists hypothesize material structures based on experience and intuition, and properties of the designed materials are assessed computationally and experimentally. Recently, machine learning technologies has been paid much attention in this area as a promising alternative that can promote enormous savings on time and costs in the laborious and time-consuming trial-and-error procedure. The aim of our study is to create a novel material design method by the integration of machine learning and quantum chemistry calculation, and to show the proof-of-concept in practical applications under industry-academia partnerships.

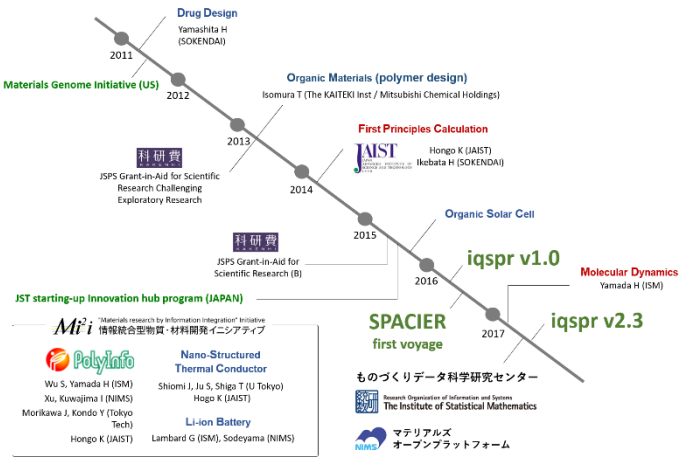

Figure1: History of our activities in materials science

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Citation: Yoshida R (2017) Materials Informatics: An Emerging Interdisciplinary Field of Materials Science. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osi.2

Artificial intelligence and neuroinformatics

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Era of 'data deluge' is approaching in neuroinformatics. Accompanied by the developments of various high-throughput imaging technologies, functional and structural images of neural circuits will be accumulated tremendously. One of such emerging neuroinformatics fields is connectomics, in which the structures of neurons and neural networks are comprehensively examined, leading to understanding the structural bases of their functions. If the data are taken by magnetic resonance imaging device, optical microscope, and electron microscope, it is called macro-connetomics, meso-connectomics, and micro-connectomics, respectively. Especially in meso- and micro-connectomics, it is almost impossible for human analysts to process the images interactively, so it would be inevitable to rely on computer analyzers, i.e., artificial intelligence.

I first explain artificial intelligence techniques to deal with connectomics data. In terms of macro- and meso-connectomics, high-throughput energy-based optimization technology based on fiber-structure modeling was employed on parallelized computing environments. In terms of micro-connectomics, deep neural networks equipped with a powerful regularization mechanism were employed to lower the efforts of human proofreading.

Then, I introduce an application to brain machine interface, in which connectomics data were used for transferring brain decoders trained based on the database covering many human participants, into the one for a new human user whose data was only available in the connectomics part. This application suggests that connectomics can be a basis to discuss commonality over and difference between individuals, which will lead to developments of new neuroscience-based applications.

Accordingly, artificial intelligence techniques and neuroinformatics like connectomics could have tighter collaborations, which will incubate further interdisciplinary research fields.

Acknowledgements

This study was supported by the AI project led by New Energy and Industrial Technology Development Organization (NEDO), the Brain/MINDS project led by Japan Agency of Medical Research and Development (AMED), and the Post-K project led by Ministry of Education, Culture, Sports, Science, and Technolog

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Organized Session II

Selected papers

Development of a hypertext tutorial for construction of a standard brain

Hidetoshi Ikeno [1], Daisuke Miyamoto [2], Tomoki Kazawa [2], Chika Iwatsuki [2], Yoshihiro Okumura [3], Yoko Yamaguchi [3], Ryohei Kanzaki [2]

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The model animal are using for analysis of relation between behavior and brain function. There are various experimental techniques for investigating brain mechanisms. However, it is impossible to obtain enough knowledge from one individual, so it is needed to integrate data obtained by different way of experiments and observations. The standard brain, which has standard shape and location of brain regions, could be very useful for a platform to register and integrate neurons and neuronal connections in the brain. The standard brain for famous model animals, such as mouse, drosophila and so on, already constructed and published. But it is still needed to develop and provide it for other animals, because many kinds of animals are using for difference of investigation and experiment. In this work, we are making a tutorial text for developing a standard brain image and model from confocal images. We are introducing a procedure of construction for standard brain step by step with text document (https://cns.neuroinf.jp/modules/pico/index.php?cat_id=4), movie and exercise on the virtual machine of Simulation Platform (http://sim.neuroinf.jp). The contents on the Internet are used on various terminals, such as laptop, tablet, and useful not only for scientists, but also students who are learning biology. It could be accelerated to develop and use of a standard brain for integration of experimental results for comparative neuroscience studies.

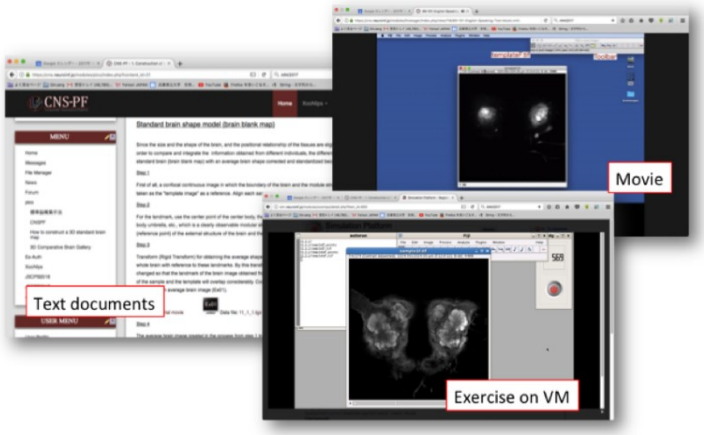

Figure1: Tutorial hypertext for construction of a standard brain

Acknowledgements

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Citation: Ikeno H, Miyamoto D, Kazawa T, Iwatsuki C, Okumura Y, Yamaguchi Y, Kanzaki R (2017) Development of a hypertext tutorial for construction of a standard brain. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osii.1

The experimental-data-driven construction of neural circuit simulation of insect brain using estimations on a single neuron and circuit level

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In order to understand the intelligences originate from the brain, we chose the road via a reproduction of a simple but adequate insect brain by a detailed simulation on the big computational resources. The real-time simulation of a whole insect brain on post K computer is our big milestone at 2020.

An antennal lobe, the first olfactory center in the insect brain, is a good model system for building simulation model due to the abundant data and easiness of physiological experiment.

As a test bed of the experimental-data-driven construction of insect brain simulation, we built the simulation model of silkmoth antennal lobe based on the pheromonal receptor activities, dose response characteristics of projection neuron, pharmacological experiments to GABA receptor, and so on. Normalized olfactory response of antennal lobe projection neuron to tetanus pheromonal stimuli observed in our experiment (Fujiwara 2014) were reproduced in our simulation model that use GABA-B receptor as the mutual inhibition mechanism among local inter neuron on the point neuron H-H model.

For the more detailed simulation, we introduced multi-compartment models based on the morphology of silkmoth antennal lob neuron stored in the our Bombyx Neuron Database(BoND). The pheromonal stimuli to MGC in the dorsal antennal lobe and mechnosensory input in the ventral part of antennal lobe from AMMC were implemented in the simulation for the multisensory integration in the natural environment.

However, it may be accompanied by a vast work to define the values of numerous parameters of the biophysical detailed model. We have been developing a massively parallelized parameter estimator on supercomputer in order to treat massive parameters not by hand but automatically.

We succeeded the estimation of more than a few thousand parameters about synapse mechanisms in neural circuit simulation consist of a few of ten neurons. simultaneously by the combination of our massively parallelized simulator on K com

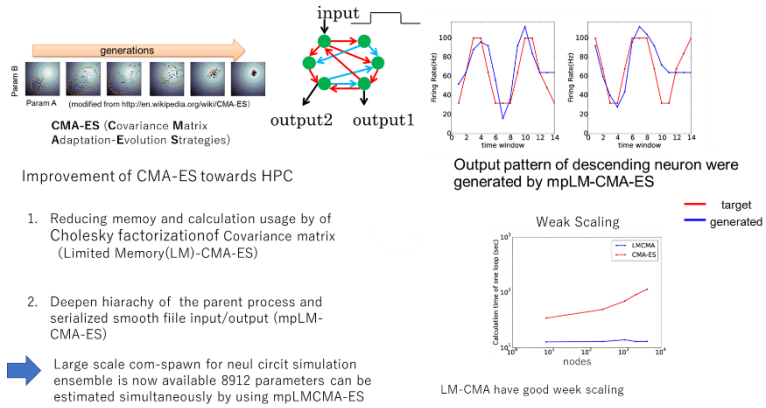

Figure1: Improvement of CAN-ES for the circuit simulation of large scale circuit

Acknowledgements

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Citation: Kazawa T, Arase K, Fukuda T, Park H, Miyamoto D, Kanzaki R (2017) The experimental-data-driven construction of neural circuit simulation of insect brain using estimations on a single neuron and circuit level. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osii.2

NEST: A mature simulation tool for spiking neuronal networks

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Efficient and reliable simulation tools are essential for progress in brain research. Like other fields of neuroscience, computational neuroscience is maturing and network simulations are increasingly based on the use of standard tools, instead of building home-brew solutions from scratch.

The NEST simulator is an open-source software tool that is developed by a team of about 20 core developers with contributions from over 50 neuroscientists on GitHub and used by a growing community of neuroscientists from all over the world. With a user-friendly Python interface [1], integration with PyNN [2] for simulator-independent scripting and MUSIC support [3] for integrated multi-scale simulation, NEST is a powerful simulation tool for brain-scale simulations today. The software runs on a wide range of computer architectures from laptops to leading-edge supercomputers, where streamlined data-structures allow NEST to efficiently exploit the capabilities of the machine. This led to a world-record simulation of a network of 1.86×10^9 neurons connected by 11.1×10^{12} on the Japanese K supercomputer [4, 5].

The most recent release version NEST 2.12 [6] provides over 50 neuron models and 10 synapse models including short-term plasticity and different variants of spike-timing dependent plasticity and the NEST topology module allows the construction of spatially structured networks. Recent developments include the integration of continuous interactions between spiking neurons via gap junctions [7] as well as rate-based neuron models [8], and models of structural plasticity. Furthermore, the domain specific language for neuron models NESTML allows the user to define custom neuron models in an easy and precise manner.

NEST is regularly taught at computational neuroscience summer schools and new developments are discussed in the annual NEST user conference, that was first held in 2016. It is the Network Simulation Component of the Human Brain Projects's Collaboratory.

Acknowledgements

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Quantitative Evaluation of Motor Control in Smooth Pursuit Arm Movement on Kinect v2 Sensor

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On daily life, human can precisely and quickly control arm movements in various situations in the basis of the internal model which represents motor information in the brain. In previous studies, we obtained that patients with cerebellar diseases lost function of the internal model in reaching movements when offline-feedbacks were fed to the cerebellar patients. On the other hand, nobody knows effects of online-feedback information in movements of the cerebellar patients. We developed to measurements of the whole body movements and proposed a new method to evaluate the motor functions at the level of movement kinematics by using the Kinect v2 sensor (Microsoft Inc.). In our task, the participants were requested to follow to a moving target presented on a display with a pointer which position reflects his/her index finger. We analyzed the error which is the differences between the finger-pointer position and the target position on the display were measured in real-time. We found that the errors of the cerebellar patients were larger than the healthy subjects. Especially, vertical elements of the error in the cerebellar patients were six times greater than the healthy subjects. This implies that cerebellar patients lost the internal model for gravity. The quantitative evaluation will help to diagnosing cerebellar ataxia. In future, a task program and data sets will be obtained or provided by using a database system through internet. This system may connect patients with medical doctors on-line and may ubiquitously provide a practical test of motor control. We are going to connect the system with a cloud database system (e.g., Microsoft Azure) so that the system will truly put remote diagnosis into practice.

Acknowledgements

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Citation: Honda T, Yoshida H, Lee J, Yozu A, Kondo T, Kakei S (2017) Quantitative Evaluation of Motor Control in Smooth Pursuit Arm Movement on Kinect v2 Sensor. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osii.4

Visiome data for computational study on the receptive fields of the primary visual cortex

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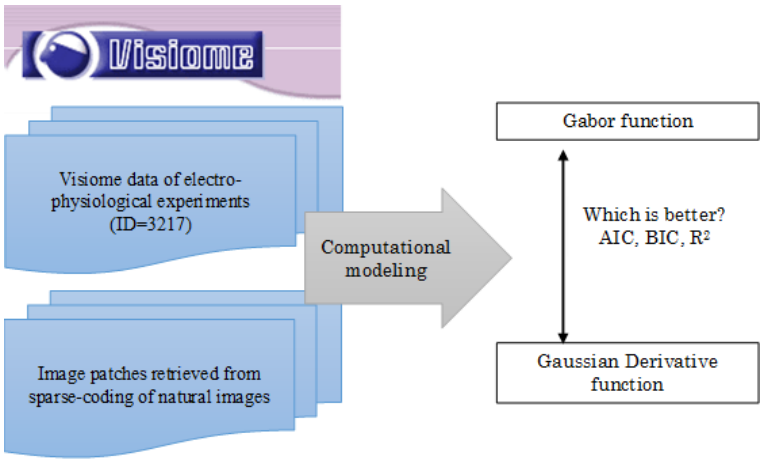
The Gabor function has been employed as a physiologically plausible model of the spatial receptive fields of simple cells in the primary visual cortex (V1) (Marcelja, 1980). Almost all researchers conclude that "those are Gabor functions" when observing localized sinusoidal gratings in experimental data or in numerical solutions of computational theories (e.g. sparse coding and ICA to obtain image bases of image patches or model of receptive fields). But is the Gabor function one and only computational model of V1 receptive fields or sparse-coding pathces? This simple questions motivate this research.

The fractional order Gaussian derivative function (fGD) is introduced as an alternative model. We evaluate the Gabor and fGD functions using physiological data of V1 simple receptive fields [1] available in Visiome Platform [2] (a database for vision research; https://visiome.neuroinf.jp/). Model comparison using AIC reveals that the fGD functions are better for 12 of 14 physiological data, and better for 52 of 64 sparse-coding patches.



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Citation: Satoh S, Ueda I (2017) Visiome data for computational study on the receptive fields of the primary visual cortex. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osii.5

The INCF Neuroinformatics for Aging Special Interest Group – Cooperation in neuroinformatics to accelerate validation of aging interventions

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Societies in many countries are rapidly aging which is increasing the burden of care while negatively affecting the sustainability of economic wealth and output. Advances in neuroimaging [1, 2], wearable sensors and genetic profiling technologies will contribute new data with unprecedented quantity of temporal and spatial detail on anatomical, functional and lifestyle factors which influence degeneration in aging. However, building capability to use rich data to assess efficacy of aging interventions and translate it to clinical use is beyond the capability of individual research labs. In addition, we have incomplete knowledge and control over the numerous factors that influence degeneration in aging such as lifestyle, socio-cultural and cognitive capacity. The lack of scale, capacity and diversity in the content of the study and number of participants hinders clear identification of influential factors.

Trans-disciplinary, multi-center and multi-country research cooperation is a useful way to address this shortfall [3, 4]. We have conducted a neuroimaging study to compare the effects of short-term intervention between Japan (fMRI) and Singapore (EEG), finding compatible results in the anterior salience network modulation in response to the cognitive / physical training as a potential biomarker [5, 6]. A prototype platform for fMRI analysis pipeline using deep learning was also demonstrated [7].

To expand these achievements into a multi-country scale, as a SIG of the INCF, we will work together to define minimum common elements for data, protocols and processing steps. Subsequent collaborative research will verify and optimize them. Then, the outcomes will be seeded to develop computational models of the aging brain, to validate and deploy aging interventions and to assess the role of nutrition with neuroimaging. Partners will continue to identify the best outcome for each country and to bridge the gap between clinicians and scientists.

Acknowledgements

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Organized Session III

Dynamics of genes expressed in neurons and brain, their associated phenotypes and potential links to neuroinformatics

Evolution of V1R pheromone receptor genes in vertebrates: its diversity and generality

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Pheromone sensing plays an important role in eliciting innate behaviors such as reproduction and predator avoidance. However, the origin and the evolution of pheromone detection system in vertebrates mostly remain to be elucidated. In the present study, I focus on the V1R pheromone receptor gene family, whose repertoire varies greatly depending on animals due to species specific gene gain and loss. Our phylogenetic and genome wide comparative analyses on the V1R genes of broad vertebrates from ancient fish (polypterus, gar, and coelacanth) to tetrapods led us to obtain several interesting results. I will introduce these results, which shed light on the origin and diversification of pheromone detection system over five hundred million years of vertebrate evolution.

Acknowledgements

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Differential and tissue-specific gene expression in the mouse brain

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ViBrism DB (http://vibrism.neuroinf.jp/) is a platform aiming at showing brain architecture based on molecular distribution of many genes on the three dimensional (3D) anatomical context. Comprehensive gene expression densities in the mouse brain were measured with microtomy-based technology, which we invented, Transcriptome Tomography1, and were mapped on the 3D MRI space compatible to the mouse standard brain coordinate. Now 172,023 maps of overall gene expression in the three maturation stages after the birth and in the adult brain are searchable by gene IDs. The results are shown as 2D/3D maps on the MRI images. Also, the measured densities at each stage are subjected to gene-by-gene correlation analysis of co-expression using Pearson correlation coefficient as a similarity measure2, and then co-expression search results can be browsed as network tables and graphs associated with the 2D maps. These frameworks enable to comprehensively assess differential gene expression underlying brain structures and functions. In this talk I will introduce analyses of anatomy/function association based on gene expression.

Acknowledgements

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Citation: Okamura-Oho Y (2017) Differential and tissue-specific gene expression in the mouse brain. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osiii.2

Transcriptome dynamics during in vitro neuronal differentiation with allelic distinction

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Mammals have a distinct gene expression mechanism called genomic imprinting, where only one allele, either the maternal or paternal is expressed. Approximately 100-200 genes are known to be imprinted. Among these imprinted genes, some are imprinted only in particular cell types or tissues.

We have been investigating neuron-specific imprinted genes, utilizing in vitro differentiation system. In order to distinguish the maternal and paternal alleles, we made use of genetic polymorphisms existing between two inbred mouse strains, MSM/Ms (MSM) and C57BL/6 (B6). We established male F1 hybrid embryonic stem (ES) cells, derived from embryos obtained by breeding MSM and B6.

The RNA samples from the cells during in vitro neurogenesis were subject to RNA-seq, and the dynamic expression changes during differentiation were analyzed with the maternal and paternal allelic distinction. We performed RNA-seq not only for poly(A)+ RNA (mRNA), but also for total RNA including poly(A) - RNA. With these considerations for RNA-seq, we could observe interesting aspects of mammalian transcriptome.

We would like to present general landscapes of our data, and some loci and genomic regions of great interest.

Citation: Kiyosawa H (2017) Transcriptome dynamics during in vitro neuronal differentiation with allelic distinction. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osiii.3

Transcriptional dynamics of monoallelically expressed genes during neuronal development of F1-hybrid mice

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The paired autosomal genes in the two chromosomes of distinct parental origins (alleles) could, in theory, express equally, though, expression of certain genes show clear allelic bias toward a particular sex (imprinted) or mouse strain (strain-specific). In F1-hybrid mice generated by crossing two distinct mouse strains whose genomes differ by 0.1 ~ 1%, thousands of genes have been identified as monoallelically expressed (MAE) genes in distinct tissues including embryonic stem cells (ESC) and neuronal precursor cells (NPC). Many imprinted genes are associated with neuronal disorders, and some strain-specific genes are implicated in human diseases. In this talk, I will first mention features of MAE genes including their potential functions, association with neuronal diseases and evolution. Next I will describe transcriptional dynamics of MAE genes observed during neural development from ESC to NPC and mouse brain, together with dynamics of epigenetics including DNA methylation, histone modifications and biding of transcriptional and elongation factors in and around the MAE genes. I conclude summarizing potential contribution of the allele-specific transcriptional study based on F1-hybrid mice to neuroinformatics.

Citation: Kondo S (2017) Transcriptional dynamics of monoallelically expressed genes during neuronal development of F1-hybrid mice. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osiii.4

Organized Session IV

Brain signal: Measurement, data analysis and modeling

Unraveling Individual Differences in Human Brain Dynamics

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We propose a novel perturbational paradigm to assess individual differences in nonlinear neural dynamics in the human brain. We investigated how and to what extent macroscopic human neural signals as measured by electroencephalography (EEG) exhibit consistency to noisy visual inputs on an individual basis. A total number of 130 volunteers participated in the study after giving informed consent. Participants were repeatedly presented with two distinct sequences of 5.5 s noisy visual stimuli. We evaluated the degree of consistency of EEG responses to noisy visual sequences across single trials by applying a canonical correlation analysis (CCA)-based method within and across different individuals. Next, we tested if a support vector machine (SVM) combined with the CCA-based method could classify single-trial EEG signals for the two distinct realizations of visual stimuli. Finally, we estimated if the method could successfully classify different individuals. The CCA-based method significantly classified EEG trials for two distinct realizations of visual stimuli. Crucially, the SVM classifier showed the average accuracy of more than 99 % to classify different individuals on a single trial basis. The results were stable over time as shown by the high accuracy of verification of individuals from follow-up sessions tested for 32 participants. We also found a significant positive correlation between the degree of separation between two distinct realizations of noisy visual sequences and the degree of separation from other individuals. Moreover, resting-state EEG showed a lower accuracy in verification performance. Taken together, we conclude that noisy inputs can harness individual human brain dynamics as was observed in other nonlinear dynamical systems such as laser systems (Uchida et al. 2004) and single neurons (Mainen et al. 1997). Our novel perturbational paradigm should be useful for the manipulative dissection of individual variations in brain dynamics and functions.

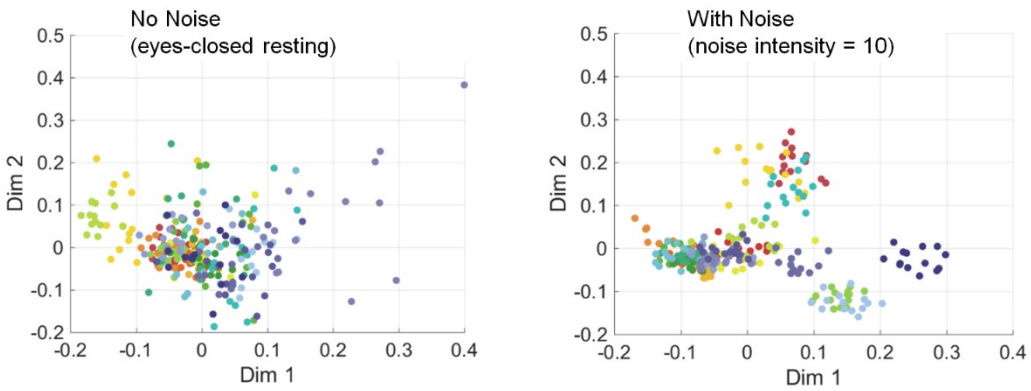

Figure1: MDS visualization of EEG trials. Trials from 20 participants are shown for the eyes-closed resting condition (left) and high-intensity visual noise condition (right). Same markers correspond to same individuals. Better separation between individuals was observed for noise-induced EEG dynamics.

Acknowledgements

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Citation: Kitajo K, Sase T, Mizuno Y, Suetani H (2017) Unraveling Individual Differences in Human Brain Dynamics. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osiv.1

MEG-fMRI multimodal integration to investigate neural dynamics while perceiving 3-D object shape from motion

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We used both MEG and fMRI to precisely visualize the dynamic brain responses to 3-D object perception from random-dot motion [1]. Also, we employed causality analysis to infer driving relationships between the neural activities along the two visual pathways.

The visual stimuli consisted of 1000 random dots whose motion coherence was manipulated parametrically to create different levels of 3D perception and to study the associated changes in brain activity. MEG signals were measured using a 306-channel MEG system and fMRI data were collected using a 3-Tesla scanner with the single-shot EPI sequence. The results of the block-design fMRI data were used to impose plausible constraints on the MEG inverse calculation using a weighted minimum-norm approach [2]. In order to test the directional influences between the active regions detected in the spatiotemporal activity estimates, Granger causality test [3] was applied on the raw MEG time-series extracted from ROIs where significant activities were observed in the MEG-fMRI analysis.

The results showed that the activities in the posterior inferotemporal (pIT), the parietooccipital (PO), and intraparietal (IP) regions were increased at different latencies during highly coherent motion conditions in which subjects perceived robust 3D objects. The interactions inferred by the Granger causality showed that there were significant directional influences from MT to PO, IP to pIT, and pIT to PO only in the conditions where robust 3D objects were perceived.

The results indicate that these regions were involved in a large-scale neural network underlying the perception of 3-D object structure from 2-D motion [4]. The results also support the idea that PO, which was investigated in detail in the previous fMRI studies on 3-D SFM, receives feedback input from pIT as well as feedforward input from MT to form robust 3-D percept by integrating the global motion and the object information processed in the ventral visual system.

Acknowledgements

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Citation: Iwaki S, Belliveau JW (2017) MEG-fMRI multimodal integration to investigate neural dynamics while perceiving 3-D object shape from motion. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osiv.2

Challenge to the brain functional measurement during parent-child interaction.

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Magnetoencephalography (MEG) is a noninvasive method of recording neural activity. MEG measures a direct consequence of the electrical activity of neurons. This technique has a temporal resolution of approximately one millisecond, which is the typical resolution of measurable electrical phenomena in the brain.

In the past decade, MEG has emerged as an important investigatory tool in neurodevelopmental studies of infants and young children regardless of their typical or atypical development. Conventional whole-head MEG systems have fixed sensor arrays designed to accommodate most adult heads. Therefore, it was difficult to investigate the brain activities of the right and left hemispheres simultaneously in young children. After the development of the custom child-sized MEG in 2010, researchers could focus on brain activity in young children (e.g., 3–7 years old). In the past decade, MEG studies have substantially contributed to the understanding of brain function during both typical and atypical development.

In Kanazawa University, using a combination of child-customized MEG and conventional adult-sized MEG device, as shown in Figure, we developed the new system in order to record brain activities during the live, real-time social communication between mother and infant simultaneously. We introduce this system which will contribute to brain science on the development of communications skills during childhood. Using this system, we have been focusing on the social interaction between a mother and her child because this interaction has a crucial role in childhood development and is critical in the development of social minds. The cognitive and emotional interactions between a mother and her child are induced by their behaviors, and such brain-to-brain interactions must play a crucial role in forming social minds.

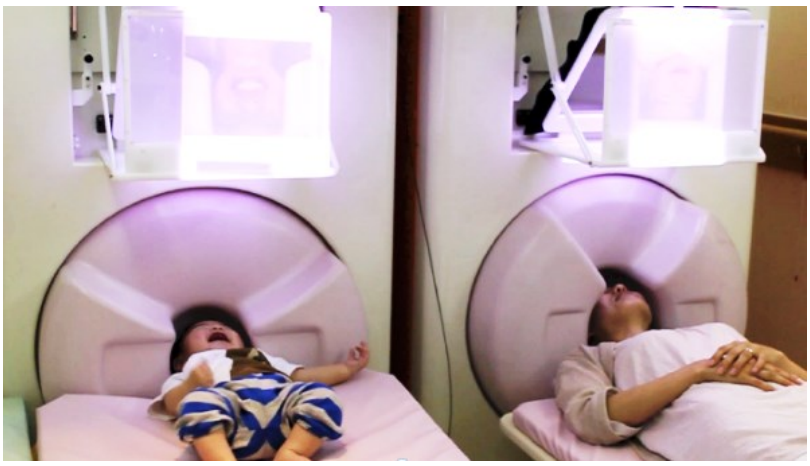

Figure1: MEG hyperscanning system

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Mathematical Structures in the Brain Dynamics of Epilepsy

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Motivated by the success of interpretations of observed data in terms of nonlinear dynamical systems, we have formulated a mathematical theory for measurements, experiments, data, and trajectories including transient and asymptotic motion. In this respect, it can be supposed that one will find mathematical structures embedded in the data of brain dynamics, whose structure may represent mental states. Under this assumption, we applied nonlinear time series analysis on ECoG datasets which were recorded during epileptic seizures of two patients. As studied in [1], DC shift before seizure onset and high frequency oscillation (HFO) during seizures are typically observed by power spectrum analysis.

Throughout our analyses we tried to extract mathematical structures which are embedded in the ECoG datasets. On one hand, during the HFO time interval of the ECoG data, we found that power spectral densities obey either power law distribution of exponent around -2 which is similar to Brownian motion or the power law with 150 Hz peak. We also applied an embedding technique [2] to the data, and found that a type of one-dimensional dynamical systems, like, so called, a circle map, are embedded in the data. The results suggest that a class of low-dimensional dynamical systems describe the brain dynamics during the seizure onset though high degrees of freedoms are expected in general.

On the other hand, an interictal epileptic slow shift which we call a red slow is observed in the wideband ECoG datasets. The rate of occurrence of a red slow increases near onset and is expected as a factor of prediction of seizure. We found that the shape of power spectral density in log-log scale dynamically changes during a red slow, that is, fluctuations of the power spectrum in high frequency area become relatively small compared with the results on power spectrum in non-ictal case. We can detect the occurrences of a red slow by tracing the changes of the fluctuations.

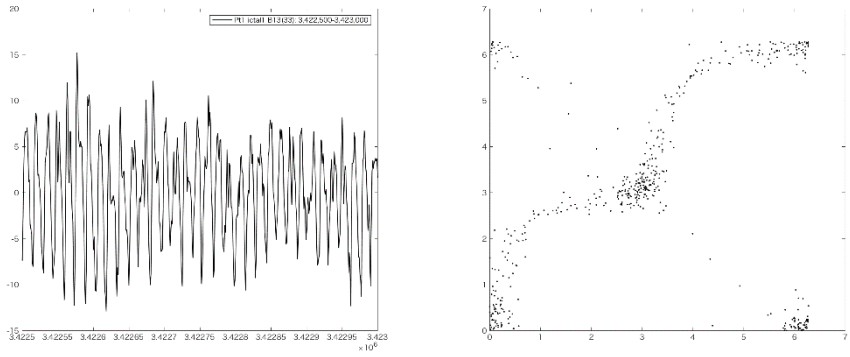

Figure1: Left: difference of wideband ECoG dataset. Right: result of embedding of the time series. A discrete dynamical system is clearly appeared.

Acknowledgements

This work was partly supported by Grant-in-Aid for Scientific Research 15H05878.

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Citation: Namiki T, Tsuda I (2017) Mathematical Structures in the Brain Dynamics of Epilepsy. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.osiv.4

Poster Session

Brain Transcriptome Database (BrainTx)

Akira Sato [1], Yo Shinoda [2], Yoshitake Sano [1], Tetsushi Sadakata [3], Noriyuki Morita [4], Michisuke Yuzaki [5], Takafumi Inoue [6], Mitsuhiro Hashimoto [7], Hayato Ohwada [1], Hirozumi Nishibe [8], Yoko Yamaguchi [8], Teiichi Furuichi [1]

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The Brain Transcriptome Database (BrainTx) (http://www.cdtdb.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. These neuroinformations help to understand the genetic mechanisms underlying complicated neural processes on the brain and nervous system. BrainTx has already been demonstrated to be valuable for neuroscience research (for example, identification of several brain genes important for neural circuit development).

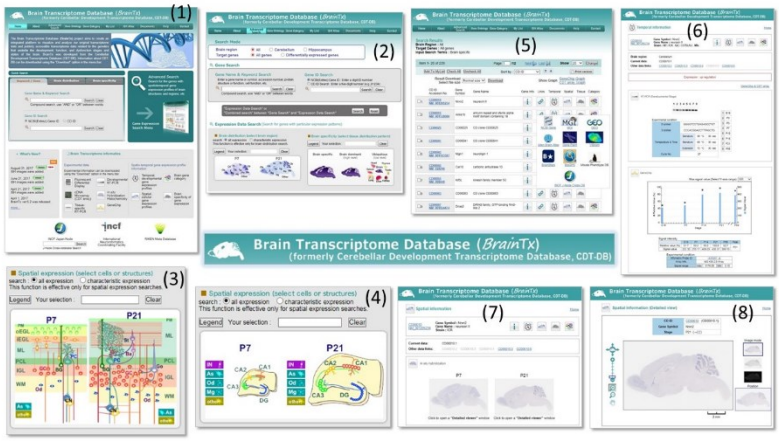

Figure1: BrainTx Top page (1), Search page (2), Search functions for cerebellum (3) and hippocampus (4), Search results page (5), Temporal (6) and Spatial (7) gene expression pages, and ISH brain image viewer page (8).

Acknowledgements

The project is supported by the NIJC, RIKEN-BSI and is also partly supported by the research grants from the Japan Society for the Promotion of Science (JSPS), the Japanese Ministry of Education, Culture, Sports, Science, and Technology (MEXT), and the Japan Science and Technology Agency (JST).

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Citation: Sato A, Shinoda Y, Sano Y, Sadakata T, Morita N, Yuzaki M, Inoue T, Hashimoto M, Ohwada H, Nishibe H, Yamaguchi Y, Furuichi T (2017) Brain Transcriptome Database (BrainTx). Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.1

Development and Aging of Motor Control for Smooth Pursuit Arm Movement

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Quantitative evaluation of human motor function is key technology for evaluating effects of aging and effectiveness of treatments for neurological disorders. In addition, it is desirable to make the evaluation available anywhere and anytime (e.g. at home). In our previous study, we developed a system for quantitative evaluation of wrist motor control using a simple tracking task with a manipulandum. Although the system was effective in terms of evaluating motor control, its custom-made device was costly.

We developed a new system for quantitative evaluation of motor function using a Kinect v2 sensor (Microsoft Inc.), which is available worldwide at a low cost. In our experiment, participants sat in front of the Kinect and were instructed to pursue a moving target displayed on a screen with a pointer whose position reflects the position of the tip of his/her index finger. We analyzed the tracking error, which is defined as the distance between the pointer and the target position on the display, in real-time. The ideal path of the target was not visible to the participants during the task, however they had some knowledge about the target motion due to preceding practice trials. We compared the performance of tracking movements of 10 children (8-12yo), 10 young adult participants (20-29yo), and 10 elder participants (70-79yo). The tracking error of the young adult group was significantly smaller than that of the elder group. Among the elder group, those over 70 years old tended to show larger tracking error. Interestingly, the tracking error in the child group quickly decreased with the increase in age. However, the tracking error of the child group was significant larger than that of the young adult group.

The present system could be further improved by connecting it to a cloud database system through internet (e.g. Microsoft Azure). Such a system will connect patients to medical doctors on-line and may make remote diagnosis into an effective, cheap and fast practice

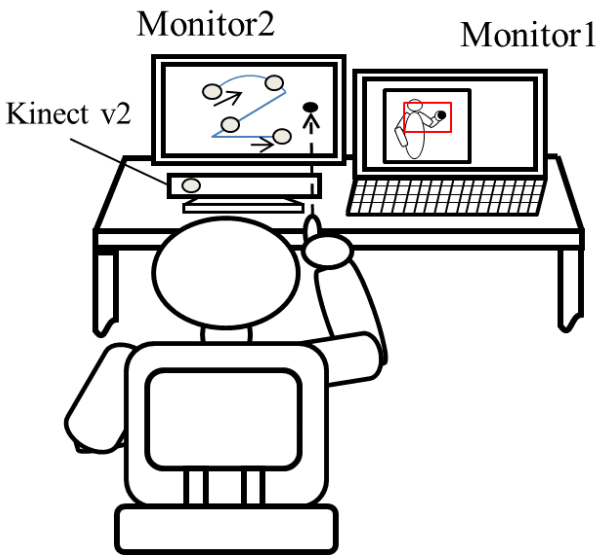

Figure1: Quantitative evaluation system

Citation: Yoshida H, Honda T, Miyata Y, Kumada S, Manabe M, Yozu A, Lee J, Kakei S, Kondo T (2017) Development and Aging of Motor Control for Smooth Pursuit Arm Movement. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.2

EEG metastable states in nonlinear human brain dynamics

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The human brain generates highly complex but ordered nonlinear dynamics spontaneously, especially in the resting state. The dynamics transitions among multiple states on the large-scale network, possibly depending on the activity of, for example, cognition. Such spontaneous brain dynamics can be translated into mathematics from a dynamical system point of view (Kelso, 2012). Kelso pointed out that metastability is a key for unraveling functional roles of spontaneous brain activity. However, metastable dynamics, macroscopically emerging from the large-scale network, has not been well understood.

In this presentation, we introduce the following three topics of our recent work: (i) Developing a new clustering method that can label time-series data as multiple metastable states by a data-driven approach; (ii) applying the method to 63-channel scalp electroencephalography (EEG) signals recorded from 130 healthy individuals in an eyes-closed resting condition for 180 s; and (iii) modelling the obtained phenomenon by a coupled-oscillator system, composed of the Stuart-Landau (SL) oscillators.

More specifically, the method in topic (i) converts metastable d-dimensional tori in the high-dimensional state space into metastable zero-dimensional ones in a lower-dimensional space. Then, topic (ii) shows experimental evidence that EEG metastable states are two- or three-dimensional tori, each of which generates phase-amplitude coupling dynamics. Further, we have grasped evidence, based on the autism-spectrum quotient (AQ) score obtained after the EEG experiment, that the dynamics of the metastable states is associated with attention switching (Figure 1). Finally, topic (iii) attempts to model these results by fluctuation-induced SL oscillators for individuals.

We conclude that EEG metastable states are metastable tori with the dimension larger than d=1, of which the dynamics is associated with attention switching. How such metastable dynamics is generated is our ongoing topic.

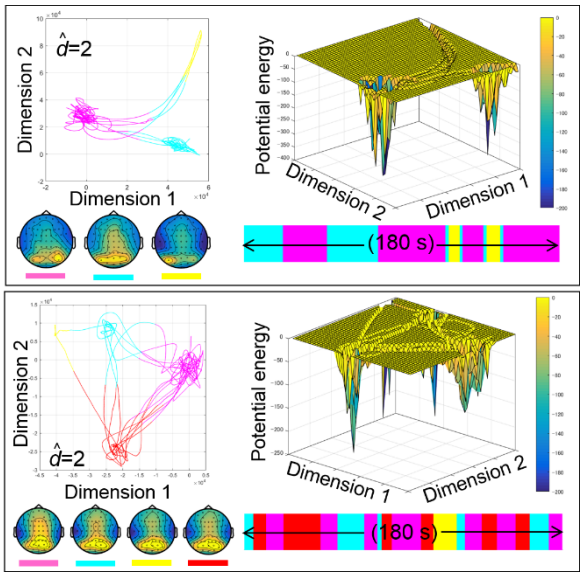

Figure1: Typical metastable dynamics for higher AQ score=30/50 (top panel) and for lower AQ score=7/50 (bottom panel)

Acknowledgements

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Citation: Sase T, Kitajo K (2017) EEG metastable states in nonlinear human brain dynamics. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.3

Parameters Exploration of DWI-based Global Fiber Tracking with Neuronal Tracer Signal as References

Carlos Enrique Gutierrez [1], Henrik Skibbe [2], Ken Nakae [2], Alexander Woodward [3], Akiya Watakabe [4], Junichi Hata [5], Hideyuki Okano [5], Tetsuo Yamamori [4], Yoko Yamaguchi [3], Shin Ishii [2], Kenji Doya [1]

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Brain Mapping by Integrated Neurotechnologies for Disease Studies (Brain/MINDS) project aims multi-scale brain mapping of the common marmoset (Callithrix Jacchus) (Okano et al., 2016). As a part of this program, we validate and optimize diffusion weighted MR image (DWI)-based fiber tracking results in comparison with information obtained by neural AAV-based fluorescent tracer injected into the prefrontal cortex of the same subject.

We explored parameters space of a fiber tracking algorithm, Freiburg Fibertools (Reisert et al., 2011, 2013), using one-subject ex-vivo DWI data. Firstly, a set of parameters was selected to obtain different tractography results; secondly tracer injection point was used to extract subsets of fibers connected to source area; after that, fibers were mapped as track-density images; finally we compared density images against tracer signal in the standard brain space and evaluated parameters based on an objective function.

On preliminary experiments we found better results than default parameters regarding both quality and quantity of our objective function.

Best results can complement information of sparse structural connectivity obtained by tracer injections, improve connections quantification between source areas and targets, and provide a reliable nondestructive 3D brain-wide connectivity mapping method.

Citation: Gutierrez CE, Skibbe H, Nakae K, Woodward A, Watakabe A, Hata J, Okano H, Yamamori T, Yamaguchi Y, Ishii S, Doya K (2017) Parameters Exploration of DWI-based Global Fiber Tracking with Neuronal Tracer Signal as References. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.4

Pattern-induced subjective hue perception is coupled with the phase of visual flicker patterns.

Jonathan Kar-Sing Lai [1, 2], Munenori Takaku [1, 2], Sutthinan Anantarattanachai [1, 3], Itsuko Ishii [1], Yoshihiro Okumura [1], Yoko Yamaguchi [1, 2, 3]

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Benham's top is a spinning disk with black and white patterns which causes the perception of colours when spun. This is known as Subjective or Pattern-Induced Flicker Colours. It is known that different people and different spinning patterns have varying perceptions of subjective colour, however not much is known about these individual differences in perceived colour. In this study, the individual differences in perceptions of subjective colour are elucidated on across a large range of age groups and gender and across four different patterns shifted in rotation on the spinning disk.

Using the result of questionnaires on the Benham's top illusion we collected colour perception reports from 280 (112 male, 168 Female, 6 age brackets under 10 to over 80) people. Circular (Anderson and Wu, 1992) and Linear Statistical Tests showed significant variation in the mean and variance of the distribution of perceived colour hues across age groups ($p<0.05$) in 3 of the 4 tested patterns. Additionally, the general hue perception when considering all four shifted bands showed a consistent change in hue related to the change in rotation for each of the patterns.

Overall, perceived hues shifted with certain hues being more likely to be perceived depending on age groups and a consistent shift in hue relating to the rotated phase of the presented patterns across all age groups. These results indicate that subjective hue perception may be coupled to the phase of visual flicker patterns and that age can play a significant factor in the perception of subjective colours and hues.

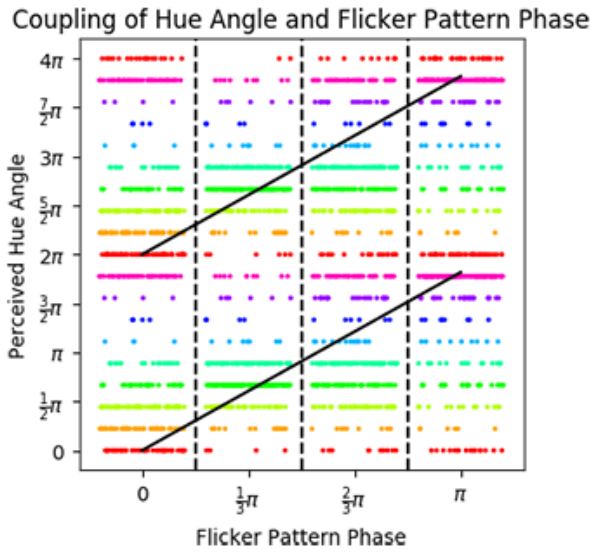

Figure1: Perceived Subjective Hues are plotted against the phase shift applied to the Visual Flicker Pattern across two complete cycles of hues. A positive relationship is seen between the hue angle and the phase shift applied to the pattern as denoted by the solid black lines.

Citation: Lai JK, Takaku M, Anantarattanachai S, Ishii I, Okumura Y, Yamaguchi Y (2017) Pattern-induced subjective hue perception is coupled with the phase of visual flicker patterns.. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.5

Comparative Neuroscience Platform: the environment for the comparative neuroscience by facilitating data analysis and collaborations through neuroinfomatics

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CNS-PF (Comparative NeuroScience PlatForm; https://cns.neuroinf.jp) is a successor of IVB-PF (Invertebrate Brain Platform) that aims to provide the integrative database of the nervous systems and behaviors about not only invertebrates like insects but various species like fishes, Reptiles, Amphibia, bird and mammals, various model organisms and non-model organisms.

IVB-PF was constructed on the CMS system called XOOPS. It was mainly composed by the collection of more than ten independent database modules(CosmoDB), each stores neuroscience data for one species with 2D pictures, and general (noneinterpreted by the server) file like physiology and 3D data, and document pages which were supported by Pico modules and describes the characteristics of each species' brain structures, behaviors and so on.

In CNS-PF now all databases is integrated to one module under XooNIps and a 3D viewer were implemented for the first result of our effort to expand the modalities of machine-readable data. Some 3d-brain data of fishes and insects were additionally registered as 3D.

Japanese Society for Comparative Physiology and Biochemistry (JSCPB) annual meeting page and JSCPB wiki is now constructed under CNS-PF domain as a cooperation with JSCPB.

To facilitate massively connection between documents and data towards deep understanding and analysis, we built test site build by semantic-media-wiki(SMW) using semantic web technology. We imported data pages, documents from IVB-PF and JSCPB-wiki and now are introducing standard ontology systems to arrange data/document structures.

The CNS-PF is organized by CNS-PF committee in INCF Japan Node in collaboration with the JSCPB. It is developing towards the environment for data analysis in collaboration with the database and for the collaborative researcher various fields, including physiology, Histology, information science, and engineering and be used efficiently for educational purposes.

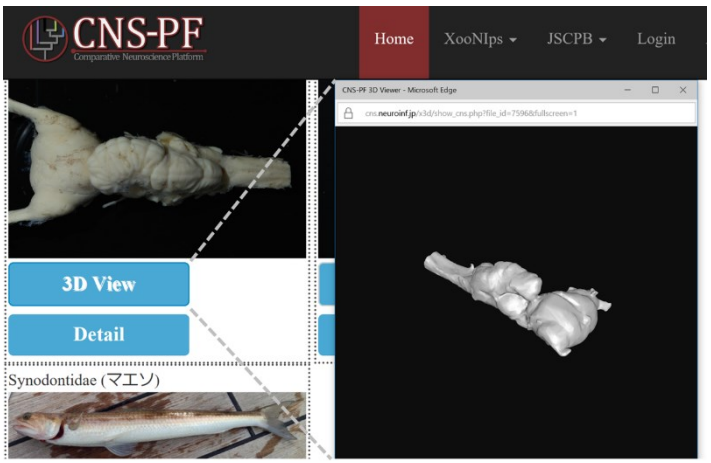

Figure1: 3D-viewer for a polygonized 3D brain

Acknowledgements

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Citation: Kanzaki R, Kazawa T, Miyamoto D, Seki Y, Yosida M, Iwatsuki C, Ando N, Namiki S, Ikeno H, Nishino H, Oota S, Murata Y, Kanazawa A, Ichishi H, Kanamoto Y, Yamaguchi Y (2017) Comparative Neuroscience Platform: the environment for the comparative neuroscience by facilitating data analysis and collaborations through neuroinfomatics. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.6

KANPHOS Platform: A comprehensive database for kinase-associated neural phosphorylation signaling

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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. Recently, we have developed an in vitro approach termed the kinase-interacting substrate screening (KISS) method [2] and an in vivo approach termed kinase-oriented substrate screening (KIOSS) method [3,4]. Here, we present an on-line database system which provides the phosphorylation signals identified by our KISS and KIOSS methods as well as those previously reported in the literature.

The database system and its web portal, named KANPHOS (Kinase-Associated PHOspho-Signaling), were built based on the Next Generation XooNIps [5]. All data are controlled for quality via review and curation by our professional staffs. In the portal site, we can search for the data of interest in three ways: 1) Search for substrates phosphorylated by a specific kinase; 2) Search for kinases phosphorylating a specific protein; and 3) Search for kinases and their target substrates by a specific signaling pathway (Fig.1, left). Each substrate is linked with external databases such as Uniprot KB (proteomics database), HGNC DB (human genomics database), and Allen Brain Atlas, enabling us to easily predict unknown functions of the protein phosphorylation. As an application of the database, we also demonstrate how to retrieve proteins and pathways in striatal medium-sized spiny neurons modulated by extracellular dopaminergic stimulation [4] (Fig.1, right).

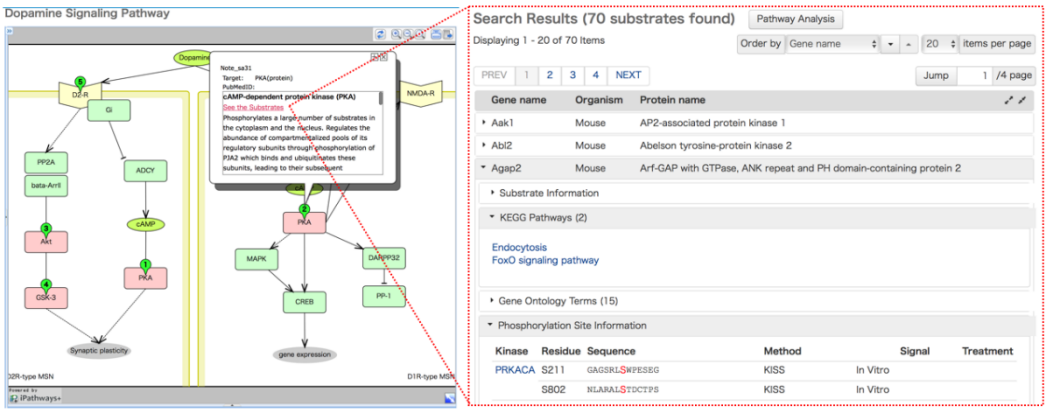

Figure1: Snapshot of searching by a specific signaling pathway (left panel) and the corresponding search results (right panel).

Acknowledgements

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Citation: Yoshimoto J, Kannon T, Amano M, Nishioka T, Usui S, Kaibuchi K (2017) KANPHOS Platform: A comprehensive database for kinase-associated neural phosphorylation signaling. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.7

A Neural Network for Pattern Separation

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The ability of signal separation in complex environments is one of the most important abilities in animals. In the case of sound signals, the ability is known as Cocktail Party effect. In case of vision, we can recognize one pattern through figure-ground separation. We can separate mixtures of signals without knowledge of the number of signal sources, and without special training. The mechanism to realize this ability is still an open question.

In this paper, we propose a neural network model for separating overlapping 2D images. Gray scale images of hand-written digits are used in the simulation. A mixture of images is given in a single-input channel setting, without knowledge of the number of inputs. Our network consists of three part, Encoder, Decoder, and Memory-Eraser system. Encoder outputs a mixture representation, which is kept as a memory vector for Memory-Eraser system. Memory-Eraser system extracts the most probable discrete codes at a time by sequentially erasing the memory vector until a terminating condition holds. Decoder receives discrete codes, forms their attention vectors to filter out individual patterns from the input mixture, and the filtered or attended inputs are used to regenerate the individual inputs.

The model was trained end-to-end by gradient-based algorithms with individual image patterns in an unsupervised manner. The results showed that the model could recover correct patterns in the mixture when a correct attention vector was selected. When an incorrect attention vector was selected, the generated output resulted in a corrupted image; thus, it can be discriminated from a complete one by a classifier. The proposed computational ideas are also compatible with physiological properties in the auditory and visual cortices. Our model might shed light on how our brain performs simultaneous separation of sound patterns in a single short-time window. Basic principles in our network might be extensively applied to sound signal separation.

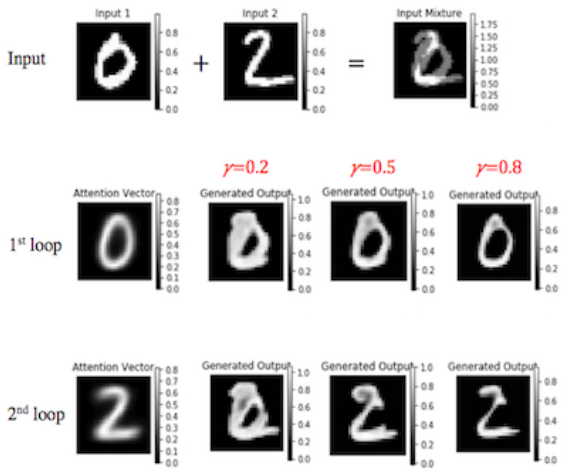

Figure1: An example of separation results. The attended input is reparameterized as $(\alpha)_{N_2} \odot |(x)_{N_2}|^{\gamma}$ where $(\cdot)_{N_2}$ is L2-normalization, $\odot$ and $|\cdot|$ are element-wise multiplication and absolute value, and γ is a control parameter of intensity.

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Citation: Anantarattanachai S, Yamaguchi Y (2017) A Neural Network for Pattern Separation. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.8

A Quantum Neural Network Based System for Handwritten Numeral Recognition

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Quantum Neural Networks (QNN) provide a good computational method over the classical neural networks, and involves some important advantages of quantum mechanics. Comparing with other classical methods, QNN can be more efficient in the field of pattern recognition. Pattern recognition is a mature and fast developing field, which underpins developments in branches such as computer vision, image processing (including image classification and recognition) and artificial neural networks. Due to the extensive application potentials of the handwritten numeral recognition in automatic postal system, automatic bank business processing and document analysis etc., it becomes an important branch of pattern recognition. Thus, in this study, a QNN-based handwritten numeral recognition system is studied. Experiments are conducted with the data from the MNIST database. During the training process of the QNN-based system, the back-propagation (BP) algorithm and particle swarm optimization (PSO) algorithm are used in order to improve the performance of the recognition system. As a result, the recognition rate of this proposed system becomes very high. The preliminary results of the experiments imply a possibility of superiority of the proposed recognition system in terms of not only the convergence speed but also the recognition rate.

Acknowledgements

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Citation: Yaxuan M, Aihara K (2017) A Quantum Neural Network Based System for Handwritten Numeral Recognition. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.9

Analyze microarray data on three mental diseases and extract common risk gene

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doi:10.14931/aini2017.ps.10

1. Background / Purpose

Currently, finding related genes for different mental disorders is a serious problem. However, the number of genes in the brain of mental illness is huge, I think that it is more effective to evaluate the importance using machine learning, and find the relevant gene after attaching some extent. Also, when dealing with a large amount of data, the development of microarray technology supplies a large amount of data in multiple fields. Therefore, we will use the microarray as the data set this time. In fact, there are many things that are currently used for cancer prediction and its diagnosis, and its usefulness is expected.

In this research, I would like to find a common risk gene for three mental diseases "depression, bipolar disorder, posttraumatic stress".

2. Methodology

First of all, genetic data is gathered from the brain "hippocampus, polaristic bodies, prefrontal cortex" for healthy subjects and each mental disease patient. Next, the data of each healthy subject and each patient were averaged, normalized, and difference between healthy subjects and patients was taken. Therefore, the data with small difference was truncated at that point. The reason is that data with small difference are considered to be less relevant to disease. I was able to reduce the data that was about 300,000 to about 2,500, so I ran from here to the classifier. This time I am thinking as a candidate of classifier using XGBoost and random forest. I hope to gather 500 data by applying it to a classifier from about 2,500 data of each disease. Among them, find a candidate group to be a common risk gene.

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Big data infrastructure for online collaboration

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In Brain/MINDS project [1], one goal is to generate integrated knowledge on the neuronal circuit of marmoset brain. Multiple measurement data ranging over microscopic and macroscopic scales by multiple research groups must be shared and analyzed through interdisciplinary collaboration. The reusability of those data is of course of importance. In order to enable this large-scale data-sharing and collaboration, we have started to construct information infrastructure. The system includes large-scale-shared storage and HPC. In order to enable access through internet, the user interface is given as the Research Portal and the Data Portal [2]. These two portals are for online-collaboration and for opening data to public.

Recently, we added semi-automatic data transfer function from Research Portal to Data Portal. Now, the data registered at the Research Portal can be comprehensively managed by attaching Brain/MINDS standard metadata until publication, including visualization and operations at data analysis pipelines. This system needs continuous development according to increases in data types and progress of knowledge integration. In addition, next challenge is association with on-going brain projects.

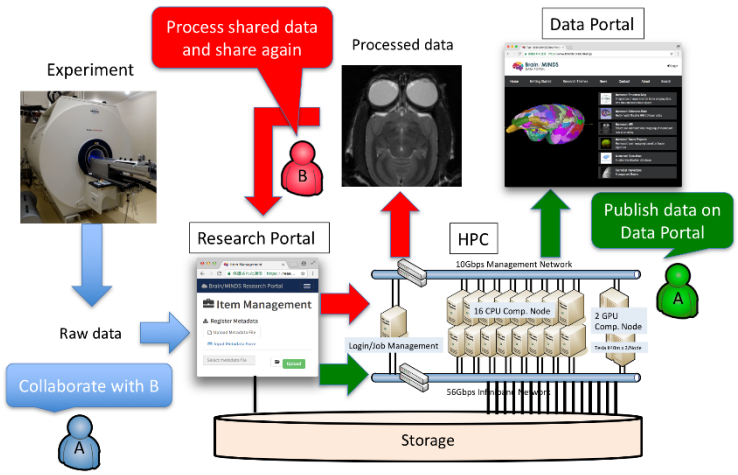

Figure1: This example of data flow includes three parts. Blue: data acquisition by experiment [3] and the sharing with others on Research Portal. Red: analysis of shared data on HPC and sharing of processed data [3] on Research Portal. Green: data publication on Data Portal with processing on HPC.

Acknowledgements

This research is 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: Maeda M, Woodward A, Gong R, Okumura Y, Morii Y, Takeuchi T, Yamaguchi Y (2017) Big data infrastructure for online collaboration. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.11

Closing the loop between neural network simulators and the OpenAI Gym

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Since the enormous breakthroughs in machine learning over the last decade, functional neural network models are of growing interest for many researchers in the field of computational neuroscience. One major branch of research is concerned with biologically plausible implementations of reinforcement learning, with a variety of different models developed over the recent years. However, most studies in this area are conducted with custom simulation scripts and manually implemented tasks. This makes it hard for other researchers to reproduce and build upon previous work and nearly impossible to compare the performance of different learning architectures.

In this work, we present a novel approach to solve this problem, connecting benchmark tools from the field of machine learning and state-of-the-art neural network simulators from computational neuroscience. This toolchain enables researchers in both fields to make use of well-tested high-performance simulation software supporting biologically plausible neuron, synapse and network models and allows them to evaluate and compare their approach on the basis of standardized environments of varying complexity.

We demonstrate the functionality of the toolchain by implementing a neuronal actor-critic architecture for reinforcement learning in the NEST simulator and successfully training it on two different environments from the OpenAI Gym.

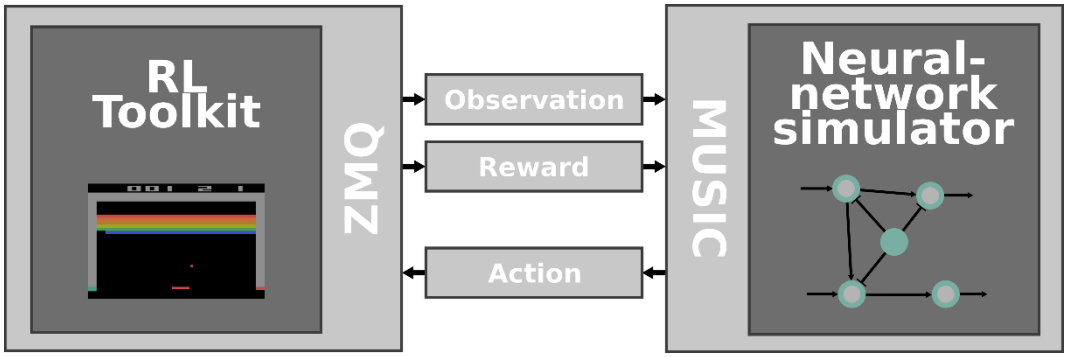

Figure1: The RL toolkit (left) emulates an environment that provides observations and rewards which are communicated via ZeroMQ sockets and MUSIC adapters (middle) to a neural network simulator (right). The activity of the simulated neural network is transformed to an action and fed back to the RL toolkit.

Acknowledgements

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DNA microarray data analysis for schizophrenia using machine learning

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Gene selection is a common task in most studies of gene expression and it allows to discover target protein and marker gene of diseases. However, most of gene expression data such as DNA microarray data are too complex and massive for researchers to analyze using conventional techniques. In this study, we applied machine learning methods such as random forest algorithm or k-means algorithm to microarray data to extract discriminative genes for classification between control and non-control. More specifically, we focused on schizophrenia and used microarray data related to the disease in the experiment. Our proposed methodology put emphasis on treating imbalance and high-dimensional data to extract meaningful genes because most microarray data contains a small number of samples especially that of positive (diseased) and the number of genes as a dimension of data is too high. In the result, we found some genes which have been investigated for their relevance to schizophrenia. We expect that these extracted genes would be mental disease-related genes and it also would be marker genes of diagnosis and monitoring of therapy.

Citation: Nishiwaki K, Furuichi T, Sato A, Ohwada H (2017) DNA microarray data analysis for schizophrenia using machine learning. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.13

Effect of Local Excitatory-Inhibitory Connection Balance in Reproducing Whole-Brain Functional Connectivity

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In recent years, methods to investigate the relationship between MRI-based anatomical and functional networks using mathematical models have been proposed in human studies [1,2]. We extend these method to the common marmoset MRI data and investigate the effect of local neural dynamics in reproducing resting state functional MRI data.

We constructed a whole brain network model based on the structural connectivity matrix of 96 anatomical areas estimated by the global fiber tracking algorithm [3] using diffusion-weighted MRI data. We compared the network activity simulated by the model and the brain activity observed by resting state functional MRI. We adopted the Wilson-Cowan model [4] for each area of the whole brain network model, and examined what parameters affect the relationship between anatomical and functional networks. The correlation between the simulated and empirical functional connectivities (FCs) had a peak in a range of the global coupling parameter. We also changed the balance of local excitatory and inhibitory connections, and found a complex landscape of the correlation between the simulated and empirical FCs in resting state fMRI (see Figure 1).

Comparison of further marmoset fMRI data (e.g. under cognitive tasks and in disease model animals) would contribute to understanding of the factors behind the disorders and development of new treatments.

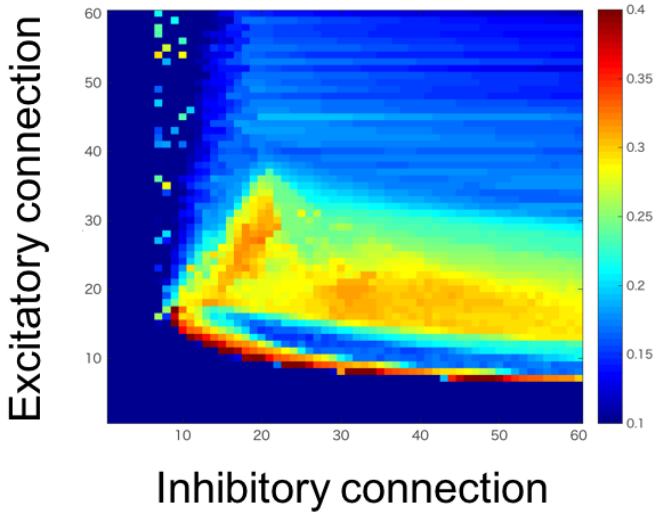

Figure1: Correlation between simulated and empirical FC in the parameter space of excitatory and inhibitory connection strength.

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, Nakae K, Ishii S, Hata J, Okano H, Doya K (2017) Effect of Local Excitatory-Inhibitory Connection Balance in Reproducing Whole-Brain Functional Connectivity. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.14

Marmoset Brain Atlas Applied to dMRI Based Connectomics

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A challenge in Brain/MINDS is to integrate multiscale-multimodal neuroimaging data first as a structural map and next as a functional map of the marmoset brain. The specification of neuronal and regional connections are key to bridging between structure and function. As a step to integrate macro connectomics, we mapped the Brain/MINDS digital marmoset atlas [1] to dMRI data.

We prepared the atlas with different variations of cortical parcellation to investigate different scales of representation. Next, computational linear and non-linear image registration was used to map between the atlas space and the individual dMRI space. After this, deterministic tractography was performed and this information along with the anatomical brain regions was used to prepare the necessary connectomics data such as region centers, track lengths and connection weights. All of the structural information was prepared in HDF5 format - making it easy to load into a number of software tools. By using this data, we simulated resting state dynamics in the marmoset brain by using the TVB (The Virtual Brain) software [2].

Thus, our approach links between the structural map, functional map and simulation studies.

Acknowledgements

We thank Junichi Hata for generating the dMRI data for this work.

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Citation: Woodward A, Gong R, Yamaguchi Y (2017) Marmoset Brain Atlas Applied to dMRI Based Connectomics. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.15

Mouse behavioral phenotype database

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The mouse is a powerful research tool for modeling human diseases and condition. Since almost all mouse genes have homologs in human, a large-scale project has been undertaken to determine the functions of genes in mice. Approximately 80% of all genes are expressed in the brain, and we have been identifying the genes that have significant impact on the brain functions efficiently by examining the final output level of gene function in the brain, that is, behavior. The influence of a given gene on a specific behavior is determined by conducting "comprehensive behavioral test battery" of genetically engineered mice. This battery includes the test that can detect the following abnormalities in those behaviors with high sensitivity: sensori-motor functions, anxiety-like behavior, depression-like behavior, social behavior, and learning and memory. So far, by using the test battery, we have evaluated the effects of nearly 200 kinds of experimental manipulations on behavior, and raw data of 164 indices in 19 tests from these strains are stored in a FileMaker file. Here, we introduce the database "Mouse Phenotype Database".

In our comprehensive behavioral test battery, the data were obtained systematically with reasonably standardized methods. Raw data for each strain are available in the Mouse Phenotype Database after publication. By secondary use of data in the database, we can evaluate the effects of factors, such as age, sex, and temperature, on behaviors. We have reported the effect of substrains of mice, cohort removal, and age on behavioral phenotypes by the large-scale analysis of behavioral data from our database (Matsuo et al., 2010; Takao et al., 2016; Shoji et al., 2016). The utilization of our database may contribute to progress in understanding gene-brain-behavior relationship.

"Mouse Phenotype Database" (http://www.mouse-phenotype.org/).

Acknowledgements

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Recent Outputs of Neuroimaging Platform for Brain Researchers and Younger Generation

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In this paper, we present recent activities and outputs of Neuroimaging platform (NIMG-PF) for brain researchers. NIMG-PF opened to the public in 2009 to accumulate and to share articles regarding non-invasive neuroimaging approaches. At present, it contains 5497 items in the categories of books, published papers, tutorial and documentation items, acquired data by experiments, tool information including software and hardware for experiment, and brain coordinate data.

One of the most remarkable function available for advanced brain researchers is document retrieval/searching function using "Search with Brain Atlas." It can be searching for published papers which include the description of brain activity for specified brain coordinate position. Currently 2394 articles for normal and patient subjects are accumulated from pubMED including the categories such as Vision, Audition, Somatosensory, Gustation, Olfaction, Sensory integration, Motor, Sensory-motor integration, Learning and memory, Language, Executive function, Emotion, Awareness/Consciousness, Rhythm/Sleep, Development/Aging, Social cognition and Resting State Network. Currently, we start a discussion to realize the function of automatically collecting bibliographic and brain coordinate data using artificial intelligent technology.

For supporting beginners, we are uploading neuroimaging experimental data for analysis skill training. We have uploaded two fMRI datasets, one with basic experimental paradigm and the other with advanced technique, with analysis training manual. In addition to that, we are planning to upload MEG data for basic visual and auditory stimuli with analysis training manual using Statistical Parametric Mapping (SPM).

As part of activities to introduce brain science to younger generation, we have just started to hold a demonstration event showing functional MRI experiment for high school students (Fig.1). This event includes basic science as well as imaging technology.

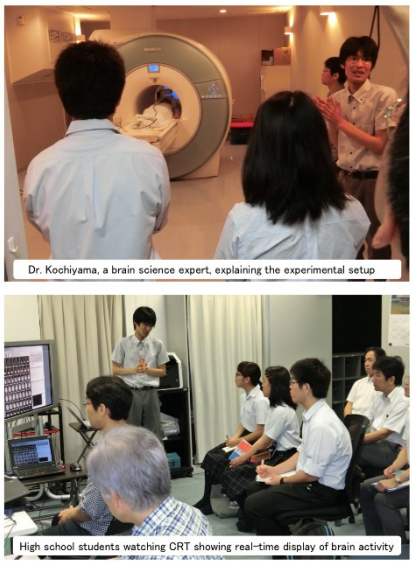

Figure1: Demonstration event showing functional MRI experiment for high school students at ATR Brain Activity Imaging Center.

Citation: Kashioka H, Masaki S (2017) Recent Outputs of Neuroimaging Platform for Brain Researchers and Younger Generation. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.17

Simulating the retinal cone mosaic with eye optics

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In the human eye, light passes through eye optics and refracts to form an image on the retina. Cone photoreceptors convert the image into neural signals. Cones show maximal sensitivity to either the long (L), medium (M), short (S) wavelength light. Anatomically, cones form a distinctive spatial arrangement, the cone mosaic. Since optical aberrations limit the quality of the retinal image, it is important to clarify the influence of the optics on our vision. In the present study, we developed a computational model of the cone mosaic with eye optics (Figure 1). By convoluting the image with the polychromatic point-spread function (PSF), we were able to calculate a retinal image with aberrations. The PSF was computed from the pupil function which includes chromatic and spherical aberrations. The cone mosaic was generated by a stochastic algorithm to position the cones randomly. To generate S-cone nonrandom distribution we use the exclusion zone method. The response of cones to chromatic light was modeled by spectral sensitivity and the equations of the membrane dynamics.

In the simulation, the S-cones respond to wider spatial images than the L- and M-cones, the chromatic aberration is large in short wavelength light. The simulation results suggested that S-cones are able to catch a retinal image with the sparse but nonrandom distribution.

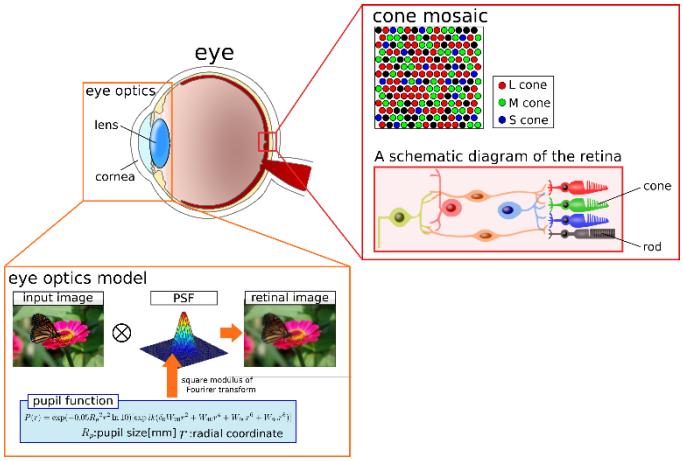

Figure1: A model of the cone mosaic with eye optics. PSF: Point-spread function, L: Long, M: Medium, S: Short

Acknowledgements

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Statistical analysis and inference from olfactory EEG studies: from sensor to source space

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The ability to smell is essential for taste, crucial for social bonding, and survival (e.g., detecting life threatening gas fumes). Yet, when compared with other sensory modalities, olfaction is the least studied and understood one. Specifically, neuroimaging research on human olfactory behavior is fairly young and still emerging. Whereas fMRI studies have helped in identifying brain regions that mediate various olfactory tasks, their inference lack the temporal resolution required to estimate the temporal course of the brain activity. EEG can provide more temporally precise measurements, e.g., olfactory event related potential (OERP), to summarize the time course of the neural activity. However, most OERP studies still rely on waveform-based analysis with few midline electrodes with spatially limited inference. With recent advancements in source reconstruction techniques, high-dimensional EEG can provide both spatio-temporal and cortical information. Indeed, reconstructed brain data from the source space is difficult to analyze, because it comprises thousands of voxels with spatially and temporally dependent structures. This causes a huge multiple comparison problem. Most source reconstruction toolboxes offer limited statistical options lacking sufficient power to detect significant voxels. The goal in this study is to highlight such issues and suggest new alternative approaches to improve the statistical reliability (1). We demonstrate their application with 3D current source density maps generated by a source reconstruction method (e.g., sLORETA) (2), using example datasets from olfactory experiments.

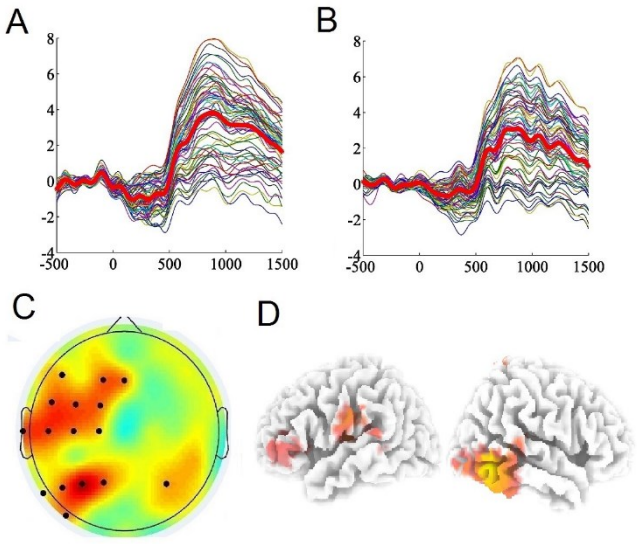

Figure1: Comparing P3 component between two olfactory conditions in sensor and source space. (A-B) butterfly plots of OERP for two conditions show higher P3 peak, A>B, (~800 ms) (C) electrodes with significant difference in sensor space. (D) brain regions with significant effect (fdr<.05) in source map.

Acknowledgements

This work was supported by ERATO Touhara Chemosensory Signal Project from JST Japan.

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Citation: SIngh AK, Okamoto M, Ogura S, Okumura T, Touhara K (2017) Statistical analysis and inference from olfactory EEG studies: from sensor to source space. Advances in Neuroinformatics 2017. doi:10.14931/aini2017.ps.19

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