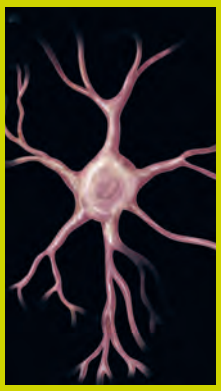
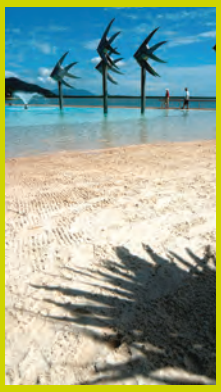
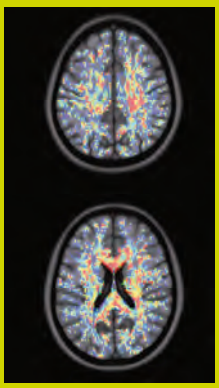
incf | Neuro Informatics 2015




August 20-22

Cairns, Australia

Neuroinformatics 2015
8th INCF Congress

Program & abstracts

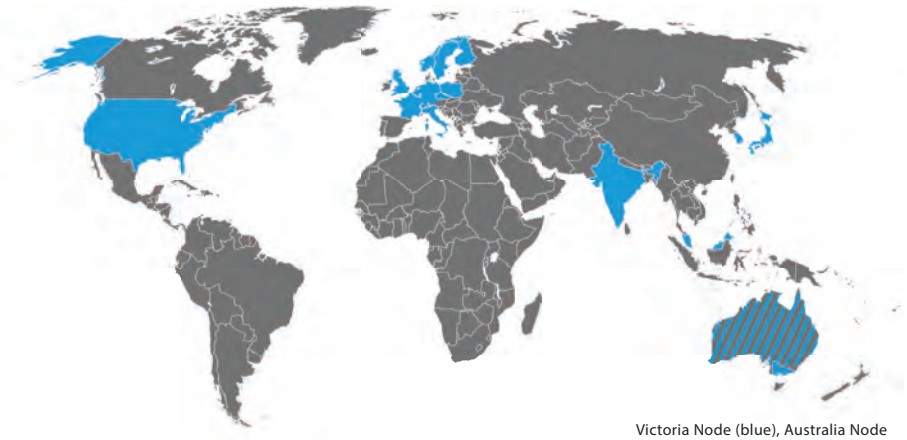
August 20 - 22, 2015
Cairns, Australia

incf International Neuroinformatics Coordinating Facility

The International Neuroinformatics Coordinating Facility (INCF), together with its 18 member countries, coordinates collaborative informatics infrastructure for neuroscience and manages scientific programs to develop standards for data sharing, analysis, modeling, and simulation in order to catalyze insights into brain function in health and disease. INCF is an international organization launched in 2005, following a proposal from the Global Science Forum of the OECD to establish international coordination and collaborative informatics infrastructure for neuroscience. INCF is hosted by Karolinska Institutet and the Royal Institute of Technology, and the Secretariat is located on the Karolinska Institute Campus in Solna. INCF currently has 18 member countries across North America, Europe, Australia, and Asia. Each member country establishes an INCF National Node to further the development of Neuroinformatics and to interface with the INCF Secretariat. The mission of INCF is to share and integrate neuroscience data and knowledge worldwide, with the aim to catalyze insights into brain function in health and disease.

Learn more: incf.org
software.incf.org
neuroinformatics2015.org

INCF Member Countries as of August 2015



Victoria Node (blue), Australia Node from 1 Jan 2016 (hatched blue)

8th INCF Congress in Cairns, Queensland, Australia.

General Information

The 8th INCF Neuroinformatics Congress, organized by INCF, International Neuroinformatics Coordinating Facility, took place at the Pullman International Cairns Hotel, August 20-22 in Cairns, Queensland, Australia.

The 8th INCF Congress on Neuroinformatics meets this year in sunny Cairns, Australia, home to the Great Barrier Reef place at the Pullman International Hotel, In such exciting environment, the Congress program reflects a growing interest in neuroinformatics and big data analytics. On behalf of the organizers and Program Committee, I welcome you and hope you enjoy it! Neuroinformatics 2015 is organized by INCF together with the INCF Australian Node. Overall the program structure is similar to previous years, mostly single track with 4 keynotes, 3 workshops, and 2 poster and demo sessions. The keynote speakers shed light on neuroinformatic challenges for understanding the molecular mechanisms of brain organization and its connectivity, as well as discuss recent development in brain-machine interfaces and big data analytics. Workshops will focus on neuromorphic computing and present both large and small scale brain initiatives. For the investigator presentations session, the Program Committee selected 6 out of 40 submitted abstracts that requested an oral presentation. This session has brought the newest science and reflects topics that are of special interest to the attendees. The final day of the Congress has hosted by the INCF Australian Node. It shows how neuroscience drives next generation neuroinformatics, presents imaging informatics, simulation and visualization environments, as well as modern brain atlases.

Katrin Amunts
Research Centre Jülich/Heinrich Heine University Düsseldorf, Germany
INCF 2015 Program Committee Chair

Program Committee
Alan Evans, McGill University, Canada
Tianzi Jiang, The Chinese Academy of Sciences, China
Hidetoshi Ikeno, University of Hyogo, Japan
Romain Brette, Vision Institute, France

Jeanette Hellgren-Kotaleski, Royal Institute of Technology/Karolinska Institutet, Sweden
Gary Egan, Monash University, Australia
Mary Kennedy, California Institute of Technology, USA
Mathew Abrams (secretary), INCF Secretariat, Sweden

Local Organizing Committee
Gary Egan, Monash University, Australia
Ramesh Rajan, Monash University, Australia Hsin-Hao Yu, Monash University, Australia
Elizabeth Arsenault, Monash University, Australia
Wojtek Goscinski, Monash University, Australia Duwage Alwis, Monash University, Australia
Geoff Goodhill, University of Queensland

Registration fees

Registration fees (USD)	Early Bird	After July 15	One Day Pass
Regular	470	630	230
Postdocs/Students	160	240	90
Social Program			
Welcome Reception	Complimentary		
Banquet	90 USD		

Neuroinformatics 2015 registration fee included:

- Participation in the scientific program
- Conference kit including program booklet, name tags, etc.
- Three lunches, coffee and refreshments in the coffee breaks twice a day for three days
- Welcome reception during the poster session August 20, 2015 at the Pullman Hotel

SOCIAL EVENTS There has been be a complimentary welcome reception at the Pullman hotel during the poster and demo session on August 20. On August 21, INCF hosts a Congress Banquet at the beautiful waterfront restaurant Salt House, August 22.

Financial Budget:

ISN generous contribute of the 205 Neuroinformatics congress was announced on the website, in the program book, on postcards, on posters and in the abstract book. The ISN contribution has been used as shown below:

Venue: 4500 USD
Invited speakers expenses: 10000 USD
Posters and networking reception: 5500 USD

210 Participants including invitees	**Budget USD for 200 participants**	**Forecast USD for 118 participants**
Expenses		
Venue	5000	4250
Printed materials	5400	2130
Registration	5500	1600
Cost for invitees	43000	36000
Staff	27000	23000
Posters, demo, exhibit	9400	2900
Catering, welcome reception	31000	20500
Banquet	3500	2050
Others	4200	2950
Total cost	**134000**	**94000**
ISN	10000	10000
Registration fees	59000	21150
Sponsors	24000	5850
Total revenue	**-93000**	**-37000**
Balance	**41000**	**57000**

Sponsors

In addition to the 20,000 USD received from ISN, the meeting was sponsored by: BNA, Scientific Data, Frontiers, Springer, National Bernstein Network, F1000Research, Neurotechnix, GigaScience, Massive, NIF and CIBF as follows:

Organization/person to contact	Email address	Type of collaboration	Agreed	Amount committed AUD
BNA		marketing exchange - no cost	Yes	0
Scientific Data (NPG journal)		marketing exchange plus advert in program book	Yes	730
Frontiers		Abstract hosting in exch for advert in program book	Yes	0
PLOS		booth and/or session sponsring		
Springer		booth	Yes	1300
F1000		poster session sponsring	Yes	1200
GigaScience (BMC)		marketing exchange	Yes	
Neurotechnix		marketing exchange - no cost	Yes	
MASSIVE			Yes	1000
NIF			Yes	1000
CIBF			Yes	2500
TOTAL				7730

frontiers

ISN International Society for Neurochemistry

F1000Research Open for Science.

Australian Research Council Centre of Excellence for Integrative Brain Function

Springer the language of science

National Imaging Facility

SCIENTIFIC DATA

MASSIVE

(GIGA)n SCIENCE

ALLEN INSTITUTE for BRAIN SCIENCE Fueling Discovery

Participants

It welcomed 118 researchers in Neuroinformatics and in other related fields such as data and knowledge bases of the nervous system from molecular to behavioral levels, tools for the acquisition, analysis, and visualization of nervous system data, as well as theoretical, computational, and simulation environments for modeling the brain. The meeting included a series of keynote lectures, workshops, poster sessions, and live demonstrations of neuroinformatics tools. 59 abstracts were accepted for either poster presentations or live demonstrations, and 6 of these abstracts were selected for oral presentations.

Participant Demographics

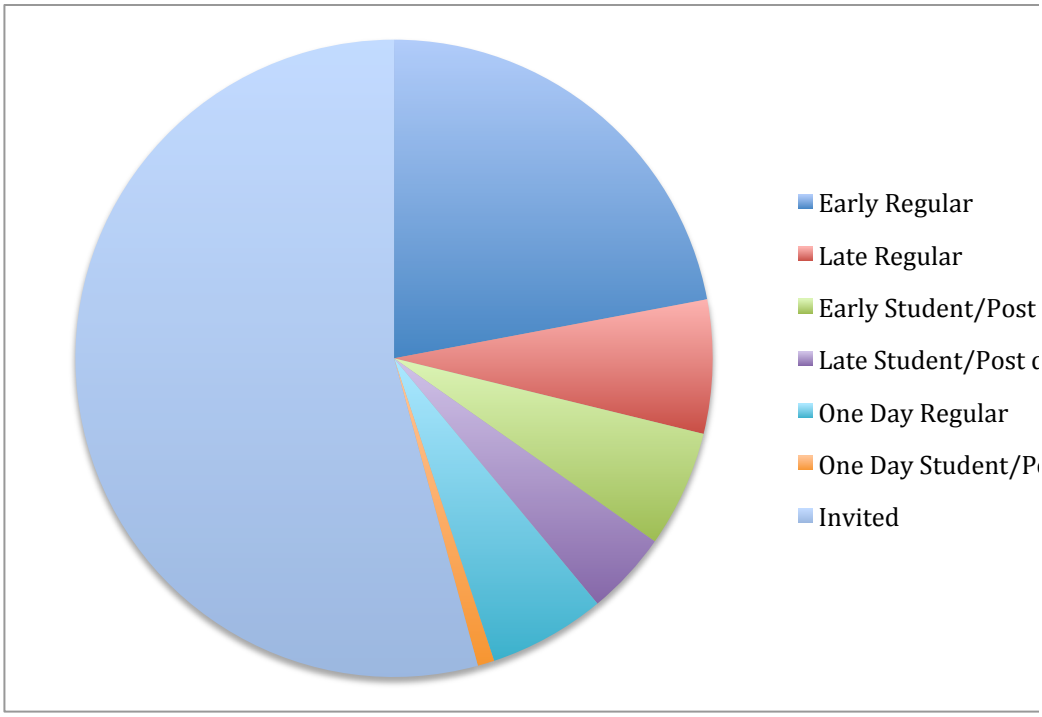


Figure 1: Participant demographics based on registration level. Data presented as total number of participants.

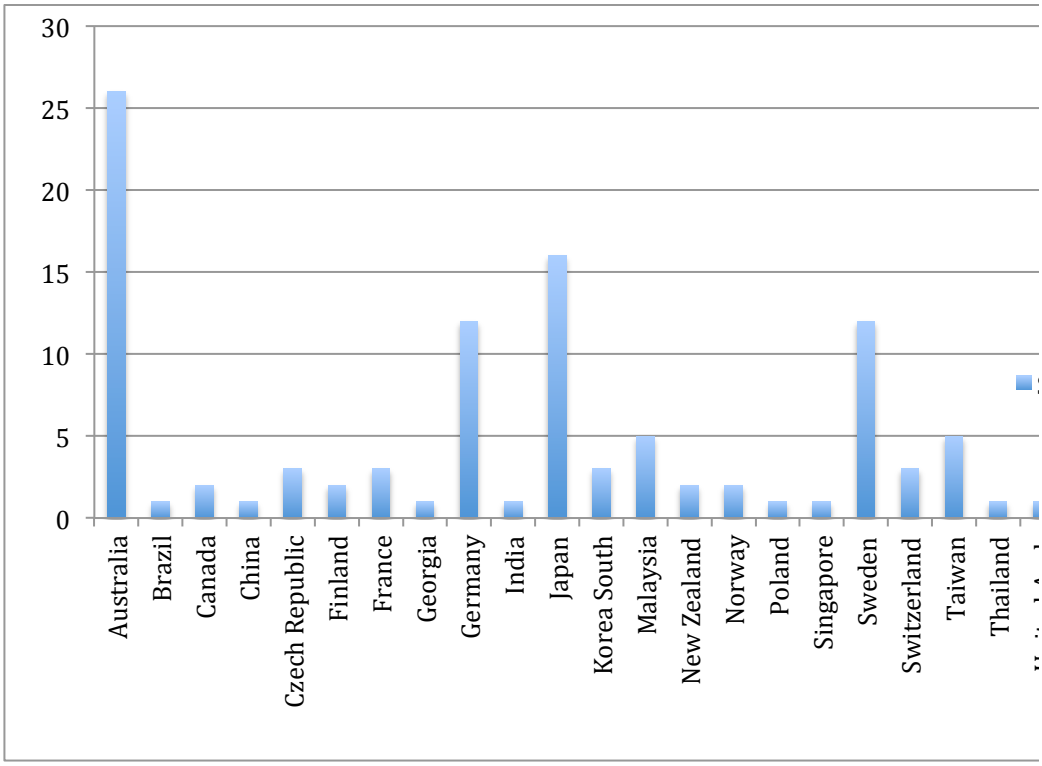


Figure 2. Registered participants based on country of origin. Data presented as the total number of participants.

Participant list:

First name	Middle Name	Last name	Email	Country
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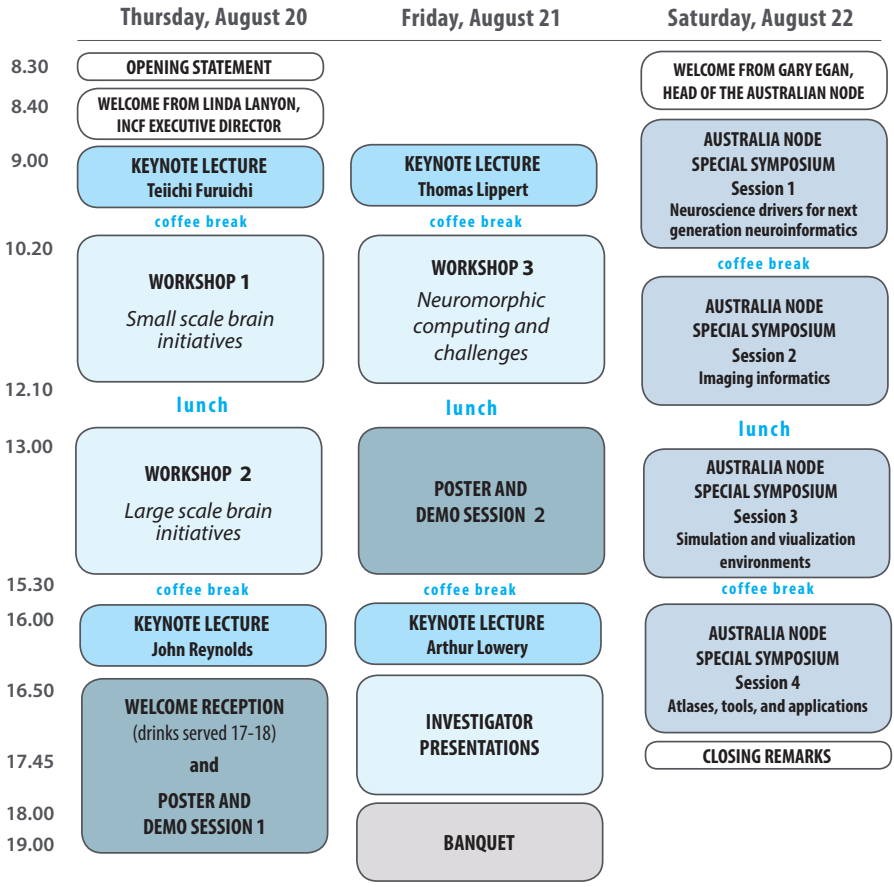
Krzysztof	Jacek	Gorgolewski	krzysztof.gorgolewski@gmail.com	America

Congress program at a glance



Thursday, August 20, 2015

08:30 **OPENING STATEMENT**
Katrin Amunts, Program Committee Chair, Research Centre Jülich/Heinrich Heine University Düsseldorf

08:40 **WELCOME**
Linda Lanyon, INCF Executive Director, Sweden

09:00 **KEYNOTE** ▶ *The molecular mechanisms of brain development and disorders*
Teiichi Furuichi, Tokyo University of Science

09:50 Coffee break

10:20 **WORKSHOP 1** ▶ *Small scale brain initiatives*
Chair: **Romain Brette**, Vision Institute, France
Ann-Shyn Chiang, National Tsing Hua University, Taiwan
Vladimir Brezina, Mount Sinai School of Medicine, USA
Paul S. Katz, Neuroscience Institute, Georgia State University, USA

12:10 Lunch

13:00 **WORKSHOP 2** ▶ *Large scale brain initiatives*
Chair: **Sean Hill**, INCF, Sweden, and HBP, Switzerland
Walter Koroshetz, NIH, NINDS, USA
Richard Frackowiak, EPFL, Switzerland

15:30 Coffee served

16:00 **KEYNOTE** ▶ *Dopamine and learning mechanisms in the basal ganglia*
John Reynolds, University of Otago Medical School, New Zealand

17:00 **WELCOME RECEPTION** (drinks served 17-18)
POSTER AND DEMO SESSION 1

19:00 End

Friday, August 21, 2015

09:00 **KEYNOTE** ▶ *Supercomputing and big data analytics in the neurosciences*
Thomas Lippert, Research Centre Jülich/University of Wuppertal, Germany

09:50 Coffee break

10:20 **WORKSHOP 3** ▶ **Neuromorphic computing and challenges**
Chair: **Jeanette Hellgren-Kotaleski,** KTH/KI, Sweden
Tadashi Yamazaki, University of Electro-Communications, Japan
Giacomo Indiveri, University of Zurich/ETH Zurich, Switzerland
Runchun Mark Wang, University of Western Sydney, Australia
Romain Brette, Vision Institute, France

12:10 Lunch

13:00 **POSTER AND DEMO SESSION 2**

15:30 Coffee served

15:40 **KEYNOTE** ▶ *Monash Vision Group's Cortical Bionic Eye System: a wireless cortical stimulator*
Arthur Lowery, Monash University, Australia

16:20 **ORAL PRESENTATIONS OF SELECTED ABSTRACTS**

16.50 David Keator - *Standardizing metadata in brain imaging*

17.00 Chris Gorgolewski - *Brain Imaging Data Structure-a new standard for describing and organizing human neuroimaging data*

17.10 B. Nolan Nichols - *The National Consortium on Alcohol and Neurodevelopment in Adolescence (NCANDA): A framework supporting neuroimaging data integration and analysis*

17.20 Junichiro Yoshimoto - *Neural PhosphoSignaling Database: A neuroinformatics platform for protein phosphorylation with quality control*

17.30 Tianzi Jiang - *Genetic sculpture of fine grained human cortical regionalization*

17.40 Cameron Craddock - *The preprocessed connectomes project quality assessment protocol - a resource for measuring the quality of MRI data*

17:50 End

18:00 Banquet at the Salt House

Saturday, August 22, 2015

08:30 Introduction by **Gary Egan**, CIBF, Monash University, Australian INCF node

08:45 **SESSION 1 ▶ Neuroscience drivers for next generation neuroinformatics**

Sponsored by the ARC Centre of Excellence for Integrative Brain Function

Chair: **Gary Egan**, Monash University, Australia

08:45 *Predictive coding circuits in the brain* - Michael Ibbotson, University of Melbourne, Australia

09:15 *How do populations of neurons incorporate recent stimulus statistics?* - Nicholas Price, Monash University, Australia

09:35 *Investigating human attention and prediction* - Marta Garrido, University of Queensland, Australia

Physiology-based quantitative modeling and analysis of brain dynamics underlying attention and prediction - Peter Robinson, University of Sydney, Australia

10:15 Discussion

10:30 **Coffee break**

11:00 **SESSION 2 ▶ Imaging informatics**

Sponsored by the Australian National Imaging Facility

Chair: **Graham Galloway**, University of Queensland, Australia

11:00 *INCF Neuroimaging Data Sharing Model* - Jean Baptiste Poline, University of California Berkely, USA

11:30 *Automated neuroimaging biomarkers computed on the cloud* - Olivier Salvado, CSIRO, Australia

11:50 *Integrating data-driven and model-based analysis tools for functional MRI* - David Abbott, The Florey Institute of Neuroscience and Mental Health, Australia

12:10 *Workflows for large cohort neuroimaging datasets* - Parnesh Raniga, Monash University, Australia

12:30 Discussion

12:45 **Lunch**

Saturday, August 22, 2015 (cont.)

13:45 **SESSION 3 ▶ Simulation and visualization environments**

Sponsored by the MASSIVE Computational Facility

Chair: **Paul Bonnington**, Monash University, Australia

13:45 *Supercomputing and big data analytics in the neurosciences* - Thomas Lippert, Research Centre Jülich, Germany

14:15 *MASSIVE CVL: a specialized imaging and neuroinformatics facility* - Wojtek Goscinski, Monash University, Australia

14:35 *Visualisation architectures* - Stefan Eilemann. EPFL, Switzerland

14:55 *Immersive visualisation environments for investigating the brain* - Paul Bonnington, Monash University, Australia

15:15 Discussion

15:30 Coffee

16:00 **SESSION 4 ▶ Atlases, tools, and applications**

Sponsored by the Allen Brain Institute

Chair: **George Paxinos**, University of New South Wales

16:00 A next generation common coordinate framework of the adult mouse brain for data integration and discovery - Lydia Ng, Allen Brain Institute, USA

16:30 Tissuestack: an open source HTML5 web based imaging viewer - Andrew Janke, University of Queensland, Australia

16:50 Scalable atlases for non-human primate brain research - Daniel Wojcik, Nencki Institute, Poland

17:10 Discussion

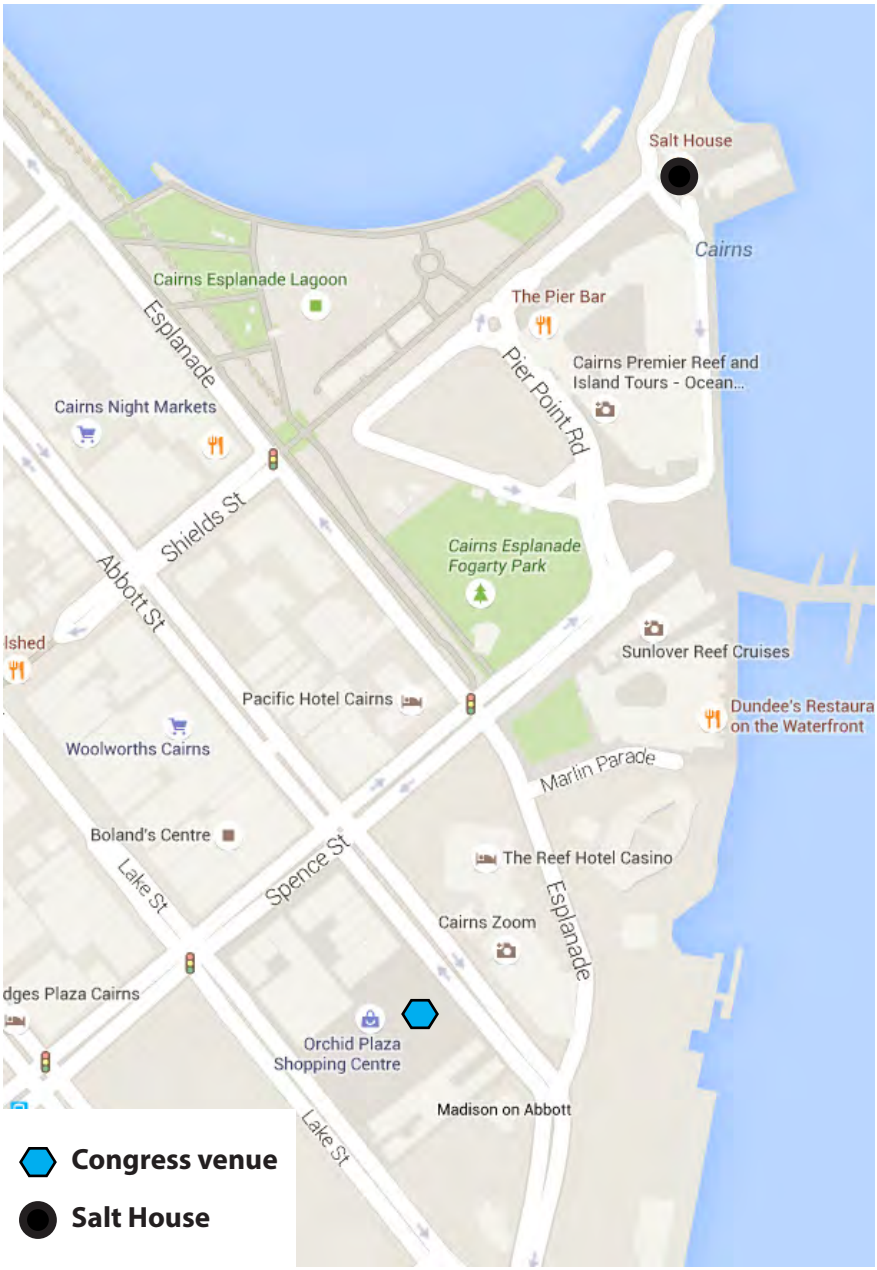
17:25 **CLOSING REMARKS**

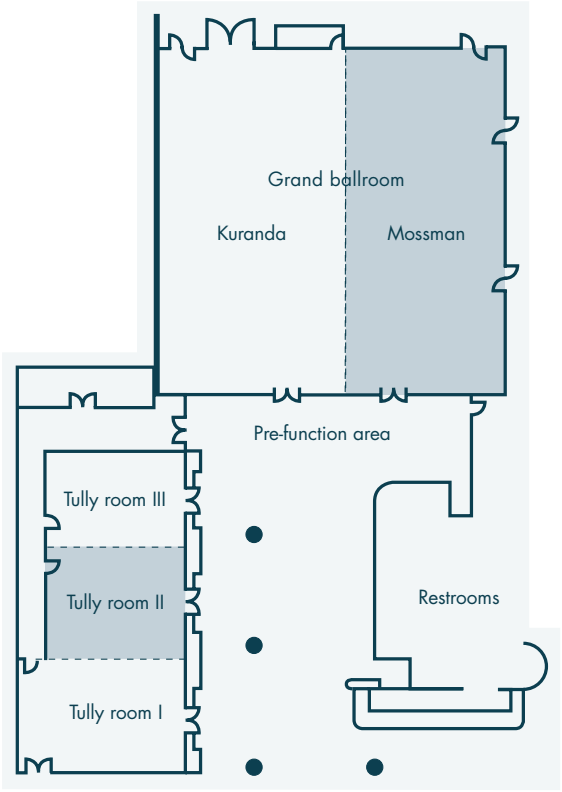
Jan G Bjaalie, INCF Governing Board Chair

17:30 End

INCF looks forward to welcoming you to the 9th Neuroinformatics Congress in Reading, UK, on September 3-5, 2016!

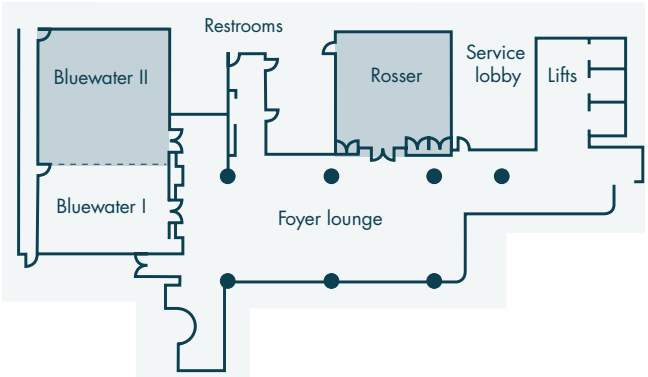
www.neuroinformatics2016.org


Salt House
Cairns
Cairns Esplanade Lagoon
Esplanade
The Pier Bar
Pier Point Rd
Cairns Premier Reef and Island Tours - Ocean...
Cairns Night Markets
Shields St
Abbott St
Cairns Esplanade Fogarty Park
Sunlover Reef Cruises
Pacific Hotel Cairns
Dundee's Restaura on the Waterfront
Woolworths Cairns
Marlin Parade
Boland's Centre
Spence St
Lake St
The Reef Hotel Casino
Cairns Zoom
Esplanade
Orchid Plaza Shopping Centre
Madison on Abbott
Lake St
Congress venue
Salt House



Ground floor

Grand ballroom:
Keynotes & workshops

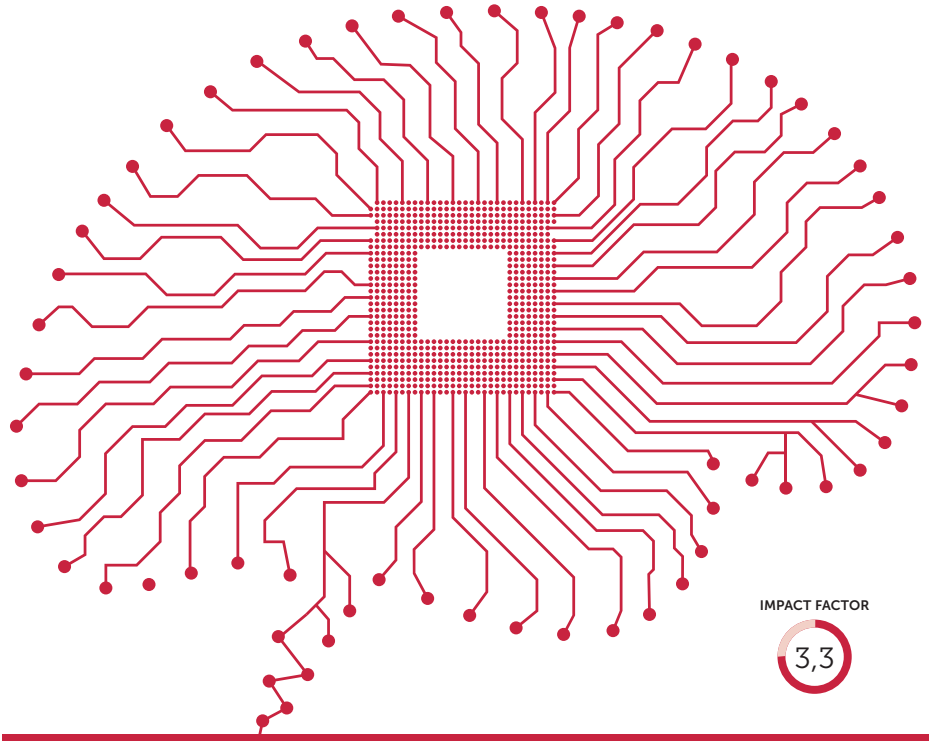


First floor

Bluewater I & II:
Demos

Foyer lounge:
Posters and welcome reception

frontiers in Neuroinformatics



IMPACT FACTOR

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Frontiers in Neuroinformatics is an open-access journal devoted to studies on the creation of data and knowledge bases, together with the development and use of numerical models and analytical tools for the sharing, integration and analysis of experimental data and the advancement of theories of nervous system function.

frontiersin.org/neuroinformatics

Other titles in the Frontiers in Neuroscience Journal Series:
journal.frontiersin.org/journal/neuroscience

Abstracts

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ABSTRACT INFORMATION

The abstract list is sorted in alphabetical order by the corresponding author's last name.

P Poster

OP Poster which will also be presented in the oral session at 16:20 on Friday, August 21.

D Demo

Session 1

Thursday, August 20 17:00 - 19:00

Abstracts with uneven numbers will be presented

Session 2

Friday, August 2113:00 - 15:40

Abstracts with even numbers will be presented

All abstract presenters have been asked to be available during both sessions if possible.

Corresponding author	Abstract title	Abstract number
David B. Keator	Standardizing metadata in brain imaging	OP01
Junichiro Yoshimoto	Neural PhosphoSignaling database: a neuroinformatics platform for protein phosphorylation with quality control	OP02
Tianzi Jiang	Genetic sculpture of fine-grained human cortical regionalization	OP03
B. Nolan Nichols	The national consortium on alcohol and neurodevelopment in adolescence (NCANDA): a framework supporting neuroimaging data integration and analysis	OP04
Chris Gorgolewski	Brain imaging data structure – a new standard for describing and organizing human neuroimaging data	OP05
Cameron Craddock	The preprocessed connectomes project quality assessment protocol – a resource for measuring the quality of MRI data	OP06
Rajan Kashyap	Neuroanatomic localization of priming effects for famous faces with latency-corrected event-related potentials	D01
Chao-Chun Chuang	A web based remote visualization architecture for big neuroimaging data	D02
Yuko Okamura-Oho	*Ex vivo* transcriptomic analysis on the web: a new platform of ViBrism DB for gene expression mapping and analysis	D03
Roman Mouček	Advances in Building Infrastructure for Electrophysiology Research	D04
Makoto Takemiya	The BrainLiner platform for exploring time-aligned neurophysiological data	D05
Petra Ritter	TVB-EduPack – an interactive learning and scripting platform for the virtual brain	D06
Yoko Yamaguchi	Integrative development of multidisciplinary neuroinformatics platforms in Japan node	D07
Adrian Stoewer	Integrating data storage and annotation in the data workflow using the NIX format and libraries	D08
Hidetoshi Ikeno	Development of an on-line simulation platform for neuroscience research	D09
Zeeshan Ahmed	Lipid-pro: a bioinformatics tool for rapid identification of lipids in pre-processed DIA data	D10
Yoko Morii	Neuroinformatics Platform for Data Sharing and Global Collaboration in the Brain/MINDS Project	D11
Zeeshan Ahmed	GenomeVX: bioinformatics solution towards understanding the genome-wide comparative analyses of different human populations	D12
Mayu Ichiki	Simultaneous recording of EEGs and eye-tracking for investigating situation awareness and working memory load in distracted driving: a prospective analysis toward the neuro-driving framework	P01
Prasun K. Roy	MRI-analysis of neurodevelopmental inversion of allocortex for fast screening of seizure patients: a clinical informatics approach	P02
Georgia Theocharopoulou	Modeling protein interactions in neurodegenerative disorders using automata	P03
Heewon Park	Realistic neural circuit simulation of the moth antennal lobe that recognizes relative pheromonal concentration	P04
Petra Ritter	Constructing subject-specific virtual brains from multimodal neuroimaging data	P05
Masato Gosui	Realtime simulation of memory consolidation in a large-scale cerebellar model	P06

KEYNOTES

Teiichi Furuichi
Thomas Lippert
Arthur Lowery
John Reynolds

The molecular mechanisms of brain development and disorders

Teiichi Furuichi

Tokyo University of Science
Tokyo, Japan

Teiichi Furuichi is a Professor in Molecular Neuroscience in the Department of Applied Biological Science at the Tokyo University of Science in Japan. He graduated from Shinshu University, did doctoral studies in microbial development and genetics at the State University of New York at Stony Brook and received his Ph.D. from the Tokyo Metropolitan University in 1986. He joined the faculty staff at the National Institute for Basic Biology (Research Associate in 1989) and the Institute of Medical Science, University of Tokyo (Associate Professor in 1992) to study molecular and developmental neuroscience focusing on the IP3 receptor-mediated intracellular Ca^{2+} signaling. He became a Team Leader at the RIKEN Brain Science Institute and started a project of systematizing the transcriptomic basis underlying the postnatal development of mouse cerebellum in 1999. His group released the Cerebellar Development Transcriptome Database (CDT-DB), one of the publicly-accessible database platforms supported by the Japan Node of the INCF, in 2005. His current research interests are in (1) studying the molecular mechanisms of brain development and its disorders and (2) attempting to systematize the transcriptomic basis underlying the development, function, and dysfunction stages and states of the brain. He now acts as the project leader of the Brain Transcriptome Database (BrainTx) (http://www.cdtdb.neuroinf.jp), formerly the CDT-DB.

Talk abstract: The brain is a complex structure and its basic design is attributable to the controlled expression of thousands of specific genes in time and space. We aim to create an integrated database platform BrainTx (formerly CDT-DB) for visualizing and analyzing the transcriptome that underlie the various stages and states of the mammalian brain. Abnormalities in gene expression patterns are thought to affect normal brain development and behaviors. The involvement of multiple-genetic factors in the risk of autism-spectrum disorder (ASD), a neurodevelopmental disorder, is strongly indicated besides possible association with environmental factors. In combination with the information on genome-wide association studies of ASD, the transcriptome database is expected to provide a foundation for mining and analyzing ASD-associated gene candidates. In this presentation, I will talk about our brain transcriptome database project and mouse models with ASD-associated mutations.

Creating the HPC and Data Analytics Infrastructure for the Human Brain Project

Thomas Lippert

Forschungzentrum Jülich/University of Wuppertal
Jülich,Germany

Bio sketch: Thomas Lippert has received his diploma in physics in 1987 with a study on supersymmetry from the University of Würzburg, Germany. He has completed doctoral theses at Wuppertal University, Germany, on simulations of lattice quantum chromodynamics in 1992, and at Groningen University, The Netherlands, on massively parallel computing with systolic algorithms in 1998. Thomas Lippert is director of the Institute for Advanced Simulation and head of the Jülich Supercomputing Centre at Forschungszentrum Jülich, were he has created a simulation and data support laboratory for neuroscience together with colleagues from the institute for medicine. He is spokesman of the Programme on Supercomputing & Big Data in the research field Key Technologies of the German Helmholtz Association. He acts as executive director of the John von Neumann Institute for Computing (NIC) and he is chair of the German Gauss Centre for Supercomputing (GCS); both institutions are responsible for the national provision of computer time in Germany. On the European level he is director of the HPC platform within the human brain flagship project (HBP), he coordinates the series of Europe-funded implementation projects for the Partnership for Advanced Computing in Europe (PRACE) as well as the exascale hardware projects DEEP and DEEP-ER. Thomas Lippert holds the chair for Computational Theoretical Physics at the University of Wuppertal. His research interests include high precision simulations of quark properties, gravitational anomalies in galaxies and beyond, numerical and parallel algorithms, cluster computing hardware and software, and quantum information processing.

Talk abstract: HBP, the human brain project, is one of two European flagship projects foreseen to run for 10 years. The HBP aims at creating an open neuroscience driven infrastructure for simulation and big data aided modelling and research with a credible user program. The goal of the HBP is to progressively understand structure and functionality of the human brain, strongly based on a reverse engineering philosophy. In addition, it aims at advancements in digital computing by means of brain inspired algorithms with the potential to create completely novel analogue computing technology called neuromorphic computing. The HBP simulation and data analytics infrastructure will be based on a federation of supercomputer and data centers contributing to specific requirements of neuroscience in a complementary manner. It will encompass a variety of simulation services and data analytics services ranging from the molecular level towards synaptic and neuronal levels up to cognitive and robotic models. The major challenge is that HBP research will require exascale capabilities for computing, data integration and data analytics. Mastering these challenges amounts to a huge interdisciplinary software and hardware co-design effort

including neuroscientists, physicists, mathematicians, and computer scientists on an international scale. The HBP is a long-term endeavor and thus puts large emphasis on educational and training aspects. The maturity of a service is critical, and it is important to differentiate between an early prototype, the development phase, and the delivery of services, in order to assess capability levels. The services and infrastructures of the HBP will successively include more European partners, in particular PRACE sites and EUDAT data services, and will be made available step by step to the neuroscience and computer science community.

Monash Vision Group's Cortical Bionic Eye System: a wireless cortical stimulator

Arthur Lowery

Monash University
Clayton, Australia

Arthur Lowery is an electrical engineer with a long interest in systems engineering – specifically, the interaction of known sub-systems to produce highly complex phenomena. For the last 6 years, I have led Monash Vision Group from its inception through to preclinical trials of the full system. This has given me great insight into leading a multidisciplinary team, and focusing researchers on biomedical product development and verification.

I undertook my undergraduate studies in 1980 in Applied Physics and Electronics at Durham University, UK, and was also a Design Engineer at Racal Research in military communications systems. I moved to Marconi Radar Systems, then was appointed a Lecturer at Nottingham University. I developed computationally efficient models of semiconductor lasers, based on transmission-line models (of Johns and Beurle). In 1990 I moved to Melbourne University and worked in the Photonics Research Laboratory. Amongst other things, I developed a commercial product for simulating complex photonic systems, based on representing photonic components as icons on a computer – this gave designers great flexibility in trying out (simulating) different arrangements of fundamental building blocks. Phil Gurney and I, founded Virtual Photonics, which became the leading supplier of design tools for optical communications systems. In 2004 I joined Monash University as a professor, working on optical communications system, as I still do as a 2013 ARC Laureate Fellow and Science Leader of the CUDOS Centre of Excellence. In 2010 I applied my experience of systems design to proposing a cortical bionic eye, and this was funded to the tune of $10M as part of an ARC Special Research Initiative (SRI) in Bionic Vision technologies. This is now funded by generous benefactors, and has reached the stage of manufacturing and testing devices for First in Human trials. More recently, I am also working in the CIBF as a CI, with the aim of incorporating my systems engineering experience to brain-machine interfaces and also numerical modelling.

Talk abstract: Monash Vision Group– comprising Monash University, MiniFAB, The Alfred hospital and Grey Innovation – MVG is developing a visual prosthesis based on a cortical implant. A cortical implant provides high-acuity vision because a large area of the visual cortex is dedicated to foveal vision. It also bypasses the optical system, eyeball and optic nerve. Thus it is suitable who have lost their sight through traumatic injury, as well as disease in the eyeball or optic nerve.

The implant itself is 7-11 autonomous tiles, each with a wireless receiver, 500,000-transistor mixed signal chip, and 43 active electrodes. The implant tiles are fed with power and data

from a common transmitter. Sophisticated signal processing algorithms use information from multiple sensors to provide maximum utility for the user.

This presentation will cover the first five-years of this project. I will address the design choices that have been made in the initial stages of the project, and the challenges in manufacturing and testing the implanted tiles and system as a whole. I will address the multiple skill-sets required to design and test the device and the make-up of our 60-strong team. I will also address the possibilities of using these technologies, and our experience, to produce bidirectional interfaces to the brain.

This work is supported by the Australian Research Council's Special Research Initiative in Bionic Vision and Sciences (SRI 1000006), Monash University and pubic benefactors.

Dopamine and learning mechanisms in the basal ganglia

John Reynolds

University of Otago Medical School
Dunedin, New Zealand

Bio sketch: John Reynolds is an Associate Professor in Neuroscience in the Department of Anatomy at University of Otago in New Zealand. His research team studies the application of neuroplasticity approaches to Parkinson's disease and stroke. His interest is in understanding the natural conjunction and timing of neurmodulator signals underlying synaptic plasticity in affected brain areas. John graduated in Medicine in 1994, and then returned to University of Otago after a few years in practice to undertake PhD studies. He has received an international Brain Research Young Investigator Award and a National Tertiary Teaching Award, and he currently holds a Rutherford Discovery Fellowship from the Royal Society of NZ. He chairs the Scientific Advisory Committee of the Neurological Foundation of NZ.

Talk abstract: Organisms with multifunctional capability but limited motor resources must decide which competing action will be best to perform in any given situation, to maximize the likelihood of a positive outcome and minimise negative consequences. This requires a brain system specialized to solve the problem of selection, ie. capable of deciding which functional system should be allowed access at any given time to the machinery driving behavioural output. The re-entrant loop architecture connecting the basal ganglia subcortical nuclei to external brain structures such as cortex and thalamus can be viewed as an ideal substrate providing a solution to this problem. A major control point within these loops is the synapses between the cortex and the major input structure of the basal ganglia, the striatum. Efficacy of these corticostriatal synapses can be modified via a three-factor learning rule, involving the interaction between cortical inputs influencing the firing of striatal neurons, and phasic activity in midbrain dopamine systems reporting the presence of salient events. Thus the basal ganglia can be viewed as a selection system with an integral reinforcement learning mechanism, biasing the system towards specific behavioural outcomes based on prior experience. In this talk, I will review the basic structure of the selection machinery of the basal ganglia, and the rules for synaptic plasticity within the striatum as they might relate to reinforcement learning. I will present *in vivo* data from our laboratory that is pointing to a critical timing requirement for dopamine in corticostriatal synaptic plasticity and links dopamine reinforcement on a second by second timescale with the millisecond sensitivity of spike-timing dependent plasticity.

Workshops

1: Small scale brain initiatives

2: Large scale brain initiatives

3: Neuromorphic computing and challenges

Workshop 1: Small scale brain initiatives

Chair: **Romain Brette**

In recent years, considerable efforts have been devoted to the development of large scale measurements of entire mammalian brains, in the hope that they would provide decisive insights into brain function. Yet connectomes have already been obtained in smaller circuits, including the entire nervous system of C. Elegans, and their relation to circuit function has turned out to be not straightforward. In this workshop, we will discuss some of these attempts to understand the function of small nervous systems, and what we have learned about the relation between structure and function.

Speakers:

Vladimir Brezina
Mount Sinai School of Medicine, New York, United States
Ann-Shyn Chiang
National Tsing Hua University, Hsinchu City, Taiwan
Paul S. Katz
Georgia State University, Atlanta, GA, United States

Making the connectome work: Lessons from simple systems

Vladimir Brezina
Mount Sinai School of Medicine, New York, United States

Bio sketch: Vladimir Brezina is an Associate Professor at the Mount Sinai School of Medicine. His research focuses on the central pattern generating and neuromuscular circuits that participate in various feeding behavior of the mollusc Aplysia. For example, their output is controlled, both centrally and in the periphery, by complex local networks of interacting neuromodulators. The experimentally advantageous Aplysia system permits the cellular effects of the modulators to be dissected, using such techniques as voltage and patch clamp, optical recordings of contractions of single muscle fibers, and intracellular calcium measurements. The effects can then be functionally reconstructed in the behavioral context in semi-intact and intact preparations, and understood conceptually with the use of realistic as well as more abstract mathematical modeling techniques. The goal is to understand not just the Aplysia system but to derive from it more general principles governing the operation of such control mechanisms in biological systems.

Talk abstract: Great progress is being made in mapping the neuronal wiring diagrams—the connectomes—of nervous systems. It is hoped by some researchers that once the full complement of the connections has been mapped, reassembling the connections in a model of the nervous system will allow the "emergent" properties of the nervous system to manifest themselves: the brain will simply work. Yet we already have connectomes mapped at the level of the individual neurons for some simple circuits, such as the crustacean stomatogastric ganglion, and even the complete connectome for one entire nervous system, that of the nematode worm Caenorhabditis elegans, and from none of these connectomes has the function of the brain simply emerged. These simple systems have enabled analysis of this failure. I will discuss in particular one cause of the failure. In these simple systems, it has become clear that the static connectome is dynamically modified and supplemented by multiple actions of neuromodulators—neurotransmitters, neuropeptides, diffusible gaseous messengers—that can be so complex that they can be thought of as constituting a biochemical network that combines with the neuronal network of the connectome to perform the computations of the nervous system. Thus the connectome alone is not sufficient to specify, and permit us to understand, the computations that underlie behavior. In my presentation I will discuss this and other lessons that simple systems offer for making more complex connectomes, including that of the human brain, work.

Neuroinformatics of the Fly Brain

Ann-Shyn Chiang
National Tsing Hua University
Hsinchu City, Taiwan

Bio sketch: Ann-Shyn Chiang is one of Asia's most distinguished neurobiologists. Born in Taiwan (1958), graduated from National Chung-Hsing University (1981), received M.S. from National Taiwan University (1983), obtained Ph.D. (1990) and trained as a postdoctoral fellow (1992) in Rutgers University, Chiang joined Department of Life Science, National Tsing Hua University as an associate professor (1992), promoted as professor (1997), took sabbatical to study Drosophila memory at Cold Spring Harbor Laboratory (2001) and became the adjunct International Faculty of Kavli Institute for Brain and Mind (KIBM) at the University of California, San Diego (2011). For his outstanding contribution to our understanding of memory formation using a connectomics approach, Chiang has received many awards, including: Outstanding Research Award, National Science Council (2004, 2009, 2012), Outstanding Scholar Award, Foundation for the Advancement of Outstanding Scholarship (2007), Academic Award of Ministry of Education (2007), Outstanding Contributions in Science and Technology of Executive Yuan (2008), and TWAS Prize in Biology (2012). Chiang is currently the Dean of College of Life Science, the Director of Brain Research Center, the Distinguished Chair Professor of National Tsing Hua University and the Academician of Academia Sinica.

Talk abstract: Animal behavior is governed by the activity of interconnected brain neurons. To understand how genes and circuits orchestrate complex behaviors in the fruit fly, we have previously generated a comprehensive brain wiring map containing specialized systems sketched by diversity of individual neurons. An open-access image database, named FlyCircuit, has been constructed for online data archiving, cell type inventory, browsing, searching, analysis, and 3D visualization of 16,000 single neurons in the standardized Drosophila brain [1,2]. Here, I announce the release of FlyCircuit 1.2 which has several new features: (1) added image data to 30,000 neurons; (2) assigned axon/dendrite polarity for each neuron; (3) created a sequence ID for each individual neuron by transforming 3D skeleton into 1D sequence for high throughput data mining; and (4) provide a novel image matching algorithm for searching genetic drivers containing specific target neurons [3]. I will also demonstrate how FlyCircuit helped us to study information flow [4] and memory formation [5] in the fly brain.

1. Chiang AS, Lin CY, Chuang CC, Chang HM, Hsieh CH, Yeh CW, Shih CT, Wu JJ, Wang GT, Chen YC, Wu CC, Chen GY, Ching YT, Lee PC, Lin CY, Lin HH, Wu CC, Hsu HW, Huang YA, Chen JY, Chiang HJ, Lu CF, Ni RF, Yeh CY, Hwang JK (2011) Three-dimensional reconstruction of brainwide wiring networks in Drosophila at single cell resolution. Curr Biol 21, 1-11.

2. Lin CY, Chuang CC, Hua TE, Chen CC, Dickson BJ, Greenspan RJ, Chiang AS (2013) A comprehensive wiring diagram of the protocerebral bridge for visual information processing in the Drosophila brain. Cell Rep 3, 1739-1753.
3. Shih CT, Sporns O, Yuan SL, Su TS, Lin YJ, Chuang CC , Wang TY, Lo CC, Greenspan RJ, Chiang AS (2015) Connectomics-based analysis of information flow in the Drosophila brain. Curr Biol (in press).
4. Lin HH, Chu LA, Fu TF, Dickson BJ, Chiang AS (2013) Parallel neural pathways mediate CO2 avoidance responses in Drosophila. Science 340, 1338-1341.
5. Chen CC, Wu JK, Lin HW, Pai TP, Fu TF, Wu CL, Tully T, Chiang AS (2012) Visualizing long-term memory formation in two neurons of the Drosophila brain. Science 335, 678–685.

Comparative neural circuitry in sea slugs; a multiplicity of mechanisms to produce species-specific behaviors

Paul S. Katz
Georgia State University, Atlanta, GA, United States

Dr. Katz is interested in understanding how neuronal circuits operate. He uses sea slugs (Mollusca, Gastropoda, Heterobranchia, Nudipleura) because they have fairly simple brains and simple behaviors. His lab determines the neural mechanisms for these behaviors at the cellular level. Furthermore, because there are many species with similar nervous systems, they can compare the neural circuits in these species to learn about the evolution of neural circuits and behavior. Individual animals exhibit variability in behavior and/or variability in circuit properties. It is important to understand the implications of these differences. Sea slugs offer a great opportunity for studying such inter-individual variability because the neurons in neural circuits are individually identifiable. So, one can examine how particular neurons and particular synapses differ between individuals. Furthermore, one can perturb those neurons and synapses to make them more or less similar to each other using techniques like dynamic clamp or expression of exogenous genes. A new direction in the lab involves using Next Generation RNA sequencing to determine all of the genes that are expressed in slug brains, the so-called transcriptome. This has been completed in six different species, allowing the researchers to determine differences and similarities in their genes and then to map those genes onto the neural circuits and the behavior.

Talk abstract: Gastropod molluscs, including sea slugs, have highly tractable nervous systems with large, identifiable neurons, allowing neural circuitry to be determined using pairwise intracellular microelectrode recordings. We have been investigating central pattern generator (CPG) circuitry underlying rhythmic swimming behaviors in six different species. The CPGs contain as few as four neurons in some species, allowing unparalleled control over each neuron in the circuit. Homologous neurons have been identified across species using neurochemical and neuroanatomical criteria. A limitation for identifying homologous neurons has been the paucity of molecular markers. New single-neuron transcriptomic methods promise to provide more markers and thus more readily allow homologous neurons to be identified. We found that species with homologous neurons that exhibit similar behaviors nonetheless used different neural mechanisms to produce the behaviors. This was explored by replacing synapses with computer-generated synapses using the Dynamic Clamp technique and rewiring the CPG of one species into that of another. In addition to synaptic connectivity differing across species, we found differences in neuromodulation, which account for some behavioral differences. Thus, even in these very small brains, there are important species-differences in the neural connectivity and modulation of that connectivity. Our results suggest that the swim CPGs evolved independently using homologous neurons in different configurations thus demonstrating that there are alternate ways to configure a CPG circuit.

Workshop 2: Large scale brain initiatives

Chair: **Sean Hill**

To come

Speakers:

Richard Frackowiak
EPFL , Lausanne, Switzerland
Walter Koroshetz
NIH, NINDS , Bethesda, MD, United States

What can modern informatics bring to an understanding of diseases of the brain?

Richard Frackowiak
EPFL , Lausanne, Switzerland

Bio sketch: Richard Frackowiak is a clinical neurologist who has spent his life researching the human brain with non-invasive brain imaging techniques. He is Professor and head of the Department of Clinical Neurosciences (DNC) at the Université de Lausanne (UNIL) and its Centre Hospitalier Universitaire Vaudois (CHUV). He also holds a titular professorship at the Ecole Polytechnique Fédérale de Lausanne (EPFL) and is a co-executive director responsible for "Future Medicine" in the EU's Flagship of Enterprise and Technology (FET) "The Human Brain Project". He is leading sub-project 8 (SP8), which is putting together the medical informatics infrastructure in the ramp-up phase. He is a pioneer of human brain imaging research, developing a number of techniques and applying them to the investigation of human brain structure and function relationships in health and disease. There is also a translational component to his research involving novel image classification techniques for studies in individuals. His scientific output is highly cited with an h-index of 158 and he has received the Ipsen, Wilhelm Feldberg and Klaus Joachim Zulch prizes.

Talk abstract: We now know that a single human gene mutation may present with any of multiple phenotypes, and vice versa, that a range of genetic abnormalities may cause a single disease phenotype. These observations lead to the conclusion that a deeper understanding is needed of the way changes at one spatial or temporal level of brain organisation integrate and translate into others, eventually resulting in behaviour and cognition or their abnormalities. The traditional approach to determining disease nosology - eliciting symptoms and signs, creating clusters of like individuals and defining diseases primarily on those criteria has not generated fundamental breakthroughs in understanding sequences of pathophysiological mechanisms that produce the repertoire of psychiatric and neurological diseases.

It is time to radically overhaul our epistemological approach to such problems. We now know a great deal about brain structure and function. From genes, through functional protein expression the mechanisms are known in some detail. When it comes to cerebral microcircuits, to networks and to functionally specialised areas defined by physiological cell recording, microanatomy and human neuroimaging we have accumulated a mass of knowledge about the brain that so far defies easy integration and hence interpretation. Europe's Human Brain Project proposes a medical informatics platform that capitalises on modern advances in information technology, from supercomputers to distributed and interactive databases, allied to new mathematics and statistics, to federate and integrate existing and future clinical and neuroscientific data for a more biologically based, mechanistic approach to brain disorders. The implications for drug discovery range from more accurate, biologically supported diagnostics, new ways of identifying treatment targets, a priori profiling of primary and secondary effects of potential therapies in silico, a rethink about drug trial methodology and a route towards precision and personalised medicine.

The NIH Brain Iniative: computing from action potentials to behavior

Walter Koroshetz
NIH, NINDS , Bethesda, MD, United States

Bio sketch: Dr. Koroshetz became the Acting Director of NINDS in October, 2014. Previously, he served as Deputy Director of NINDS under Dr. Story Landis. Together, they directed program planning and budgeting, and oversaw the scientific and administrative functions of the Institute. He has held leadership roles in a number of NIH and NINDS programs including the NIH's BRAIN Initiative, the Traumatic Brain Injury Center collaborative effort between the NIH intramural program and the Uniformed Health Services University, and the multi-year work to develop and establish the NIH Office of Emergency Care Research to coordinate NIH emergency care research and research training.

Before joining NINDS, Dr. Koroshetz served as Vice Chair of the neurology service and Director of stroke and neurointensive care services at Massachusetts General Hospital (MGH). He was a professor of Neurology at Harvard Medical School (HMS) and led neurology resident training at MGH between 1990 and 2007. Over that same period, he co-directed the HMS Neurobiology of Disease Course with Drs. Edward Kravitz and Robert H Brown.

A native of Brooklyn, New York, Dr. Koroshetz graduated from Georgetown University and received his medical degree from the University of Chicago. He trained in internal medicine at the University of Chicago and Massachusetts General Hospital. Dr. Koroshetz trained in neurology at MGH, after which he did post-doctoral studies in cellular neurophysiology at MGH with Dr. David Corey, and later at the Harvard neurobiology department with Dr. Edward Furshpan, studying mechanisms of excitoxicity and neuroprotection. He joined the neurology staff, first in the Huntington's Disease (HD) unit, followed by the stroke and neurointensive care service. A major focus of his clinical research career was to develop measures in patients that reflect the underlying biology of their conditions. With the MGH team he discovered increased brain lactate in HD patients using MR spectroscopy. He helped the team to pioneer the use of diffusion/perfusion-weighted MR imaging and CT angiography/perfusion imaging and intra-arterial reperfusion therapy in acute stroke.

Active in the American Academy of Neurology (AAN), Dr. Koroshetz chaired the professional organization's Public Information Committee, led the AAN's efforts to establish acute stroke therapy in the US, founded the Stroke Systems Working Group, and was a member of the AAN Board of Directors.

Workshop 3: Neuromorphic computing and challenges

Chair: **Jeanette Hellgren-Kotaleski**

Future computing systems will capitalize on our increased understanding of the brain through the use of similar architectures and computational principles. During this workshop, we bring together recent developments in this rapidly developing field of neuromorphic computing systems, and also discuss challenges ahead.

In the neuromorphic systems field, emulation of neural systems is done using the implementation of neural elements in silicon. Typically, parallel analog and/or digital VLSI circuits are used; and the stochastic behavior of event driven communication between simple devices resembling neurons embedded in massively parallel and recursive network architectures is exploited. Such hardware systems, whose design is inspired by the brain, have the potential to create a paradigm shift in terms of energy efficiency, fault tolerance, adaptability as well as information processing capabilities.

For example, neuromorphic systems may in the future be able to mimic the capabilities of adaptive pattern recognition and motor control capabilities found in the vertebrate brain. Also, already today neuromorphic systems allow emulation and simulations of computational neural models in real time or faster.

Speakers:

Romain Brette
Vision Institute, Paris, France
Runchun Mark Wang
University of Western Sydney, Sydney, Australia
Giacomo Indiveri
University of Zurich/ETH Zurich, Zurich, Switzerland
Tadashi Yamazaki
The University of Electro-Communications, Tokyo, Japan

Brian for neuromorphic computing

Romain Brette
Vision Institute, Paris, France

Bio sketch: Romain Brette is a research director leading the Computational Neuroscience of Sensory Systems group in the Vision Institute (Paris, France). He is a nominated member of Institut Universitaire de France, and a laureate of the European Research Council. He is the co-editor of the Springer series in computational neuroscience, and a program board member of the OCNS and INCF. He has published about 50 peer-reviewed articles on single neuron models, sensory systems, psychology of perception, acoustics, neural simulation and electrophysiology techniques (including Neuron, eLife, PNAS, J Neurosci, PLoS Comp Biol). He is the co-author of the Brian simulator, the most popular spiking neural network simulator; and of one of the most popular simplified neuron models (the AdEx model). His main interests are neural excitability, spike-based computation, neural computation in ecological environments, auditory and visual perception, neural network simulation.

Talk abstract: Neuromorphic computing relies on tools to simulate neuron models on various platforms, including dedicated electronic devices. This diversity of simulation platforms is a challenge. To address this challenge, there is a trend towards the standardization of models. Here I will argue that neuron and plasticity models are likely to evolve quite drastically in the near future, and that standards face the risk of getting rapidly outdated. I will then expose the alternative strategy used in the Brian neural simulator, where models are defined directly by their mathematical equations and code is automatically generated for each specific target.

Neuromorphic Engineering: New computational paradigms inspired by the brain

Runchun Mark Wang
University of Western Sydney, Sydney, Australia

Biosketch: Runchun Mark Wang is a postdoctoral fellow at The MARCS Institute. Dr Wang's supervisor is Professor André van Schaik and his research field is Neuromorphic Engineering. The project he is working on is Hardware Acceleration for Neural Systems. As part of this project, Dr Wang will help build an electronic system, which includes both FPGA implementation and mixed/signal analogue VLSI, which is capable of simulating neural networks of a size similar to that of the human brain. Mark will provide open source software, so that other researchers can also use the system. His PhD topic was "Neuromorphic Implementations of Polychronous Spiking Neural Networks". The work includes the design of a polychronous spiking neural network using a novel delay-adaptation algorithm, an FPGA implementation of the proposed neural network, an analogue implementation of the proposed neural network, and their integration into a mixed-signal platform. Before Mark started his PhD study, he worked as a SoC/ASIC design engineer in industry. — See more at: http://marcs.uws.edu.au/people/mark-wang#sthash.fcWmOmAg.dpuf

Learning and plasticity in neuromorphic systems

Giacomo Indiveri
University of Zurich/ETH Zurich, Zurich, Switzerland

Bio sketch: Giacomo Indiveri is a Professor at the Faculty of Science of the University of Zurich, Switzerland. He obtained an M.Sc. degree in electrical engineering and a Ph.D. degree in computer science from the University of Genoa, Italy. Indiveri was a post-doctoral research fellow in the Division of Biology at Caltech and at the Institute of Neuroinformatics of the University of Zurich and ETH Zurich. In 2006 he attained the "habilitation" in Neuromorphic Engineering at the ETH Zurich Department of Information Technology and Electrical Engineering, and in 2011 he won an ERC Starting Grant on "Neuromorphic processors: event-based VLSI models of cortical circuits for brain-inspired computation". His research interests lie in the study of neural computation, with particular interest in spike-based learning and selective attention mechanisms, and in the hardware implementation of real-time sensory-motor systems using neuromorphic circuits and VLSI technology.

Talk abstract: For many practical tasks that involve real-time interactions with the environment, conventional computing systems cannot match the performance of biological ones. One of the reasons is that the architecture of nervous systems is very different from that of today's computers. Recently developed brain-inspired hardware architectures that emulate the biophysics of neurons and synapses in silicon represent a promising technology for implementing alternative low-power and compact computing paradigms.

In this presentation, I will present an overview of past and present neurocomputing approaches and propose hybrid analog/digital circuits that directly emulate the properties of neurons and synapses. I will show how they can be configured to implement real-time compact neural processing systems, describe hardware models of spiking neurons, synaptic dynamics, and synaptic plasticity mechanisms, and propose methods for synthesizing real-time neuromorphic cognitive systems.

Building a 1 mm³ cerebellar module on a computer

Tadashi Yamazaki
The University of Electro-Communications, Tokyo, Japan

Bio sketch: Tadashi Yamazaki is assistant professor of mathematical information science at the University of Electro-Communications (Tokyo, Japan) and a visiting research scientist at Neuroinformatics Japan Center, RIKEN Brain Science Institute. He received his Ph.D in computer science from Tokyo Institute of Technology. He subsequently was a research scientist at RIKEN Brain Science Institute. He is interested in theoretical and computational modeling of the cerebellum with the aid of modern numerical techniques and high-performance computing technology. His laboratory website is NumericalBrain.Org (http://numericalbrain.org/).

Talk abstract: The cerebellum is thought to form internal models, which simulate the dynamics of physical and/or mental objects, and assist the cerebral cortex for efficient information processing. The cerebellum has a very regular anatomical structure and contains numerous neurons with limited cell types. Neurons in the cerebellum elicit spikes spontaneously in much higher frequencies that those in the cerebral cortex. These properties echo a relationship between a central processing unit (CPU) and a graphics processing unit (GPU); if the cerebral cortex was a CPU, the cerebellum would be a GPU.

I have been developing a spiking network model of the cerebellum based on the known anatomy and physiology. The model is implemented on GPUs for realtime simulation, where realtime simulation means that a simulation of network dynamics in 1 sec completes within 1 sec in the real-world time. The latest version contains 1 million granule cells and is implemented on 2 NVIDIA GeForce TITAN Z boards that are equivalent to 4 TITAN boards, whereas in the old one, only 0.1 million cells were implemented on a single board. Thus, the latest version contains 10x more neurons, and the computer simulation still runs in realtime owing to the multi GPUs. I will explain how we use the multi GPUs for efficient numerical calculation. I will discuss potential applications in which the realtime computing is essential.

Neurons in our model are implemented as point models. On the other hand, neurons in the biological cerebellum have a variety of spatial structures. To elucidate how detailed spatial structures affect the network activity, we need to build a model composed of spatial model neurons. I will introduce our new project on simulation software for spatial model neurons and their networks designed primarily for GPUs.

Oral presentations abstracts

Topics:

OP - oral presentation

OP01 Standardizing metadata in brain imaging

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Introduction
In neuroimaging open data sharing is not a common practice [1]. While publishing a paper in many disciplines requires that data be made public, in human brain imaging there is no general agreement that data should be shared, and there is a lack of community standard for data sharing. However, the neuroimaging community increasingly recognizes that

sharing raw and processed data is critical for reproducible research, enabling meta-analyses and allowing for serendipitous discoveries. In light of this challenge, the Neuroimaging and Data Sharing Task Force (NIDASH-TF) formed by the International Neuroinformatics Coordinating Facility's (INCF) Program on Standards for Data Sharing [2] supports the development of standards and tools that will have a community-wide impact on the prevalence of neuroimaging data sharing. In this abstract we report on work to facilitate the sharing of neuroimaging metadata and analysis results.

Methods

The Neuroimaging Data Model Working Group (NIDM WG), a sub-group formed to design a metadata model for neuroimaging, holds weekly calls with participating members from the international community and organizes INCF-hosted yearly meetings. The NIDASH-TF wiki [2] is the primary resource for disseminating information and contains weekly minutes, publications, and links to products. NIDASH code is available in the GitHub repository (https://github.com/incf-nidash). The Google Group incf-datasharing [3] hosts an email list on data sharing issues, reaching out to a wider community. The NIDASH-TF meets several times a year to review progress on projects (e.g., [4]) that will make data sharing easier and fruitful for the scientific community.

Results and Discussion

The NIDM WG has developed DICOM [5, 6] and neuroimaging [6, 7] terminologies, and the Neuroimaging Data Model (NIDM) [7, 8]. NIDM is a neuroimaging-specific extension of the PROV Data Model (PROV-DM; [9]) to facilitate sharing of semantically meaningful neuroimaging provenance and derived data. Using these tools, we have developed novel applications to demonstrate federating data across relational databases and spreadsheets [10], visualizing FreeSurfer segmentations [11] across a large cohort [12], and modeling SPM and FSL statistical results [13], and have started to model results from AFNI. Further, we have developed detailed specifications of the core NIDM standard and "object models," specifying the recommended minimal set of entities, agents, and activities to describe datasets, workflows, and derived data. The SPM and FSL statistical analysis object model specifications [14] and examples are available online [15]. Under the auspices of NIDASH, Gorgolewski and colleagues have also developed a website for sharing raw statistical maps (NeuroVault.org) which uses NIDM [16]. The INCF task force meetings have encouraged adoption of these resources in various outside projects. We are linking this work with projects that are providing and hosting data, developing lexicons, and generating derived data for different purposes (e.g., data mining). The group includes developers and is in close contact with projects that plan to use these resources, or may do so in the future (e.g., Neurosynth, Neurovault, Brainspell), as well as with developers of integration platforms (e.g., NeuroDebian). Recently, we have worked with R. Poldrack and colleagues on the new version of the OpenfMRI specifications and will be describing this standard in the NIDM-experiment model [17].

Conclusion

The immediate goals of the NIDASH NIDM working group are to (1) refine existing terminologies and object models, (2) continue working with software developers to incorporate NIDM into their software, (3) create similar models for related tools such as multivariate models so that common aspects across software packages can be identified, and (4) facilitate broad and expanded use of the NIDM standard for data querying and data exchange, fostering applications such as meta-analyses. Standardization within communities is always challenging. The task force has adopted cultural practices of open source software development to carry out the specification of standards for brain imaging data sharing.

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OP02 Neural PhosphoSignaling database: a neuroinformatics platform for protein phosphorylation with quality control

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Protein phosphorylation is involved in the regulation of a wide variety of physiological processes in the nervous system. Thanks to recent developments in proteomics and genomics, it is predicted that the number of protein kinases and phosphorylated sites in human proteins amounts to approximately 500 and 650,000, respectively. On the other hand, little is known about which sites are phosphorylated by a specific kinase and which extracellular stimuli activate (or inhibit) the protein phosphorylation via intracellular signaling cascades. To uncover the basic issue, we developed a new methodology for comprehensive screening of the target phosphorylation sites of a given kinase using mass spectrometry, and succeeded in identifying hundreds of phosphorylation sites of representative kinases [1, 2]. The next step is to summarize the data systematically and extract biologically significant information. To this end, we developed a database system named Neural PhosphoSignaling Database in this study. The database system and its web portal were built based on XooNIps (http://xoonips.sourceforge.jp). As of April 2015, about 8,300 pairs of protein kinases and phosphorylated sites identified by our method, as well as about 4,000 pairs cited from the literature, have been registered in the database. All data are controlled for quality via review and curation by specialists. The web portal supports three modes of search: (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. Each protein (kinase/substrate) item is linked with external databases such as Uniprot KB (proteomics database), HGNC DB (human genomics database), HuGE Navigator (human genome epidemiology database), and Allen Brain Atlas, enabling us to easily predict unknown functions of the protein phosphorylation. As an advanced option, we also implemented a function to show a list of pathways in which the set of substrates phosphorylated by a specific condition is overrepresented more than expected, via communication with Reactome (http://www.reactome.org). As an application of this function, we demonstrate how to retrieve proteins and pathways in striatal medium-sized spiny neurons modulated by extracellular dopaminergic stimulation.

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OP03 Genetic sculpture of fine-grained human cortical regionalization

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Introduction
Mapping fine-grained, anatomically distinct, and functionally specialized cortical subregions is fundamental for understanding brain function. Various phenotypic features such as cytoarchitecture, topographic mapping, gyral/sulcal anatomy, and anatomical and functional connectivity have been used in human brain parcellation. Evidence has suggested that these phenotypes are under genetic control [1, 2]. However, whether genetic information can feasibly be used to identify fine-grained cortical subregions and reveal the genetic basis of cortical regionalization is unknown. Given that genetic factors play an important role in the process of brain development and cortical patterning, we hypothesized that the genetic mechanisms that underlie cortical segregation may be reflected by genetic correlations. These could account for the magnitude of the genetic covariation in brain anatomy at various cortical locations and be used to delineate functional boundaries in the cortex. To test our hypothesis, we used classical twin analysis to detect genetic correlations between various locations of the cortical surface area in a non-invasive manner.

Materials and Methods
Participants: Participants included a total of 222 healthy young Chinese same-sex twins from the Beijing Twin Study (BeTwiSt) of the Institute of Psychology, Chinese Academy of Sciences. The exclusion of an individual with incomplete scanning, an individual with excessive head motion, and their co-twins, resulted in 218 participants comprising 124 MZ (monozygotic) and 94 DZ (dizygotic) individuals (mean age, 19.0 years; range, 17-23 years; 62 male MZ, 62 female MZ, 48 male DZ, and 46 female DZ; all twins were complete twins). This study was approved by the Institutional Review Board of the Institute of Psychology of the Chinese Academy of Sciences and the Institutional Review Board of the Beijing MRI Centre for Brain Research.

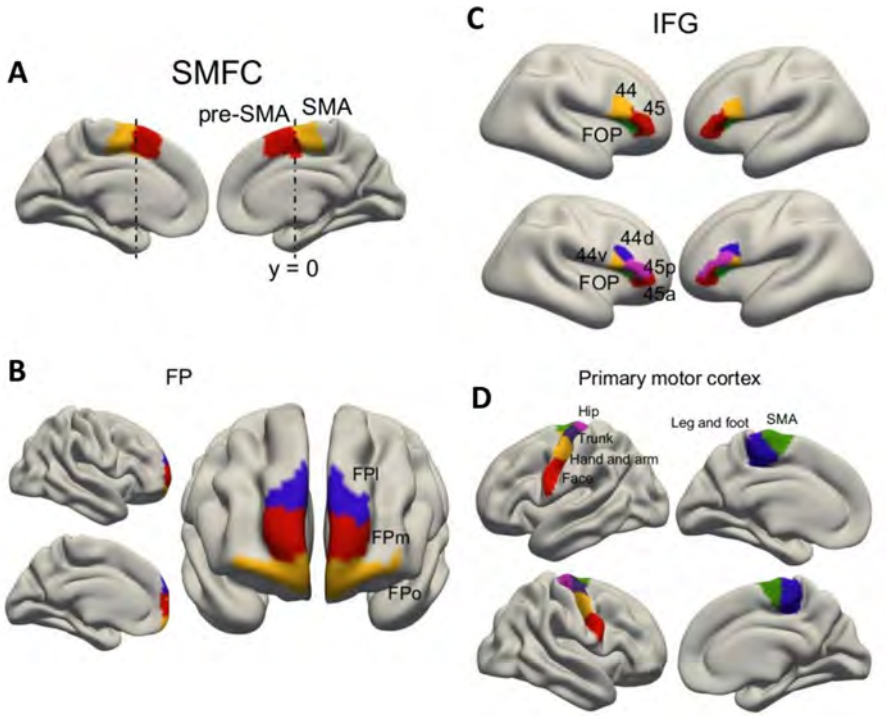
Image acquisition and processing: Images were acquired with a 3.0 T Siemens TrioTim scanner. The cortical surface reconstruction used the publicly available FreeSurfer software package, version 5.3.0 (http://surfer.nmr.mgh.harvard.edu/). The details of the processing techniques have been described elsewhere [3, 4]. Vertex-wise estimates of the surface area were calculated by assigning one-third of the area of each triangle to each of its vertices. We used 2819-iteration nearest-neighbor averaging to smooth the vertex-wise maps as previously investigated by Chen and colleagues [5].

Twin analysis: We used a bivariate model which can explain the sources of genetic and environmental covariance. Specifically, in addition to examining the genetic and environmental influences on the surface area at each vertex in the seed region, the bivariate correlated-factors model allows for estimates of the genetic (rg) and environmental (re) correlations between the surface areas at every pair of vertices. The analyses were performed using the OpenMx package. Before the model fitting, the vertex-wise surface area data were adjusted for age, sex and global effects.

Genetic correlation-based parcellation: A genetic correlation map was generated by pairwise correlations between the vertices within the seed regions. After obtaining a genetic correlation map, which consisted of the rg between the surface area measures of each pair of vertices, a spectral clustering algorithm was used for automatic clustering. Spectral clustering is an unsupervised machine learning algorithm that groups vertices which share similar genetic correlation profiles.

Results

Parcellation of the SMFC, FP, IFG and M1: Our genetically-based parcellation was performed on representative cortical regions with evolutionary and functional diversity: the superior medial frontal cortex (SMFC), frontal pole (FP), inferior frontal gyrus (IFG) and primary motor cortex (M1). In agreement with existing structural- and functional-based parcellations, we found that the genetic clustering of the SMFC showed anterior and posterior clusters that correspond to the pre-supplementary motor area (pre-SMA) and the SMA (Figure 1A). The genetic architecture of the SMA and pre-SMA is in line with cytoarchitectonic [6], anatomical [7], and functional [8] connectivity-based parcellations. In the case of the FP, we identified three separable subregions, FPo, FPm, and FPl, from the regional maps of the bilateral FP (Figure 1B) using the genetic correlations within the FP. The left and right FP subregions presented similar patterns, which were consistent with the maximum probability maps provided by connectivity-based parcellation with diffusion tensor imaging [9]. We also used a parcellation number of three in order to test the resemblance to the cytoarchitectonic division. The IFG can be divided into Brodmann's areas (BA) 44 and 45 and the frontal operculum (FOP) in a three-cluster solution (Figure 1C). Again, this finding was largely in accordance with classical cytoarchitectonics, with a boundary that aligned with the diagonal sulcus [10]. BA44 was subdivided into dorsal and ventral areas, 44d and 44v, and BA45 was subdivided into anterior and posterior areas, 45a and 45p, in the five-cluster solution, which corresponds to the subdivisions identified using transmitter receptor distribution data [11]. M1 was able to be subdivided into six subregions, five of which corresponded to motor representations of body parts: the face, hand and arm, trunk, hip, and leg and foot (from ventrolateral to dorsomedial). The single remaining subregion in the anterior medial part of M1 was the SMA (Figure 1D). This is in line with widely recognized topographic organization.



Conclusion

To the best of our knowledge, this is the first study to parcellate fine-scale, functionally distinct subregions non-invasively based on intrinsic genetic information obtained by twin analysis. Our findings suggest that genetic correlations are generally interpretable by existing phenotypic-based approaches, thereby having the potential to unravel population-based fundamental patterns of the cortex and of inter-regional connectivity. The present study is important for understanding the genetic basis of cortical regionalization and provides guidance and validation for the delineation of the next generation human brain atlas.

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OP04 The national consortium on alcohol and neurodevelopment in adolescence (NCANDA): a framework supporting neuroimaging data integration and analysis

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Introduction
Alcohol and marijuana remain the most commonly used central nervous system-active substances in the teen years [1]. The National Consortium on Alcohol and Neurodevelopment in Adolescence (NCANDA) is a multisite, longitudinal "Big Data" study using quantitative assessment tools necessary to capture the influence of adolescent alcohol and marijuana abuse on neurodevelopment. To accomplish its aims, NCANDA set out to recruit 830 participants, ranging from 12 to 22 years old, across five data collection sites nationwide. The NCANDA Data Analysis and Informatics Component (DAIC) facilitates electronic data capture, management, analysis, and distribution processes across five data collection sites. In [2], we described our data integration infrastructure for clinical and cognitive data that uses a distributed and version controlled approach to upload and harmonize multiple data sources (i.e., University of Pennsylvania Web-based Computerized Neurocognitive Battery (WebCNP) [3], LimeSurvey [4], Blaise [5], and ePrime [6]) to the Research Electronic Data Capture (REDCap) system. Since then, we have scaled up our approach by incorporating data and metadata from the eXtensible Neuroimaging Archive Toolkit (XNAT) with extensions to support automated data processing.

Dataset Description
Each data collection site carried out the same core assessment and sites worked in pairs to conduct additional studies (e.g., overnight sleep evaluation, recovery during monitored abstinence). The 831 study participants completed a core data acquisition protocol at baseline and will complete two annual followups including the neuropsychological (NP) test battery, neuroimaging session (MRI, DTI, and rsfMRI), a comprehensive assessment of substance use, psychiatric symptoms and diagnoses, and functioning in major life domains. In addition, a mid year phone interview is conducted between each visit to track substance use. The NP test battery assesses seven major functional domains including: general intelligence; executive functions; emotion regulation; multimodal and multiple component mnemonic processes; visuospatial abilities; basic visual acuity and color perception; and motor skills of eye-hand coordination, speed, and postural stability. Bio-samples for genetic analysis are collected annually. One parent of each youth completes an annual interview on the youth and family environment. Upon completing data collection, the dataset is expected to reach approximately 6TB of primary data and nearly 20TB of derived data from neuroimaging analyses.

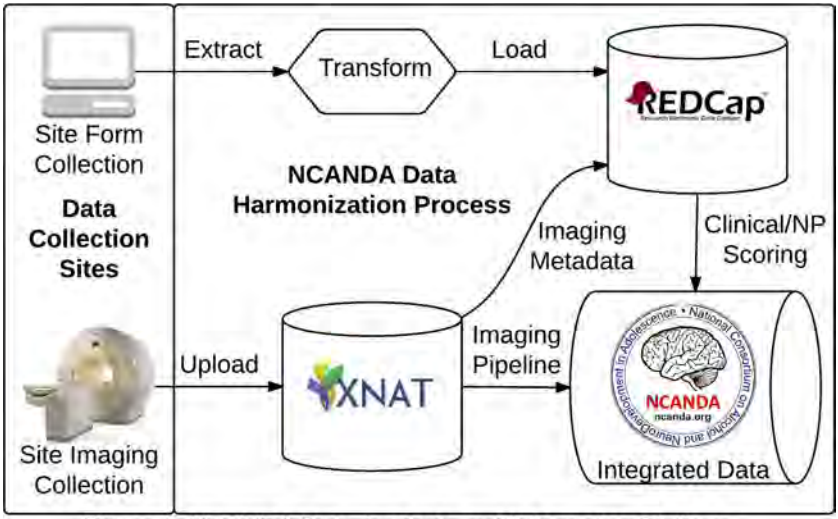

Figure 1. NCANDA Data Analysis and Informatics Platform

Data Analysis and Informatics Platform

We developed a platform to automate data harmonization processes for clinical, NP tests, and brain image measures for the NCANDA study (Figure 1). All data collected using electronic data capture were automatically merged into a REDCap server hosted by the NCANDA DAIC. Data items captured on laptops at each site, rather than being directly entered into REDCap, were automatically extracted, transformed into a compliant format, and loaded into REDCap from a secure and encrypted Subversion [8] version control system. Imaging data was first uploaded from the site specific Picture Archiving and Communication Systems (PACS) to a XNAT server hosted by the NCANDA DAIC. All data were evaluated with quality control checks that included automatic test scoring, range validation, and a neuroradiologist report for incidental imaging findings. Finally, quality control processed imaging and corresponding non-imaging data for each session were harmonized within a single REDCap project to generate data integrity reports on a biweekly basis. Identified issues were resolved with site consultation for scoring irregularities, mistyped IDs, visit dates, and any data that were not been uploaded properly [2]. Data for all future manuscripts published by the consortium will be based on quality reviewed, versioned data releases provided by the NCANDA DAIC.

Conclusions and Future Work

Heterogeneous data models and semantics are inherent to complex study protocols that capture rich neuroimaging and neuropsychological measures. The diversity of data

collected by these studies requires biomedical data management and electronic data capture systems tailored to specific use-cases. For example, the successful operation of the NCANDA study required the development of a data integration system to merge multimodel data from different information systems (e.g., WebCNP, REDCap, XNAT). This is a suitable solution for use within the NCANDA consortium, but barriers remain for broader data reuse. Without a mapping to common data elements and terminologies, data sharing and integration with external resources is limited. Incorporating metadata standards in the design of these systems may streamline data integration processes and interoperability, facilitating submission to national data repositories and querying data across studies. An implementation of metadata standards is currently outside the scope of most medical imaging studies, such as NCANDA, which is a serious limitation to the longevity of collected data. Future work aims to address these shortcomings through adoption of community-driven data exchange standards, such as the Neuroimaging Data Model (NIDM [9]).

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OP05 Brain imaging data structure – a new standard for describing and organizing human neuroimaging data

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Introduction
Typically the output of a human neuroimaging experiment is a complex, heterogeneous and multidimensional dataset that can be arranged and described in many different ways. So far there is no consensus on how to organize and share raw data obtained in such experiments. For example, two researchers working in the same lab can choose to organize their data in different ways, causing confusion and potentially losing (meta)data. Previously proposed solutions to this problem involved flexible, but complicated, file formats [1] or use of specific databases (e.g., [2]); however, lack of technical expertise in many neuroimaging labs makes adoption of such solutions challenging. Simpler data organizations, such as the standard used in OpenfMRI.org [3], lack the flexibility needed to support a wide range of experimental designs and data types. Here we introduce a simple and easy-to-adopt way to organize neuroimaging and behavioral data that facilitates sharing both within and across labs.

Methods

Initial work on the standard began during a special meeting of the Neuroimaging Data Sharing Task Force (NIDASH) held at Stanford University in January 2015. Even though the group is committed to the long term support of semantic web standards such as the Neuroimaging Data Model (NIDM, [4]), participants acknowledged that there is a need for a simpler and more easily implemented standard for the organization of neuroimaging datasets. As a starting point, the group used the existing OpenfMRI data description standard, as it has already shown its scalability and practicality through wide adoption for many datasets. The process of drafting the specification took three more months and involved weekly telephone calls and consultations with members of the community experienced in handling different types of neuroimaging data.

Results and Discussion

Within neuroimaging laboratories, it is common for metadata (such as subject ID, scan type etc.) to be encoded in the filename and folder structure. When developing the Brain Imaging Data Structure (BIDS; https://goo.gl/BOLyWR) we wanted to preserve this feature to make the structure accessible to researchers with little software expertise. In essence, BIDS describes how data should be organized into files and folders. The folder hierarchy includes subject ID, session number, modality, and imaging data are stored in the compressed NIfTI format. Key/value metadata (such as repetition time or slice timing) is stored in a JSON file. The hierarchical structure facilitates one JSON file being sufficient to describe scanning parameters for all common sessions and/or all subjects. Tabular data (variables describing each subject, events during the scan) etc. are stored in Tab Separated Value (.tsv) files. The standard covers descriptions of task and resting-state fMRI data, structural data (including, but not limited to, quantitative T1 maps), field maps, and diffusion data. The BIDS standard aims at including everything that is necessary to analyze the data given a hypothesis and thus includes population variables (e.g., age, sex or questionnaire scores) and detailed timing of stimuli presented and responses recorded in the scanner. Although BIDS requires some types data to be described in a specific way, it also accommodates extensions. Additional files collected during experiments currently not covered by the standard can be added at any level of the hierarchy. We envision that this specification will evolve through feedback from the community providing consensus for describing data types. To improve adoption we have developed a validator (https://github.com/chrisfilo/bids-validator) that checks whether the data conforms with the BIDS specification. We hope that the validator will make it easier for new users to implement BIDS in their labs. We also hope that data analysis tools and online repositories will adopt BIDS as an input (tools and repositories) and output(repositories) data layout, enabling users to apply analysis pipelines that are being developed for data formatted according to the standard. For the time being, the standard describes the data and a rich collection of relevant variables. This is necessary, but not sufficient, to replicate an analysis. In the future we plan to add an extension to BIDS that will allow specifying hypotheses in the form of a relationship between measured variables and their transformations (e.g., "Does cortical thickness correlate with the square of age?").

This will allow automated analysis of the data. Future research will also involve developing a converter from BIDS to the upcoming semantic Web based NIDM-Experiment standard, linking data with provenance and ontological information.

Conclusion
We introduced a new standard based on a file-system hierarchy, with files containing key metadata, to describe data collected during human neuroimaging experiments. It aims to be simple and easy to adopt as a standard lab practice that would later facilitate sharing and archiving.

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OP06 The preprocessed connectomes project quality assessment protocol – a resource for measuring the quality of MRI data

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Background
Although several measures have been proposed for assessing the quality of structural and fMRI data, there is no clear guidance on which of the measures are the best indicators of quality, or on the ranges of values that constitute "good" or "bad" data. This is particularly problematic for resting state fMRI (R-fMRI) data, since there is no clear means for differentiating signal from noise. As a result, researchers are required to rely on painstaking visual inspection to assess data quality. But this approach consumes a lot of time and resources, is subjective, and is susceptible to inter-rater and test-retest variability. Additionally, it is possible that some defects are too subtle to be fully appreciated by visual inspection, yet are strong enough to degrade the accuracy of data processing algorithms or bias analysis results. Further, it is very difficult to visually assess the quality of data that has already been processed, such as that being shared through the Preprocessed Connectomes Project (PCP; http://preprocessed-connectomes-project.github.io/). To begin to address this problem, the PCP has assembled several of the quality metrics proposed in the literature to implement a Quality Assessment Protocol (QAP; http://preprocessed-connectomes-project.github.io/quality-assessment-protocol). The QAP includes measures for assessing the quality of both functional and structural MRI data. The quality of structural MRI data is assessed using contrast-to-noise ratio (CNR, [1]), entropy focus criterion (EFC, [2]), foreground-to-background energy ratio (FBER), voxel smoothness (FWHM, [3]), percentage of artifact voxels (QI1, [4]), and signal-to-noise ratio (SNR, [1]). The QAP includes methods to assess both the spatial and temporal quality of fMRI data. Spatial quality is assessed using EFC, FBER, and FWHM, in addition to ghost-to-signal ratio (GSR). Spatial quality metrics were calculated for functional data using the mean image. Temporal quality of functional data is assessed using the standardized root mean squared change in fMRI signal between volumes (DVARS; [5]), mean root mean square deviation (MeanFD, [6]), the percentage of voxels with

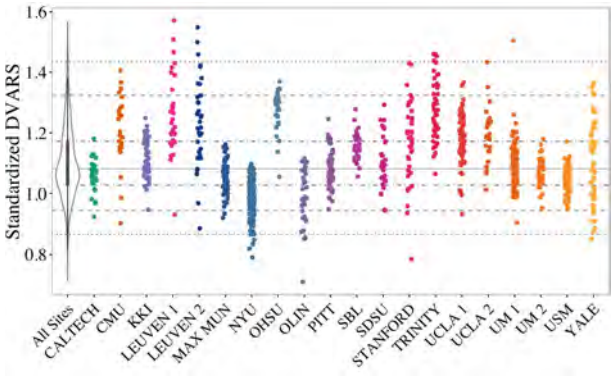
meanFD > 0.2 (Percent FD; [7]), the temporal mean of AFNI's 3dTqual metric (1 minus the Spearman correlation between each fMRI volume and the median volume; [8]) and the average fraction of outliers found in each volume using AFNI's 3dTout command. To build normative distributions of data quality we applied the QAP Python toolbox (https://github.com/preprocessed-connectomes-project/quality-assessment-protocol) to measure structural and temporal data quality on data from the Autism Brain Imaging Data Exchange (ABIDE, [9]) and the Consortium for Reliability and Reproducibility (CoRR, [10]). We further analyzed the properties of QAP measures, by analyzing the calculated measures to evaluate their collinearity, correspondence to expert-assigned quality labels, and test-retest reliability.

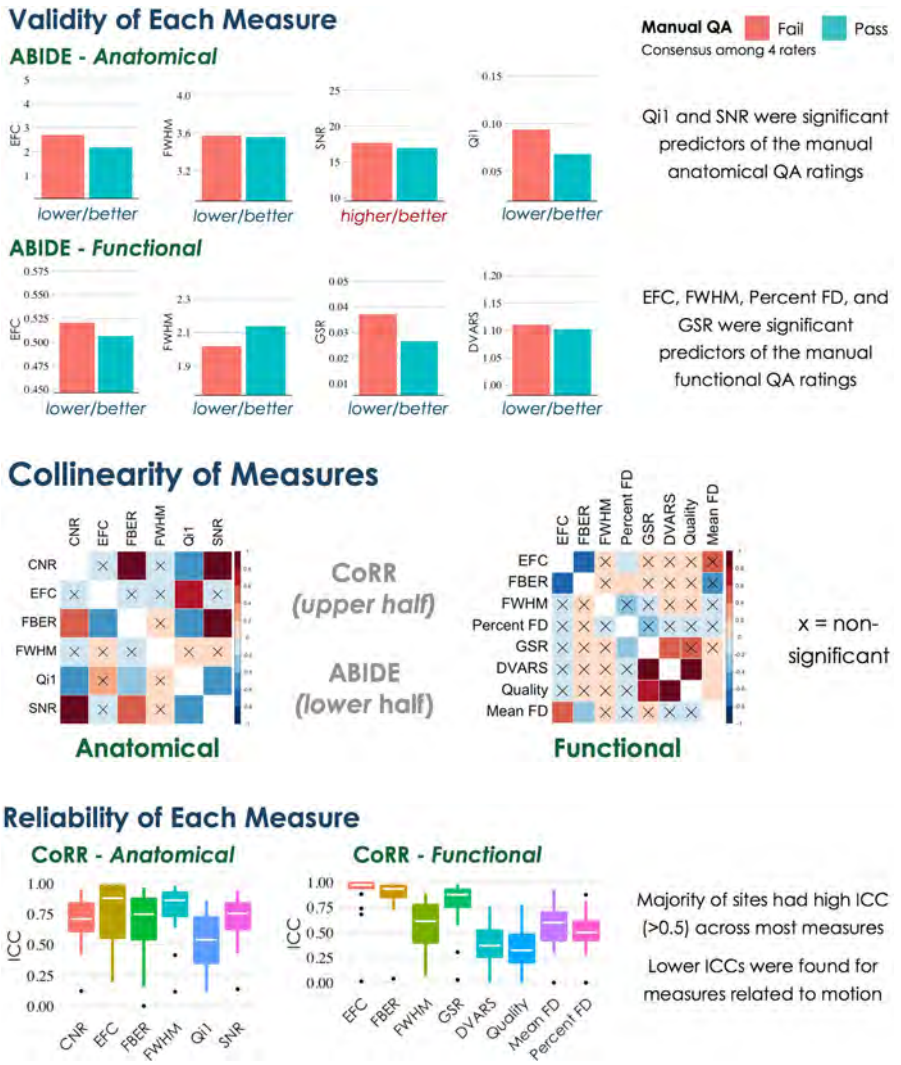
Methods

The QAP python toolbox was used to calculate spatial and temporal quality measures on the 1,113 structural and functional MRI datasets from the ABIDE dataset and the 3,357 structural and 5,094 functional scans from the CoRR dataset. For the ABIDE data, quality measures were compared to the quality scores determined from visual inspection by three expert raters to evaluate their predictive value. For both the ABIDE and CoRR datasets, the redundancy between quality measures was evaluated from their correlation matrix. Finally, the test-retest reliability of quality measures derived from CoRR was assessed using intraclass correlation.

Results

Each of the measures showed a good bit of variability between imaging sites (see Figure 1 for an example plot showing standardized DVARS for ABIDE). Ranks calculated from the weighted average of standardized quality metrics indicated that CMU was the worst performing site and NYU was the best. QI1 and SNR were the best predictors of manually applied structural data quality scores, and EFC, FWHM, Percent FD, and GSR were all significant predictors of functional data quality (Figure 2, $p < 0.0001$). A few of the measures are





highly correlated (Figure 3) such as SNR, CNR and FBER, which measure very similar constructs, indicated that there is some room for reducing the set of measures. For the functional data, the test-retest reliability of several of the spatial measures of quality were very high (Figure 4, EFC, FBER, GSR) reflecting their sensitivity to technical quality (i.e., MR system and parameters) whereas temporal measures were lower reflecting their sensitivity to

physiological factors such as head motion. Similarly in the structural data, it appears that measures can be divided into those that are more sensitive to technical quality (EFC, FWHM) and those that favor physiological variation (CNR, QI1) based on test-retest reliability.

Conclusion

We have assembled a diverse set of QA metrics for assessing the quality of R-fMRI data. The resulting Python toolbox was used to build distributions of the metrics for the ABIDE and CoRR datasets that can be used as a standard for comparing the quality of other datasets and eventually devising algorithms for automated QA. It appears as though test-retest reliability of the different measures can help distinguish those that are more sensitive to technical variation from those that are sensitive to physiology.

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Posters and demos stay up during the full meeting. Presentation of posters and demos is however divided into two sessions.

Poster session 1 (day 1): odd poster numbers
Poster session 2 (day 2): even poster numbers

Demo abstracts

Topics:

D01 Neuroanatomic localization of priming effects for famous faces with latency-corrected event-related potentials

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The late components of event-related brain potentials (ERP) pose a difficult problem in source localization; one of the reasons is due to smearing of these components in conventional averaging because of the trial-to-trial latency-variability. The smearing problem may be addressed by reconstruction of the ERP after latency synchronization with the Residue Iteration Decomposition (RIDE) method. Here we assessed whether the benefits of RIDE at the surface level might also improve source localization of RIDE-reconstructed ERPs (RERPs) measured in a face priming paradigm. Separate source models for conventionally averaged ERPs and RERPs were derived and sources were localized for both early and late components. Jackknife averaging on the data was used to reduce the residual variance during source localization compared to conventional source model fitting on individual subject data. Distances between corresponding sources of both ERP and RERP models were measured to check consistency in both source models. Sources for activity around P100, N170, early repetition effect (N250) and late repetition effect (N400) were reported. Priming effects in the sources were evaluated for 3 early and 3 late time windows. Significant improvement in priming effect was found from RERP source model, especially in the Medio-Temporal Lobe (MTL), Prefrontal Cortex (PFC) and the Anterior Temporal Lobe (ATL). Consistent with previous studies, we found early priming effects in right hemisphere and late effects in left hemisphere, indicating early processing of faces in the right hemisphere. Also, the priming effects in right hemisphere outnumbered the left hemisphere, signifying dominance of right hemisphere in face recognition. Improvement from RERP enhances the understanding of the role and the dynamics of sources in face recognition.

D02 A web based remote visualization architecture for big neuroimaging data

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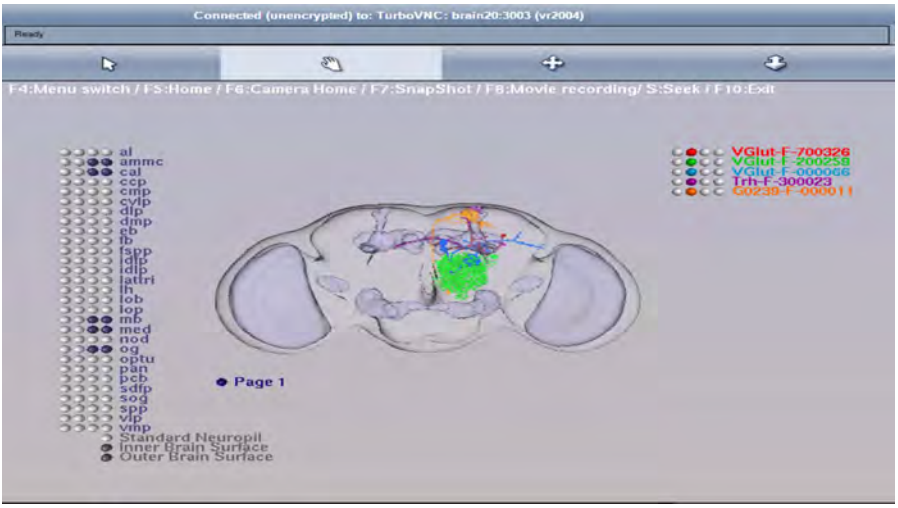
As recent neuroimaging research indicates, 3D visualization is helpful for understanding complex neuron structure. It also can help scientists share their visualization neuroimaging data and make their representation easier to understand [1, 2]. In most cases, scientists downloaded these big neuroimaging data and then visualized on a local desktop environments with 3D visualization tools. However, in recent years, higher resolution datasets in the neuroimaging research continue massive growth with higher experimental resolving power. It becomes inconvenient to download these big neuroimaging data without enough network bandwidth and difficult to display these images in user client without enough computer resources. Thus, we demo a web-based remote visualization architecture for these big neuroimaging data, and take FlyCircuit 3D viewer as an example. FlyCircuit 3D viewer uses advanced 3-layer web technologies, web server (WebSockets, Canvas), visualization server (VNC and VirtualGL) and user client (HTML5) for interactive online 3D surface, skeleton and volumetric neuroimaging data in any web browser environments without requiring any browser plugin [2–5]. The first layer, web server communicates with the second layer visualization server by WebSockets and Canvas. Then third layer user client can view 3D neuroimaging data from web page constructed by HTML5. Thus, with powerful visualization server, users can easily interactive the 3D visualization neuron imaging by web browser in a lightweight computer resource. Finally, this visualization architecture can



handle massive 3D neuronal image data collected in experiments from different research groups as well as manage bio-images with deeper neurological insight.

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D03 *Ex vivo* transcriptomic analysis on the web: a new platform of ViBrism DB for gene expression mapping and analysis

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Microtomy techniques for tomographic acquisition of thin-sliced material sections and their block-face images, followed by high-throughput measurements of gene expression densities in the materials, enable *ex vivo* transcriptomic analysis of intricate spatial expression patterns of wide varieties of RNA molecules in the whole anatomical context of any materials of interest, such as the brain and the embryos [1]. Using our microtomy technique, transcriptome tomography, we have created a database, ViBrism DB, in which measured expression densities are used for three dimensional (3D) expression map reconstruction and the maps can be superimposed on other voxel based images of the material [2]. Also the densities are directly used for co-expression analysis [3]. Here, we have launched a new platform of the DB for *ex vivo* transcriptomic analysis of mouse developing brains on the web. The platform is equipped with a WEB-GL based 3D viewer of expression maps overlaid on the MRI images and anatomical region maps. Also co-expression network graphs of genes of interest are created and can be viewed with the expression maps. We will demonstrate integrated analysis of anatomical maps and topological co-expression graphs in the developing brains on this web-based platform. All users of the microtomy technique can use this platform to upload their own data sets on the DB and view their maps and networks on the website.

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D04 Advances in Building Infrastructure for Electrophysiology Research

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Operation of electrophysiological laboratory, design and performance of electrophysiological experiments, collection, storage, management and sharing of experimental data and metadata, analysis and interpretation of these data/metadata, and final publication of results are time consuming activities. These activities need to be well organized and supported by a suitable infrastructure to increase work efficiency of researchers. Our group focuses on research of brain electrical activity using the methods and techniques of electroencephalography (EEG) and event related potentials (ERP). Except for experimental work (mostly been carried out on humans) our group develops and/or integrates a software and hardware infrastructure for electrophysiology research. This infrastructure includes the repository for managing experimental data and metadata, a library of methods and workflows for EEG/ERP signal data processing, a software tool for stimuli generation offering visual programming, a software tool for one-click control of stimulation and recording software, and hardware devices such as EEG caps/headbands using various technologies for recording electrodes, "active box" collecting and transmitting signals from various sensors, and stimulator for cognitive research. The parts of the infrastructure for which the most progress has been made in the last months are shortly described below. The central element of the whole infrastructure, EEG/ERP Portal (EEGBase), is a web-based portal that enables community researchers to store, manage, share, download and search data and metadata from electrophysiological experiments. The internal data and metadata model progressively reflects the outcomes of the INCF Task Force on standards for sharing of electrophysiology data, the NIX project of the German Neuroinformatics Node, and the outcomes of the group developing Ontology for describing Experimental Neurophysiology (OEN). Portal data are managed through several user interfaces; web and mobile user interfaces for human readers, a semantic web interface for automatic reasoners, and web services for third party tools. The data/metadata are provided in several formats/technologies (e.g., RDF/OWL, HDF5, original proprietary formats). The mobile version of EEGBase is a supplementary tool used for on-site metadata collecting and storing. The metadata are then synchronized with EEGBase using web services. Whereas measured subjects are in general different, a workflow for EEG/ERP signal processing is usually identical for the same protocol. To process and analyze large amounts of electrophysiological data automatically according to given workflows, Biosignal Processor is being developed. The hardware stimulator device for cognitive research is a universal portable ARM based Cortex

microcontroller providing a subset of often used software stimulation functions. It includes firmware and optional control software for creating various experiments in which the subject is stimulated by visual and/or auditory stimuli. It allows to change default presets or to program stimulation protocols during experiments to get desired responses. In the standalone mode the stimulator can be operated via touch screen display or used as a slave device connected via USB. By default, visual and simple audio stimuli for P300 experiments and VEP-based BCIs are supported. The device can also track reaction time separately or during stimulation. Stimulation outputs can be, e.g., simple LEDs, LED panels, patterns presented on small LCD displays, simple tones of various frequencies and lengths, or sounds. The stimulator is synchronized with recording devices and can be connected to conventional equipment.

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D05 The BrainLiner platform for exploring time-aligned neurophysiological data

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BrainLiner (http://brainliner.jp/) is a web-based platform for sharing and exploring time-aligned brain and behavioral data. Performing experiments and collecting data come with a large monetary and resource cost, thus it is an important responsibility to share data for both the advancement of science and the validation of results. Whereas contemporary database and repository sites ignore or treat behavioral and experimental task data with a lower priority than brain activity data, BrainLiner aims to enable sharing of data to support modern, data-driven neuroscience by treating both brain activity and behavioral data with equal salience. A unified data format that aligns brain activity and behavioral data on a time axis, enables analysis and ease of use. Once time-aligned, the brain and behavioral data can then be used for further analyses, such as neural decoding. The format also is built around HDF5, allowing it to be compatible across programming languages and computing environments, and uses well-defined schema such that all the properties describing data (e.g., recording modality, sampling rate, etc.) have specific meanings that are machine-readable. This lends itself towards automated analyses across large volumes of data. The standardized BrainLiner data format also enables BrainLiner to let users explore data from within the web browser. The BrainLiner Data Explorer allows users to preview data files within the browser, before investing their time to download the data and analyze it locally. The Data Explorer uses WebGL for fast viewing of high-resolution data in an interactive way. A data-driven similarity search is also integrated into the Data Explorer. For data files containing electrocorticography (ECoG) or electroencephalography (EEG) recording data, ECoG and EEG channels are split into time windows and the pairwise similarity all the time windows within a file are calculated based on correlations between spectral powers. Time windows that are highly correlated are marked as similar and stored in an index for quick retrieval. In this way, queries for similar time windows of data can be executed within a short amount of time, allowing users to explore similar time windows within the Data Explorer, just by clicking and dragging to enter queries. This can help users to find patterns within a data file and determine if they are interested in downloading the file to study it further.

D06 TVB-EduPack – an interactive learning and scripting platform for the virtual brain

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The Virtual Brain (TVB; thevirtualbrain.org) is a neuroinformatics platform for full brain network simulation based on individual anatomical connectivity data. In order to ease familiarization and to enable users to quickly start working with TVB, we developed our newly released educational module: TVB-EduPack [Matzke and Schirner (2015)] provides researchers from various backgrounds a quick start into TVB and brain network modeling. The possibility to create extendable educational content that is supported by animations, videos and textual descriptions addresses the demand for a flexible educational framework which can easily provide user group fitted interactive tutorials. In contrast to standard documentation, TVB-EduPack tutorials allow users to directly engage in complex modeling scenarios while using TVB. The educational component of TVB-EduPack comprises two different knowledge levels: (i) EduStart, an interactive introduction into the software TVB that makes the user familiar with the basic usability while guiding through concepts and methodologies in computational neuroscience and (ii) EduCase, which refers to advanced use cases in TVB, e.g., developing computational neuroscience methods further by leading the user through in-depth tutorials that exemplify typical applications like exploring dynamical regimes of different models or tuning parameters to reproduce specific types of neuronal activity. We show several use cases and demonstrate how autodidactic exercising of complex TVB simulation scenarios creates a pleasant user experience. Additionally, TVB-EduPack contains a graphical script creation tool that records GUI interactions and thereby allows users to create re-usable and modifiable batch scripts for the TVB console interface in order to automate or demonstrate their work. Like TVB, EduPack is an open source community project that lives from the participation and contribution of its users.

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D07 Integrative development of multidisciplinary neuroinformatics platforms in Japan node

Alexander Woodward[1], Ayumi Honda[1], Hideki Oka[1], Itsuko Ishii[1], Masahide Maeda[1], Sawako Suenaga[1], Shiro Usui[2,3], Takayuki Kannon[1], Tsutomu Hashikawa[1], Yoko Morii[1], Yoko Yamaguchi[1], Yoshihiro Okumura[1], Yui Isono[1]
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INCF Japan Node (J-Node) has developed 13 neuroinformatics platforms on topics of vision science, BMI, invertebrate brain, cerebellum function, neuro-imaging, cerebellar transcription, dynamical brain, comprehensive brain science, mouse phenotype, on-line simulation, brain science dictionary, transcriptome brain tomography and RIKEN BSI data and tool. In order to develop neuroinformatics beyond individual fields, J-Node is developing across platform activities. As one new platform, OpenNeuro is under construction to provide data repository for general users. Research data in any field/topics submitted to OpenNeuro is to be reviewed for open-in-public use by existing platform committees in various fields and then can be released from multiple platforms for various usage in various fields. In addition we have developed J-Node software center for software development and software catalogue in connection with various neuroinformatics platforms. As a next step for interdisciplinary data sharing, we will start across-species brain atlas project in collaboration with platform committee related with invertebrate, rodents and primate atlases. Based on the unified platform structure, J-Node looks forward to extending international collaboration of neuroscience as data science.

D08 Integrating data storage and annotation in the data workflow using the NIX format and libraries

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Increasing complexity of experimental approaches in neurosciences challenges methods for managing recorded data and metadata. Storing such information consistently is an essential part of experimental research and depends crucially on available file formats. Currently existing file formats are subject to several restrictions: some formats are vendor specific or only accessible via proprietary software. Others are highly domain specific, designed with respect to efficiency for certain kinds of data and therefore not versatile enough to be used in a wide variety of use cases. Moreover, many existing formats provide only limited support for storing metadata along with the data. A common, open file format that is versatile enough to represent various kinds of data in conjunction with metadata has the potential to increase community-based tool development as well as data sharing. The emergence of initiatives like the Electrophysiology Task Force of the INCF Data Sharing Program [1] or the NWB project [2] underlines the need for such a standardized and open file format. The NIX project [3] specifies such a format for neuroscientific data and provides libraries for accessing these files from different platforms. The NIX format is compliant with the INCF requirements for storing electrophysiology data [1]. It is based on a well defined data model [4] which can be used to represent both data and related metadata. In particular, it provides generic entities designed to store a wide variety of data types like continuous signals, spike events, image stacks, or other multi-dimensional data. Central feature is the representation of data arrays together with units and dimension descriptors, so that the stored data can be readily interpreted as recorded quantities. The data model further defines mechanisms to specify relationships between the data arrays and to describe points or regions of interest, such as areas in an image or events in a continuous signal, supporting direct access to the referenced part of the data and the linking of metadata. Based on the data model we defined a schema for HDF5 files [5] as default format. While it is possible to read and write these files using the standard HDF5 libraries, efficient use of the features of the NIX format is facilitated by specific I/O libraries provided for different languages. The C++ library [3] serves as reference implementation and basis for interfaces to other languages. Python bindings [6] provide access to the library functionality in pythonic fashion and a quick entry point to get familiar with the concepts of the format, including detailed documentation, many examples, and tutorials [7]. Matlab bindings [8] bring the benefits of the NIX features to users of this popular tool. In addition, Java bindings are under way. The NIX file format supports comprehensive annotation and efficient organization of neuroscience data, and the variety of libraries makes it easy to integrate access to data and metadata in the lab data collection and analysis workflow.

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D09 Development of an on-line simulation platform for neuroscience research

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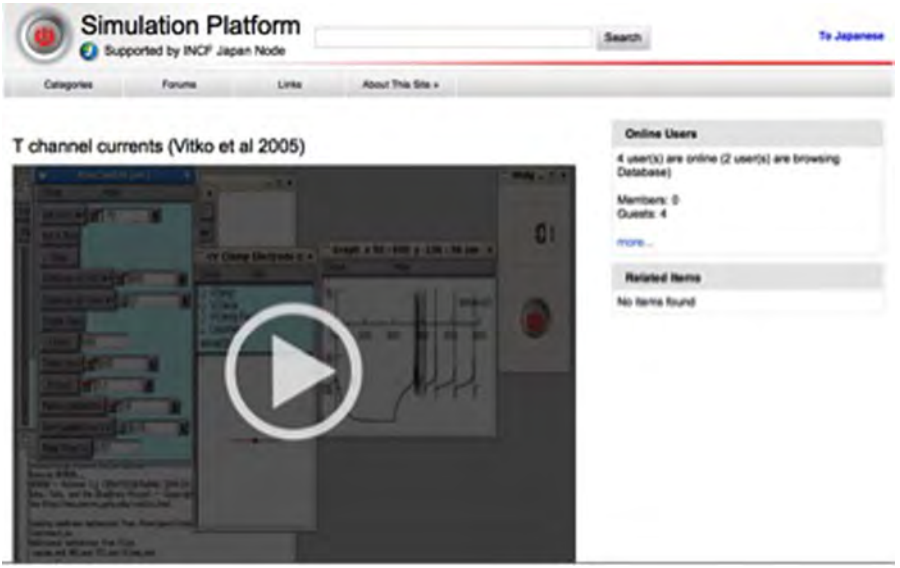
Various data analysis algorithms and computational models have been proposed and utilized in neuroscience. Especially, theoretical approach to the neuronal system is indispensable for further advance in neuroscience. Recently, a number of software packages for data analysis and simulation of computational models have been provided on the Internet, and many of them are becoming open-access for researchers. However, we should to prepare



the suitable computer environment where the numbers of software are installed for using these software resources. It will be sometimes caused problems by difference of operating system, version of software or lack of library files. In our project, we have been developing and providing a virtual machine environment for neuroscience research called Simulation Platform (Sim-PF, http://sim.neuroinf.jp) [1] to use computational model and programs on the Internet without any barrier. The virtual machine based Linux is started by user demand, then executed script for downloading model file and running it on the virtual machine (VM) automatically. The server system managing VM is developed by Guacamole 0.8.4 and OpenNebula 4.12. Now, we are setting up for providing VM with Microsoft Windows OS. It is providing standard application software in neuroscience research, such as Fiji, vaa3D for image processing and 3D viewing; NEURON and GENESIS are for neuronal simulation. The Sim-PF provides not only utilities for visualization and simulation, but also the high-speed access to the registered data for retrieving and using large amount of data. It lets users be free from preparing the environment to carry out simulation, and lets users immediately get started on simulations for reviewing and analyzing existing models as well as for reviewing newly presented models submitted for publications. Up to now we have been developing online simulation pages for ModelDB contents, and the most of models registered on the ModelDB can be run on the web browser without installing any simulation software. As some of ModelDB contents are developing on MATLAB, one wishes to use these contents have to buy MATLAB license even just for evaluation. However, in the Sim-PF, these contents are registered after pre-compiling by MATLAB compiler and executed them for evaluation very easily. The platforms running by NIJC (http://www.neuroinf.jp/) supply various kinds of contents, such as data analysis program and experimental data. We are developing new contents, which can easily review these valuable resources on our platform. As an example of collaboration contents with other platform, users can review reconstruction process and results of neuronal morphological structure from confocal image data registered on the invertebrate brain platform (IVB-PF) on the Sim-PF. Registration of neuron model into the standard brain can be understand by following our contents. The tutorial movies for supporting users and education of students are making and uploading onto the YouTube. These are used to conduct a tutorial for newly joined students to the laboratory. In this moment, these movies are developed only in Japanese, but we are translating and uploading in English near future. The Sim-PF will be improved their functions and contents for further support education and research in neuroscience fields.

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D10 Lipid-pro: a bioinformatics tool for rapid identification of lipids in pre-processed DIA data

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Mass spectra of lipid species in complex biological samples are a challenge to interpret since the lipid composition is specific to organism, tissue and cell. Additionally, thousands of lipid species are present in a biological sample and the number of lipid classes and the isomer are high and diverse. For their accurate identification different measured physico-chemical properties, such as accurate mass, fragmentation behaviour and a polarity, have to be considered in the pre-processed data.

Here, we present a recently proposed bioinformatics tool i.e., Lipid-Pro (1), a desktop application for the interpretation of LC-MS/MS data. It is a lipid identification solution towards

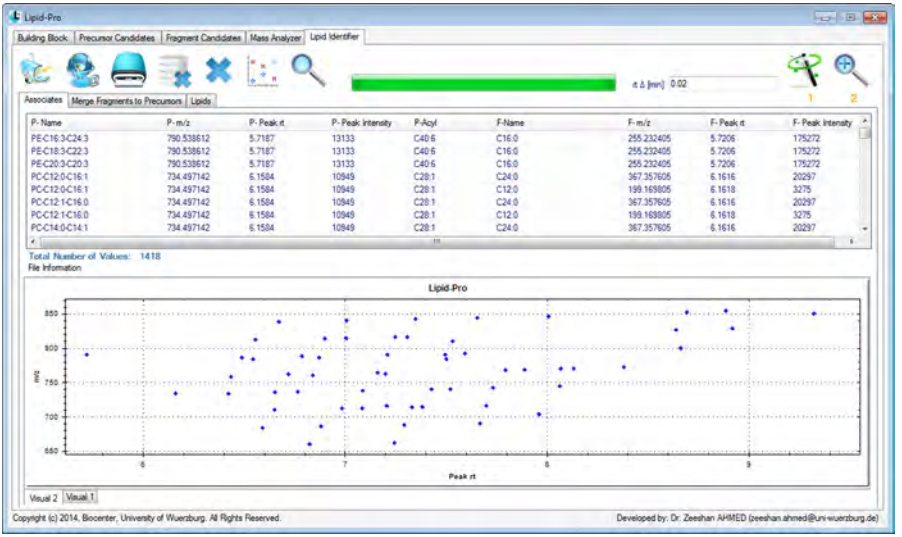

Figure 1. Lipid-pro graphical user interface.

the lipidome analysis, where defined lipid species are identified in the pre-processed data (lipid profiling). The graphical interface of the Lipid-Pro is very simple to install and use. It consists of five main modules: Building Bock, Precursor Candidates, Fragment Candidates, Mass Analyzer, and Lipid Identifier. Using these modules, user can define building blocks, compose lipid molecular ions and their fragments, calculate m/z-values of lipid molecular ions and their characteristic fragments, and identify lipid species. Moreover, it also provide comprehensive data management, sharing and integration features.

Lipid-Pro is a well-planned scientific solution, implementing the *Butterfly* paradigm (2, 3). Started with the initialization of the finalized scientific solution's requirements, then modelled and mocked using HCI guidelines. It is programmed in C# programming language, using Microsoft Dot Net Framework and only compatible to the Microsoft Windows Operating Systems (preferred OS version: 7). The most recent available version of Lipid-Pro has been tested and validated at the Metabolomics Core Unit and Department of Pharmaceutical Biology, University of Wuerzburg Germany. Lipid-Pro is a freely available tool for non-commercial, academic and scientific research, accessible at the following web link: (http://www.neurogenetics.biozentrum.uni-wuerzburg.de/en/project/services/lipidpro/).

Keywords: Bioinformatics, Lipid-Pro, Lipidomics, Mass spectra, Software

Acknowledgements
The authors would like to thank German Research Foundation (DFG SFB 1047 and TR34/Z1) for funding on this research. The authors thank to the University of Wuerzburg Germany, University of Massachusetts USA and The Jackson Laboratory USA for support in this publication. Authors also thank to all interested colleagues for critical input on the approach and anonymous reviewers for helpful comments.

Conflict of Interest
The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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D11 Neuroinformatics Platform for Data Sharing and Global Collaboration in the Brain/MINDS Project

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RIKEN, as a core institute of the 10-year (2014-2023) Brain Mapping by Integrated Neurotechnologies for Disease Studies (Brain/MINDS) project, has started constructing heterogeneous databases of the common marmoset non-human primate. The objective of this project involves gaining knowledge and insight into the diseases and functionalities of the common marmoset brain, including its ability for social communication, and their relevance to the human brain. The first goal is to construct structural and functional brain mapping across micro-, meso- and macroscopic levels by integrating heterogeneous big data of marmoset neural circuitry. To share this big data among research collaborators, we constructed an integrated neuroinformatics platform, SAKI, composed of GPFS 1.28PB storage and a VDI cloud and HPC for computational data analysis. We also developed the Biological Image Communication Cloud (BiCC) platform, which was based on the Image Communication Platform (IC) of Morita and Yokota (2014) and is now installed on SAKI. BiCC enables high performance registration, analysis and visualization of 3D/4D data. Currently, semi-automatic data registration and a 3D brain reference atlas of the common marmoset are available on SAKI. This neuroinformatics platform is designed to provide for data sharing and collaboration amongst people in the neuroscience, medical and engineering fields. By presenting SAKI, we would like to propose and discuss how to develop a state-of-the-art neuroinformatics infrastructure.

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D12 GenomeVX: bioinformatics solution towards understanding the genome-wide comparative analyses of different human populations

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We have proposed a new computational, Bioinformatics solution i.e. GenomeVX, towards the field of Genomics and Nucleic acid research. GenomeVX helps in understanding the Genome-wide comparative analyses of different human populations, as well as between species, focusing on the association studies relating genetic variation to disease with evidence of mutations. GenomeVX extracts data from the fields in VCF file [generated by the 1000 Genome Browser (1)] and displays alleles for the substitutions and variations (SNP).

The graphical interface of the GenomeVX is very simple to install and use. It is a desktop application which offers two integrated modules: VCF File Editor and VCF Extracted and Converted Information. Using these modules, user can load the VCF files in to the GenomeVX and can extract, parse and convert the nucleotides' complex respective numbers to the representative notations (e.g., ACTG). Furthermore, it helps the user to convert analysed data in to the Microsoft Excel Sheets for better analysis, statistical visualization and sharing. The overall workflow and wiring of the components of the GenomeVX is presented in Figure 1.

GenomeVX implementation follows the principles of our newly proposed software engineering paradigm i.e. *Butterfly* (2, 3). It is programmed in C# programming language, using Microsoft Visual Studio Dot Net Framework and only compatible to the Microsoft Windows Operating Systems (preferred OS version: 7). Most recent available version of the GenomeVX is in testing and in limited use, and we are focusing on the future research and development objectives by enhancing the its capabilities with more features.

The six steps installation process of GenomeVX is presented in the Figure 2 and it is freely available for any non-commercial, academic and scientific use at the following web link: (https://zenodo.org/record/13815?ln=en#.VOZSxC6ZNS0).

Keywords: Bioinformatics software, GenomeVX; Genome 1000 Browser, Genomics, Nucleic acid research

Acknowledgements
The authors would like to thank German Research Foundation (DFG SFB 1047 and TR34/Z1) for funding on this research. The authors thank to the University of Wuerzburg Germany, University of Massachusetts USA and The Jackson Laboratory USA for support in this

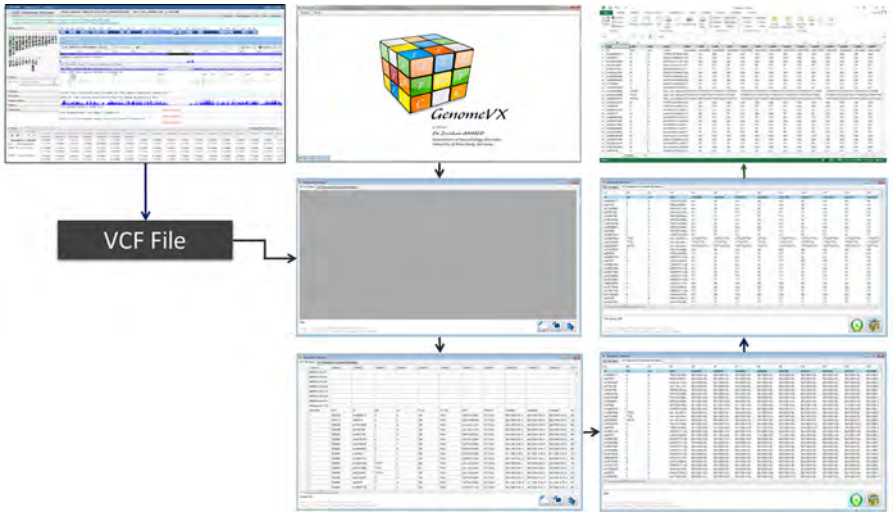

Figure 1. **GenomeVX' components and workflow.** The Figure 1 shows extracting of data from 1000 Genome Brower, wiring of components of the GenomeVX and conversion of output into the Microsoft Excel format.

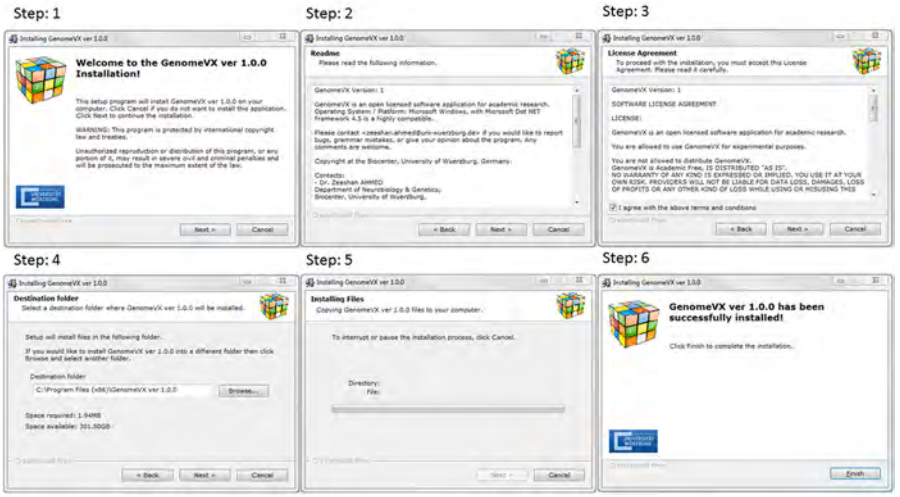

Figure 2. **GenomeVX installation process.** The Figure 2 presents six steps installation process of the GenomeVX.

publication. Authors also thank to all interested colleagues for critical input on the approach and anonymous reviewers for helpful comments.

Conflict of Interest
The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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Posters and demos stay up during the full meeting. Presentation of posters and demos is however divided into two sessions.

Poster session 1 (day 1): odd poster numbers
Poster session 2 (day 2): even poster numbers

Poster abstracts

Topics:

P01 Simultaneous recording of EEGs and eye-tracking for investigating situation awareness and working memory load in distracted driving: a prospective analysis toward the neuro-driving framework

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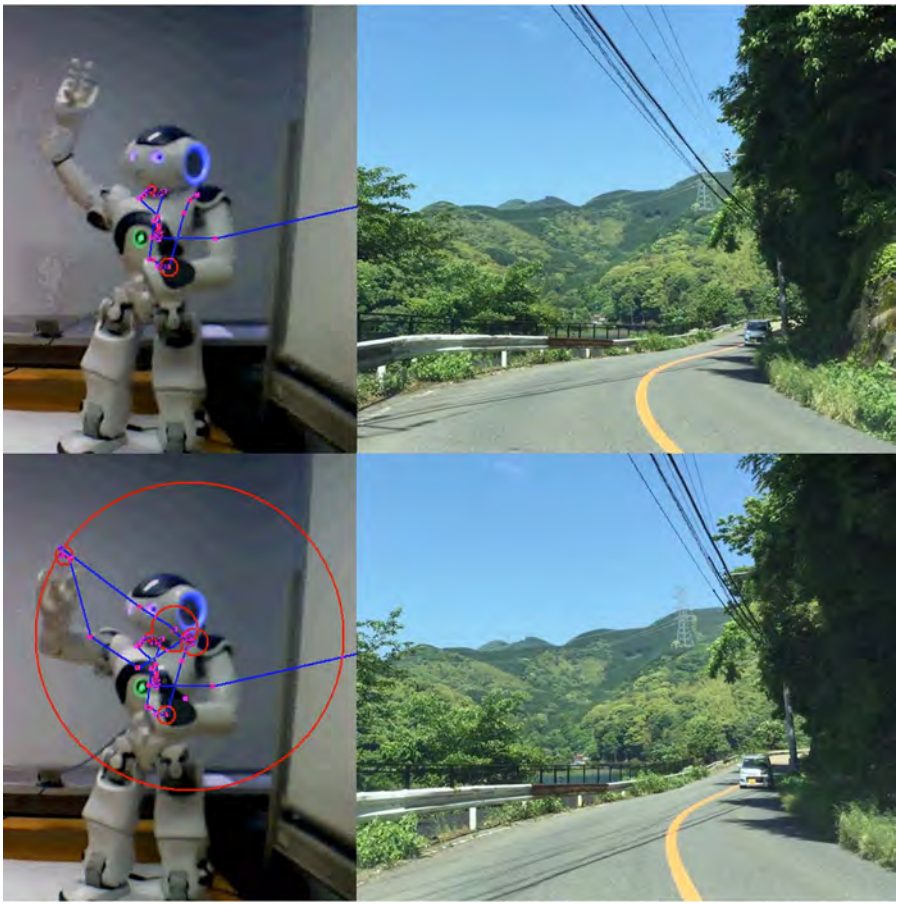
Automatic driving gains prominence not only in the automobile engineering field but also neuro-engineering research field [1, 2] to detect an abnormal brain activity for preventing serious accidents. Neuro-driving simulation frameworks were studied for the detection of



emergency situation based on ERP-related neural activity associated with emergency situations while driving [3]. In the first place, to progress such research activities, the common criterion to describe the level of driving risks is necessary for the risk assessment such as accident predictions and managements of driver's comfort levels, which is discussed as a safety zone boundary in the state space spanned by Driver-Vehicle-Environment (DVE) axes [4, 5]. The DVE state space represents three areas: the comfort zone to allow the driver the adaptive control, discomfort zone but still in the safely margin and the inevitable accident zone called lose the control [6]. In this study, we attempt to describe the DVE state space related to driver conditions (skill levels, attention controls, feelings, health status and so on) and environmental factors around the vehicle (the complexity of situations including risk levels, road and weather conditions, and so on) in a possible form of the database and car ontology [7]. In the second place, experimental framework is necessary to investigate in the dynamic environment while driving, by investigating the attention change and working memory capacity. We preliminary established the eye-tracking experiment during an interactive communication with the robot to instruct multiple sources of information, which aims to extend a test for working memory load in distracted driving (Figure 1). American Automobile Association (AAA) reports [8] that factors of distraction leading to a teen driver crash are interaction with other passengers (15%), cell phone usage (12%), looking at something in the vehicle (10%) and outside the vehicle (9%), singing/dancing to music (8%), personal grooming (6%) and reaching for an object (6%), and other distractions included eating/drinking, smoking, reading something such as a map and talking to oneself. A systematic approach to measure the attentional change and working memory capacity can be extended to analyses with a simultaneous recording of the eye-tracker and EEGs and it contributes to the establishment of the common evaluation method of social and driver competencies.

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P02 MRI-analysis of neurodevelopmental inversion of allocortex for fast screening of seizure patients: a clinical informatics approach

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Introduction
As the world population grows, there is demographic explosion of chronic diseases, as disorders of the developing or ageing brain, especially neurodevelopmental or neurodegenerative diseases. Among the neurodevelopmental disorders is Epilepsy, the most common chronic brain dysfunction with the largest global neurological disease burden. There is 50 million people having epileptic involvement, double than the population of Alzheimer's disease [1]. The percentage of patients without proper treatment ("treatment-gap") is considerable, viz. 95% and 60% in India and Spain, respectively. Much common is psychomotor or temporal lobe epilepsy (TLE), which needs to be identified or screened rapidly in a mass-scale setting at district-hospital level where there is facility of only plain brain scans (MRI/CT), without availability of customary time-consuming 3-D image analysis or morphometry. Thus the need of speedy single-slice methodology for screening, robustly implementable multicentrically.

Methods
The cortical expansion of the growing cerebrum is analyzed from a neurodevelopmental perspective of germinal neurogenesis and pruning, whereby epileptic temporal lobe dysfunction is formulated in terms of geometric malrotation of the inversion of allocortex. Possible neurodevelopmental biomarkers of TLE are deduced, in terms of 2-D rotational angles and 1-D ratiometry of the allocortex regions, which we can swiftly measure in a single MRI slice using FLASH T1 pulse sequence, with the pertinent allocortex being amygdala, hippocampus and parahippocampus. To test for large-scale multicentric applicability, our topographic analysis [2] is implemented as an India Brain Grid initiative, with 57 patients of TLE, the grid being the national-level multicentric neuroinformatics analysis platform across different regions: North (Delhi NCR), East (Calcutta), West (Bombay), South (Bangalore). We develop the architecture via Linux-Apache-MySQL-PHP bundle, using Indian National Knowledge Network connectivity and C-Brain MNI prototype system. For this study, the investigating centers are Delhi (NBRC) and Calcutta (IPGMER).

Results
We form a model of neurogenesis from germinal subventricular/subgranular zone and show how neuro-developmental impediment induces cortical dysgenesis, reduced allocortex inversion and torsion effect on paleocortex/archicortex (amygdala/hippocampus/parahippocampus). Torsion alters the ratiometry and angulation of parahippocampus and hippocampus, respectively, which we can accurately delineate in single-slice brain MRI

scan readily. In neurodevelopmental phase of infants, one knows that left cerebrum has higher hemodynamic stress, as left common carotid artery is a direct branch of aorta, unlike right artery [3]. So the neurodevelopmental inversion will be more retarded on left side in TLE. Thereby, hippocampal angular rotation is to be less on left than right in TLE, and we confirm this prediction by MRI analysis. Via the Brain Grid, we enable fast standardized accession of imaging data across distant regions (40–50 sec), whilst ratiometric and angulation thresholds can be delineated for characterizing TLE patients.

Conclusion

Feasibility of an affordable country-wide Indian Brain Grid is enabled, for rapid multi-centric collaboration and analysis, e.g., fast epilepsy screening via neurodevelopmental distortion analysis. This neuroinformatics infrastructure is expandable to other neurological and psychiatric disorders for national-level imaging trials.

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P03 Modeling protein interactions in neurodegenerative disorders using automata

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Neurodegenerative disorders are commonly characterized by the misfolding and progressive aggregation of specific proteins in selective regions of the nervous system. Increasing evidence suggest interactions of pathological proteins which points towards common pathways. The identification of causative gene and verification of proteins interactions with products are effective ways to understand correlations between neurodegenerative disorders. Modeling the protein–protein interaction networks of each neurodegenerative disorder is an important and fundamental problem in understanding the underlying mechanisms. Novel findings in the pathogenesis of Alzheimer, Parkinson, Huntington and prion diseases, suggest that by employing protein–protein interaction networks we can identify that distinct pathologies may cross talk at the molecular level. In brief, our work presents a novel approach of an abstract model that performs computations using automata in order to simulate the transitions between different configurations of protein – protein interaction networks.

P04 Realistic neural circuit simulation of the moth antennal lobe that recognizes relative pheromonal concentration

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Olfaction is the most important sensory information for a male silkmoth because of their female-searching behavior. A male moth finds a female moth via sensing pheromones which were emitted by a conspecific female. Odorants such as a pheromone are intermittently distributed in the air. When a male moth tries to find a female using olfactory information, the recognition of the pheromonal concentration in high spatio-temporal resolution is inevitable for efficient odor detection. Therefore, the concentration discrimination of intermittent pheromone plumes is the critical function for moth brain. However, the conventional research topics [1, 2] for the antennal lobe which had been studied by experiments or simulations were the discrimination of odorant species rather than concentrations. Hence, we are trying to build the realistic antennal lobe simulation of silkmoth based on experimental studies to understand dynamics and functions of this first olfactory center in the natural condition. We experimentally found that relative pheromonal concentration discriminations are processed in the antennal lobe of silkmoth, especially in macroglomerular complex (MGC). The antennal lobe, the first olfactory processing center in the insect brain, has two types of neurons. One is a projection neuron (PN), which innervates the MGC and higher olfactory centers in a protocerebrum. The other is a local interneuron (LN), most of which are inhibitory and GABAergic. We measured dynamic changes of PN's response when an antenna intermittently and consistently stimulated by pheromone [3]. Responses of PNs which were measured by calcium imaging and electrophysiology revealed following facts (Figure 1A). (1) When PNs are stimulated by high concentration pheromone, action potentials are inhibited by LNs after PNs generate a small number of spikes. (2) Repetitive stimulations by pheromone make inhibition weak. (3) After the many repetitions of same concentration stimuli, PNs show a concentration-independent and constant response at any concentration. That does not mean the antennal lobe simply desensitize the stimuli but the sensing range is tuned to stimuli because the PNs' responses are enhanced or weakened when higher and lower concentration stimuli are applied just after repetitive stimuli. We preliminary build an antennal lobe network model by the single compartment H-H type model to verify two following things. First, we expected to verify abstract network connection properties obtained from our experiments. Second, we expected to verify the cause of delay between PNs' first spike after strong stimulation and strong GABAergic inhibition to PNs' response when antenna was stimulated by high

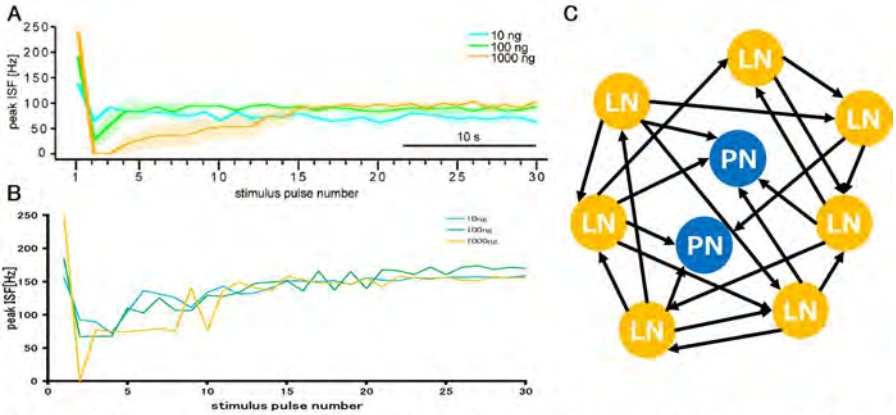

Figure 1. Responses of PNs to intermittent pheromone stimuli. **A**, Dynamics of peak ISF measured by experiment (Fujiwara et al, 2014). **B**, Dynamics of peak ISF measured by simulation. **C**, Schematic diagram of the antennal lobe neuronal circuit.

concentration pheromone. The cause of delay is predicted the time costs of the action potential propagation in the LNs. Therefore, to reproduce this delay as a physical phenomenon, it is suitable to make realistic 3D models of a neural circuit each cell is presented as a multi-compartment model. However, building a multi-compartment neural circuit model from scratch require very hard efforts such as parameter estimations, setting network connection properties. There are a lot of parameters for active and passive membrane properties and synaptic connection properties. Hence, before we make multi-compartment model of antennal lobe, we built single compartment model to verify network connection properties and reproduce dynamic changes of PN's response. Figure 1C shows the schematic diagram of single compartment antennal lobe network consisting of PNs and spiking LNs. Each arrow indicates GABAergic inhibitory synapse. There are reciprocal GABAergic inhibition synapses among LNs, and the connection probability from LNs to LNs is 0.5. And from LNs to PNs, there are also have GABAergic inhibition and the connection probability is 0.5. As a result, responses of PNs in our single compartment network model could reproduced dynamic changes like our experiments (Figure 1B). That means, the dynamic properties (1)–(3) in response of PNs can be explained by only two types of synaptic connections, among LNs and from LNs to PNs. However, as mentioned above, it is difficult to estimate realistic time delays due to spike propagations inside of neurons. Therefore, we are in progress of building multi-compartment model of antennal lobe. To make the multi-compartment model, we collected morphology data of confocal laser scanning microscope (CLSM) images of neurons in the antennal lobe. The data were brought from our database system (BoND [4]). By these kinds of data, we extracted the suitable morphology for simulation by KNEWRiTE [5] and construct the standard brain model [5] of the antennal

lobe. Using CLSM images which have a LN and a PN in one image, we could estimate synaptic connection area, and used the Peter's rule to select synapse position. Presently, we are developing the multi-compartment model simulation of antennal lobe with K computer (RIKEN AICS, Japan). Afterward, we are planning to estimate membrane potential parameters to make realistic model. In summary, we built the antennal lobe network model by the single compartment model to verify network connection properties and the cause of delay. As a result of the simulation, we were able to reproduce dynamic changes of responses of PNs. And, we were able to find out the LNs' inhibition to PNs with delay can cause the antennal lobe to modify its sensitivity in response with the stimuli from our preliminary single compartment model simulation. Furthermore, we will understand more specifically about neuronal dynamics and characteristics of the antennal lobe's microcircuit which can detect relative concentration difference in detailed 3D multi-compartment model simulation.

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P05 Constructing subject-specific virtual brains from multimodal neuroimaging data

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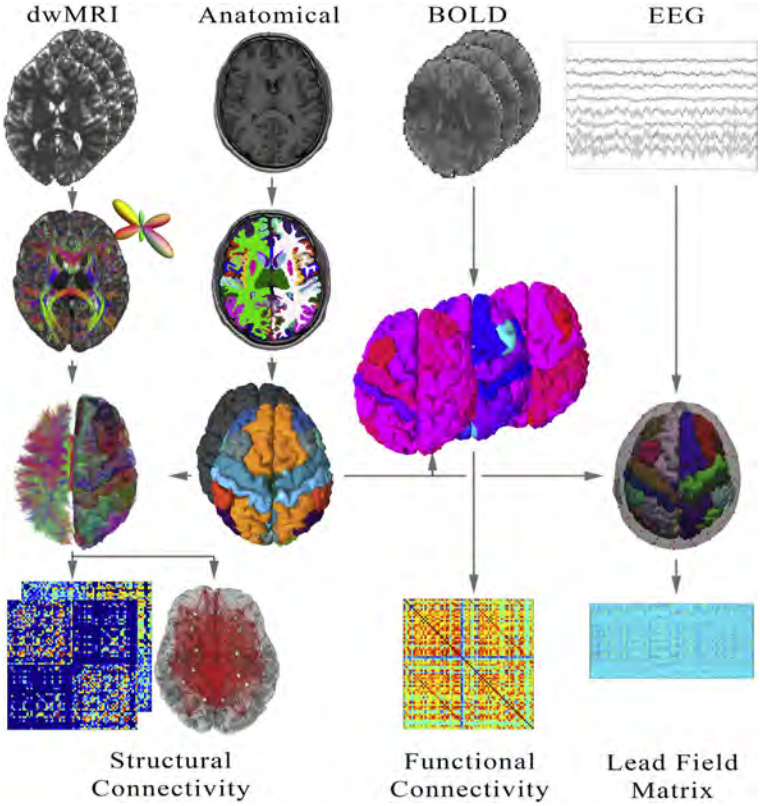
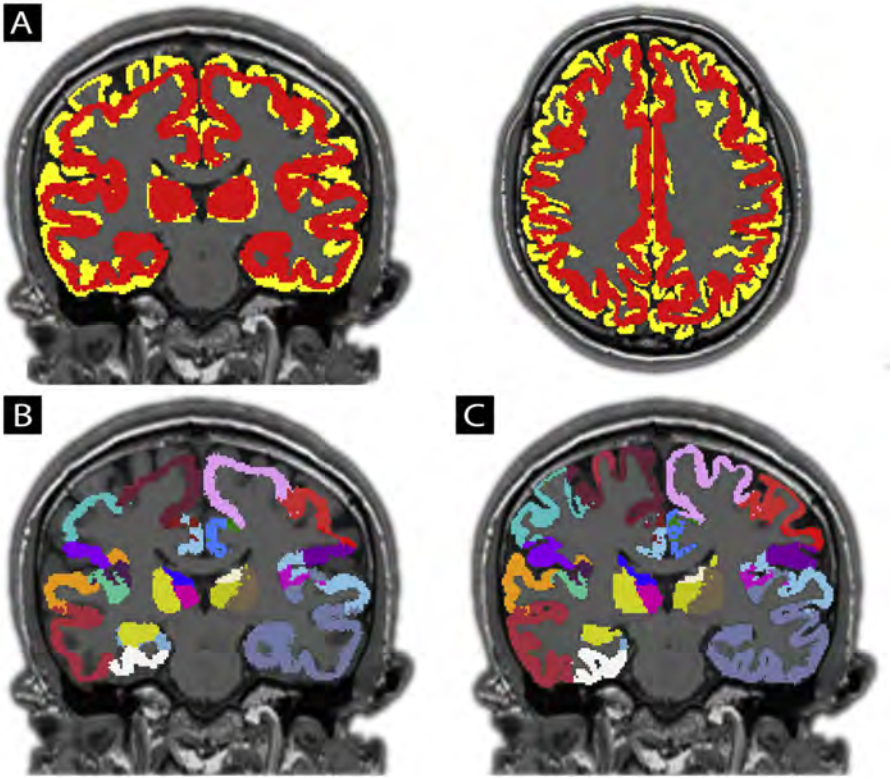
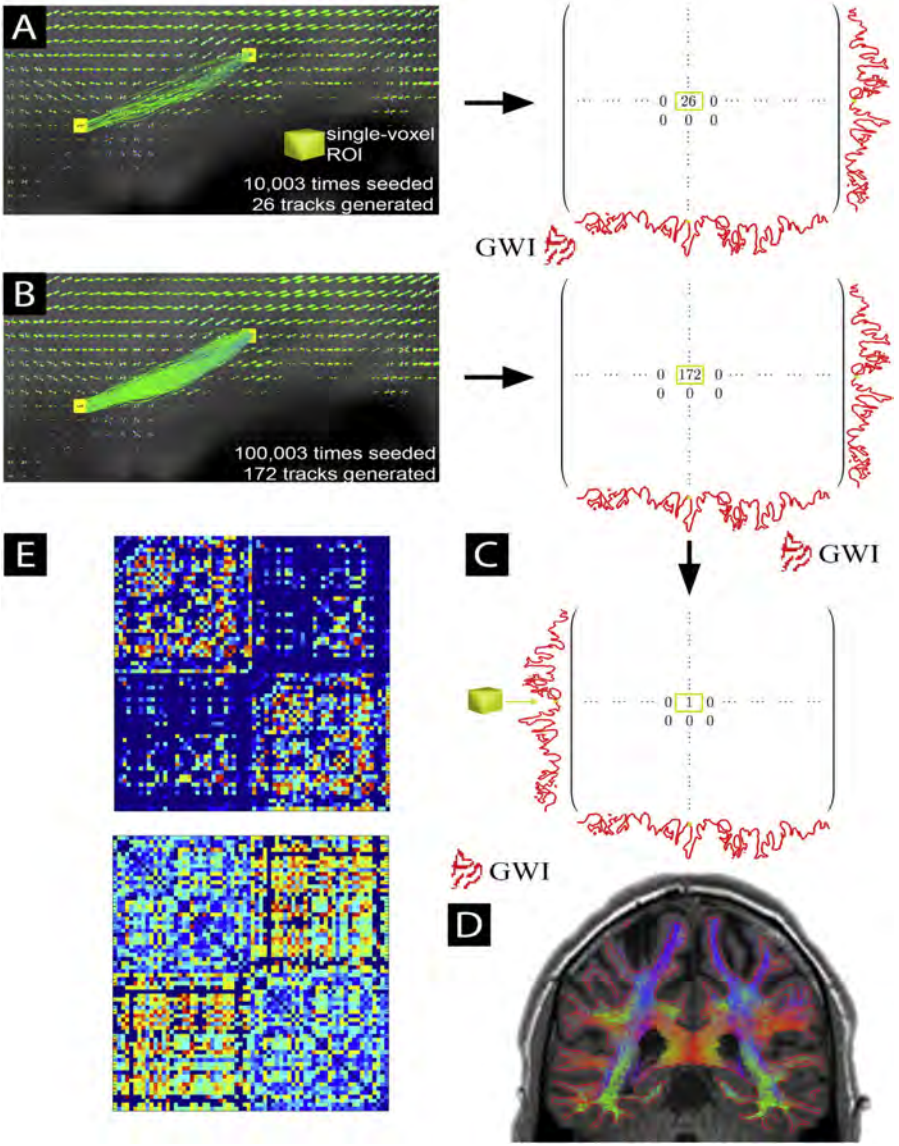
Large amounts of multimodal neuroimaging data are acquired every year worldwide. In order to extract high dimensional information for computational neuroscience applications standardized data fusion and efficient reduction into integrative data structures are required. Such self-consistent multimodal data sets can be used for computational brain modeling to constrain models with individual measurable features of the brain, such as





done with The Virtual Brain (TVB). TVB is a simulation platform that uses empirical structural and functional data to build full brain models of individual humans. For convenient model construction, we developed a shell scripted processing pipeline for structural, functional and diffusion-weighted magnetic resonance imaging (MRI) and optionally electroencephalography (EEG) data. The pipeline combines several state-of-the-art neuroinformatics tools to generate subject-specific cortical and subcortical parcellations, surface-tessellations, structural and functional connectomes, lead field matrices, electrical source activity estimates and region-wise aggregated blood oxygen level dependent (BOLD) functional MRI (fMRI) time-series. The output files of the pipeline can be directly uploaded to TVB to create and simulate individualized large-scale network models. We detail the pitfalls of the individual processing streams and discuss ways of validation. With the pipeline we also introduce novel ways of estimating the transmission strengths of fiber tracts in whole-brain structural connectivity (SC) networks and compare the outcomes of different tractography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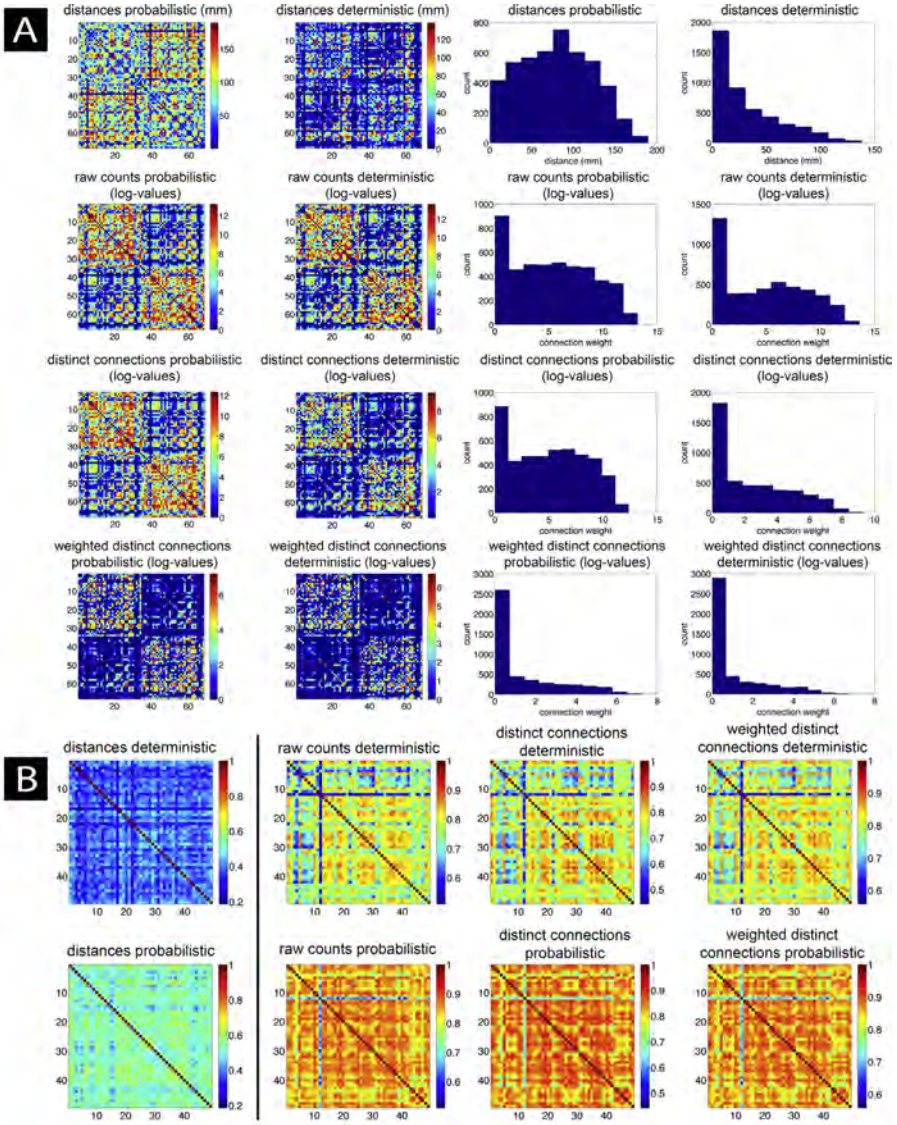
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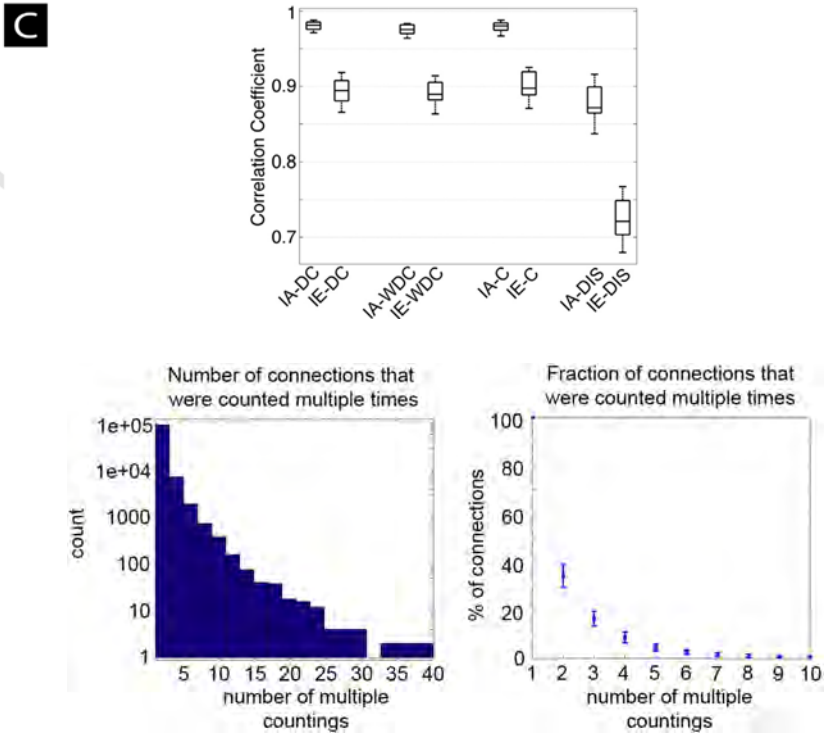

or parcellation approaches. We tested the functionality of the pipeline on 50 multimodal data sets. In order to quantify the robustness of the connectome extraction part of the pipeline we computed several metrics that quantify its rescan reliability and compared them to other tractography approaches. Together with the pipeline we present several principles to guide future efforts to standardize brain model construction. The code of the pipeline and the fully processed data sets are made available to the public via The Virtual Brain website (thevirtualbrain.org) and via Github (https://github.com/BrainModes/TVB-empirical-data-pipeline). Furthermore, the pipeline can be directly used with High Performance Computing (HPC) resources on the Neuroscience Gateway Portal (http://www.nsgportal.org) through a convenient web-interface.

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P06 Realtime simulation of memory consolidation in a large-scale cerebellar model

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Learning in the brain can be divided into two stages [1]. The first stage is called "memory acquisition," in which a short-term memory is created by a session of training. After the training, this short-term memory is erased quickly, typically within a day. The second stage is called "memory consolidation," in which a long-term memory is created by repetitive sessions of the same training over days and weeks. For studies of memory consolidation, a computer simulation can be helpful. By building a neural network model of the potentially critical part of the brain, it is possible to examine the overall process of memory consolidation and the role of responsible components of the part. However, to study the mechanism of memory consolidation by a simulation, we need to conduct a simulation long enough to observe the effects of memory consolidation. Typically, a computer simulation takes much more time than the simulated duration. In other words, if we run a simulation of neural activities for memory consolidation in a week, it will take more than a week in real-world time to complete the computation. This inefficiency imposes huge burdens on researches of models which contain long-term dynamics, especially in large-scale models. High-performance computing (HPC) could provide one of the potential solutions for the efficiency problem. HPC technologies are designed for computer applications which require processing of larger amount of data or shorter computation time. Thus, by utilizing HPC technologies, we can build neural network models consisting of large number of neurons and synapses with more detailed structure and properties compared to normal models, in a practical completion time. One of the key components of modern HPC technologies is General-Purpose computing on Graphics Processing Units (GPGPU) [2]. Graphics Processing Unit (GPU), which originates from accelerator hardware for 3-dimensinal computer graphics rendering, is a processor which has a different architecture compared to conventional CPU. The prominent feature of GPU is massively parallel computation; by the large number of cores working simultaneously, a GPU can provide much more computational throughput than a CPU. Therefore, GPU can be exploited as a high-performance parallel processor. However, this parallel characteristic of GPU could be a challenge. In order to maximize the performance of GPU, computationally-intensive parts in programs should be the same computations which can be done independently. Large-scale neural networks tend to have many neurons and synapses which share the same computational mechanism, respectively, enabling us to write efficient program relatively easily. Considering the advantage of GPU and the inherent parallelism in the computation of the large-scale models, it is natural to adapt GPGPU to accelerate the simulation. In this study, we focused on memory consolidation in cerebellar motor learning, specifically optokinetic response (OKR) adaptation. OKR is an oculomotor reflex, occurred as eye movement to reduce retinal

slip (temporal slide that eyes observe when visual world moves). In OKR adaptation, the amount of eye movement (called "gain") is increased during a training session, resulting in memory acquisition. After a training session ends, the gain gradually decreases to pre-training level. As training sessions followed by rest repeat, the acquired gain increases in per-training basis. To inspect the neuronal activities of the adaptation, we built a large cerebellar neural network model which consists of more than one million spiking neurons and ran a simulation with four GPUs (2 x NVIDIA GeForce Titan Z), which extends our previous model [3]. During the simulation, the computation required to express the entire model was completed in real-time, that is, the computation for activities in a second completed in a second. The temporal resolution of the simulation (called "time step") was 1 millisecond. In the network, we introduced plasticity at two different places. One place was synapses between parallel fibers and Purkinje cells (PF-PKJ) and the other was synapses between mossy fibers and deep cerebellar nuclear cells (MF-CN). We ran a one-week simulation as 5 iterations of 1 hour training session and following 23 hours rest with 24 hours rest at the beginning and the end of the simulation. We observed the following process during a simulation. In the first training session, the synaptic weights at PF-PKJ decreased by long-term depression (LTD). This resulted in a modulation of average firing rate of Purkinje cells out-of-phase to the retinal slip information. Additionally, the average firing rate of the deep cerebellar nuclear cells modulated in-phase to the retinal slip increasingly, showing memory acquisition. In the post-training rest, the average synaptic weights of PF-PKJ increased to the original level by long-term potentiation (LTP), suggesting PF-PKJ synapses store a short-term memory. As the training and rest repeated, the modulation in the average firing rate of the deep cerebellar cells increased, showing memory consolidation. These dynamical properties are consistent with the theory we recently proposed [4]. In summary, it is possible to simulate the dynamics of a large-scale network model in real-time manner and examine the results practically, thanks to HPC technologies. The method we employed would present an efficient and practical way for researches involving large-scale network models. Finally, we will release the source code on Cerebellar Platform [5].

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P07 The linking via active maintenance model: defining neuronal representations of memory processing

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Modern neuroscience has been grappling with the nature of memory for over 100 years, yet basic questions pertaining to the neural representations of mnemonic processing, and the substrates and structures of memory systems, are still far from resolved [1]. These questions have led to a proliferation of abstract, theoretical frameworks, addressing myriad experimental paradigms. We argue that such competing approaches cannot properly be evaluated without explicit neuronal implementations of memory theories. We introduce a simple neuronal network model for short term list recall, as a biophysical implementation of our Linking via Active Maintenance Model (LAMM) [2]. LAMM constitutes mnemonic processing in the maintenance of persistent, elevated neuronal activity in subpopulations of cells, and associative learning as synaptic strengthening between those subsets. The model encodes and recalls sequences of stimuli automatically, as a result of its simple network structure. Comparison of model and human behavioral performance indicates the value and limitations of simple associative memory networks. At the same time, implemented as a biophysical model, LAMM simulations define explicit neuronal codings for memory representation and processing which can be accountable to experimental neuroscience.

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P08 FlyDriver: a connectomic approach to find specific drivers of target neuron in the FlyCircuit

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We collected about 4000 driver expression images of Drosophila melanogaster, which included Gal4, LexA, flipase and spilt-Gal4 system for manipulating neuronal circuit function. All confocal microscopy images was archived into a database, named FlyDriver. FlyDriver was followed the same platform of FlyCircuit. Therefore, we can compare single neuron image with driver image. Here, we used image-matching algorithm on both neuron-driver image pairs and driver-driver image pairs between FlyCircuit and FlyDriver, which amount over the 100 million image pairs was been calculated. The overlap information of neuron-driver image pairs could help user to find a specific driver with a target neuron. In addition, user could also find similar driver with overlap information of driver-driver image pairs. We have illustrated the utility of these image-matching data for identifying the putative driver expressed target neuron and finding the specific driver from a set of neuron images. For some expression pattern that did not exist in one single driver, we could use the overlap information to predict expression patterns that comes from the intersection region from two driver images. As a result, FlyDriver provided a web interface that allows users to find the driver with different criterion. This will facilitate finding a specific driver to understanding the function of neuronal circuit.

P09 Towards a "biophysical psychiatry": a modeling approach for studying effects of schizophrenia-linked genes on single-neuron excitability

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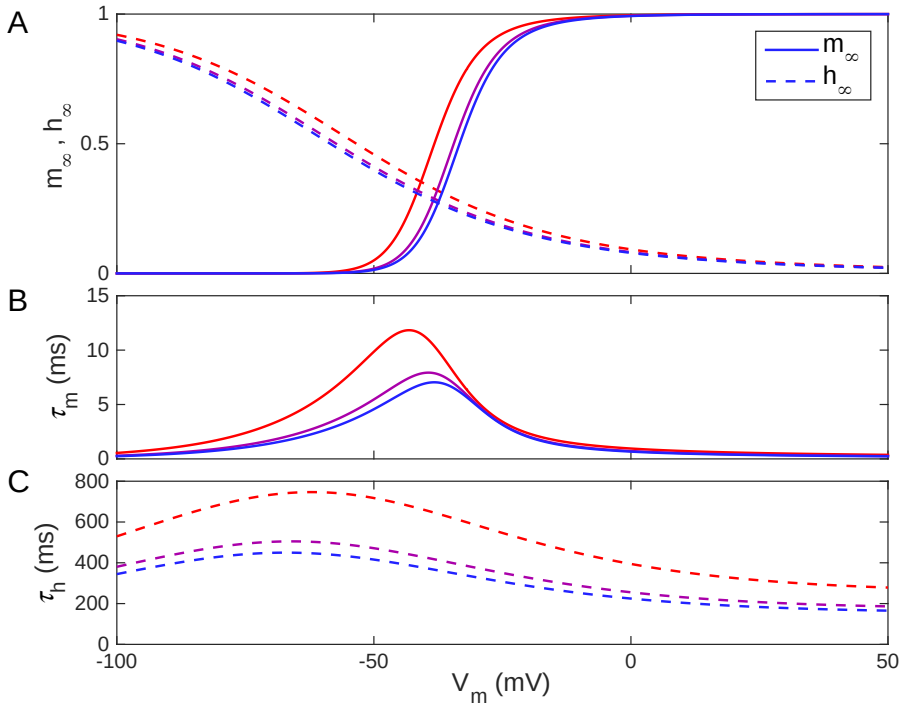
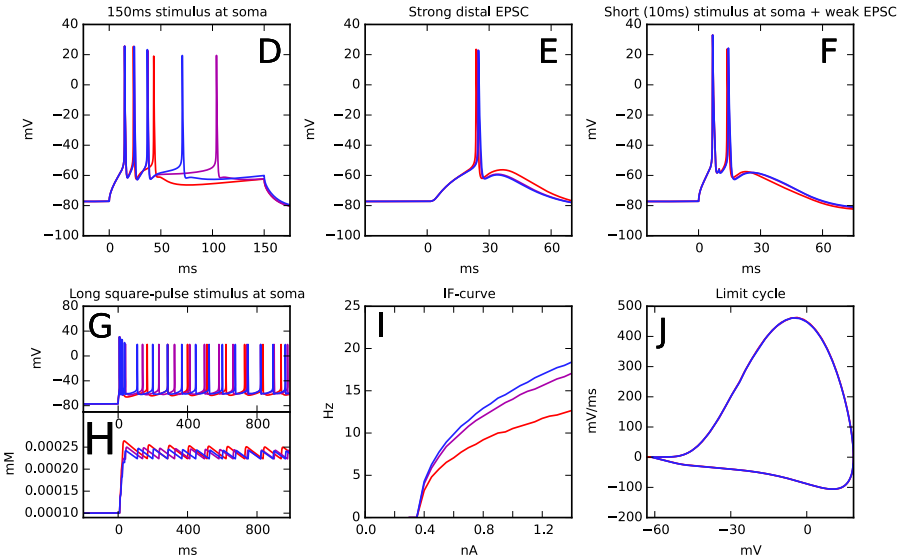
Genome-wide association studies (GWAS) employing large sample sizes and sophisticated statistical methods have recently yielded detailed information on the set of genes affected in various psychiatric disorders. This is especially important for polygenic, highly heritable disorders such as schizophrenia (SCZ) [1]. The success lately witnessed in gene discovery brings up the next big challenge for psychiatric genetics – translation of the genetic associations into biological insights [2]. In this study, we propose a computational approach for investigating the effects of a collection of excitability-related genes on various neuronal characteristics. As a proof of principle, we apply our approach for studying effects of SCZ-linked genes on firing behavior of a layer V pyramidal cell (L5PC). An L5PC extends throughout the cortical depth with the soma located in layer V and the apical dendrite branching into the "apical tuft" in layer I. The tuft serves as an integration hub for long-distance synaptic inputs, and is often considered a biological substrate for cortical associations providing high-level "context" for low-level (e.g., sensory) inputs to the perisomatic compartment [3]. Therefore, the ability of L5PC to communicate the apical inputs to the soma has been proposed as one of the mechanisms that could be impaired in the mental disease [3]. In agreement with this hypothesis, recent psychiatric GWASs consistently reported association of genes coding for the subunits of voltage-gated Ca^{2+} channels as risk factors in SCZ and bipolar disorder [1, 4]. A total of 108 genetic loci were recently confirmed to be associated with the risk of SCZ [5]. These loci span a wide set of protein-coding genes. The disorder is associated with genes affecting transmembrane currents of all major cationic species, Na^+, K^+, and Ca^{2+}. In addition, some of the SCZ-linked genes are involved in regulation of the Ca^{2+} concentration in the intracellular medium, which is another great contributor to

neuron excitability. All above aspects of electrophysiology are included in a recent multi-compartmental model of L5PC [6], which accurately describes the perisomatic firing behavior and its interplay with the generation of an apical Ca^{2+} spike. In this work, we rely on data from functional genomics studies that describe the effects of variants of certain ion channel or calcium transporter-encoding genes on the channel activation/inactivation properties or intracellular Ca^{2+} dynamics. We carry out our study by linking these effects to a change in the corresponding neuron model parameters, and observing the implication that these variants have on the information integration in an L5PC. These effects include, e.g., shifts in channel activation or inactivation voltages, changes in time constants of channel activation and inactivation, as well as changes in resting level and decay time of intracellular Ca^{2+} concentration. It should be noted that information does not generally exist for the effect of single nucleotide polymorphism (SNP) variants identified through GWASs on the biophysical parameters required for the computational models. We instead use information obtained from *in vitro* studies of more extreme genetic variations, including loss of function mutations. A central assumption of this approach is that the effects of SNP





variants can be represented as scaled-down versions of those of the more extreme variants, and that the emergence of the full psychiatric disease phenotype results from the combined effect of a large number of subtle SNP effects. Our approach for variant implementation and downscaling is illustrated in Presentation 1. Our results show a multitude of alterations of the firing behavior and integration of inputs in neurons equipped with the considered gene variants. Most of the modeled effects of variants of CACNA1C, CACNB2, CACNA1D, CACNA1I, ATP2A2, ATP2B2, SCN1A, SCN9A, KCNS3, KCNB1, KCNN3, and HCN1 genes show a distinctive impact on the steady-state firing behavior of the L5PC. This can be observed as a gain or loss of gain in the f-I curve of the neuron, but also in its calcium homeostasis during a DC input. In addition, many variants influenced the integration of apical inputs in the L5PC and the sensitivity to their temporal precision. An especially interesting observation is that many variants affect the suppression of a second successive apical stimulus, which might have a connection with the deficit in prepulse inhibition, a condition often observed in SCZ patients [7]. Our framework is an early attempt toward understanding the disease mechanisms of polygenic psychiatric disorders by computational means. Although the analyses presented here are specific to L5PCs and SCZ-related genes, our "biophysical psychiatry" framework may be directly applicable to other cell types and other polygenic diseases, such as bipolar disorder and autism, given an identification of risk genes related to neuronal excitability. Furthermore, our approach could be directly applied to biophysically detailed models of neuronal networks and extended to consider synaptic ion channel-encoding genes that are relevant in SCZ [8].

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P10 Computational modeling of the cone mosaic based on the anatomy and physiology of the vertebrate retina

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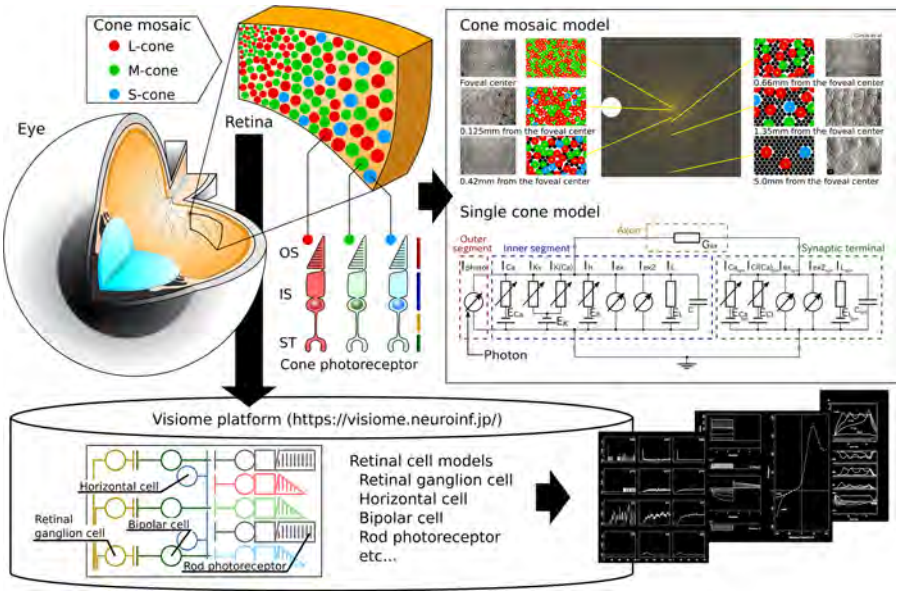
The retina converts the light into action potentials which are carried by the optic nerve to the brain. The anatomy and physiology of the retina are relatively well known. Anatomical studies have revealed the morphological principles governing the structure of the retina such as the layered structure and the spatial arrangement of the photoreceptors. Physiological studies of the retina have uncovered a number of cellular and subcellular mechanisms such as phototransduction and the characteristics of the ion channels found in retinal cells. These data provide information about the functional role of ion channels in generating and shaping the light response of the cells. We have been working developing mathematical models of the retinal cells. The models in various simulation codes have been archived in Visiome platform (https://visiome.neuroinf.jp/), and we can test, reuse and even improve the published results. It is now possible to understand some computational operations that the retina performs and to relate them to specific physiological mechanisms, on the basis of computational modeling work. In the present work, we developed a computational model of the cone mosaic based on the anatomical and physiological characteristics.



The model incorporated the anatomical characteristics such as the cone density and diameter, as well as the ratio of spectral subtypes which mediate color vision. Each cone was modeled based on the biophysical and physiological properties. The single cone model consists of three functional parts, i.e., outer, inner segments and synaptic terminal. In simulation, the model well reproduced the electrical responses similar to those observed experimentally. We also analyzed how the cone mosaic affects our ability to transform the spatial and color information in the retinal image. In conclusion, the present model can be used for analyzing the first step of visual information processing quantitatively.

P11 A combinatorial approach for mapping the interactions of multiple inputs to a biological system in a tractable number of experiments

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Multiple simultaneous inputs (e.g., neurochemical agents, drugs, therapeutic interventions) act together to affect the output of complex biological systems such as neurons and neural circuits or organs such as the heart. Describing how all these inputs act together on a system is difficult because the inputs often interact in ways that cannot be predicted from their individual actions. This happens because biological systems are non-linearly coupled networks of many components through which the presence of one input can change the effect of another on the output. Full experimental mapping of all interactions between inputs is currently impractical for non-trivial input sets because of the combinatorial explosion: there are simply too many combinations of inputs to test each combination individually. To solve the problem, we have developed a block-design approach in which we construct a small number of test sets, each containing a number of pairs (or higher tuples) of the inputs, such that together all the test sets contain all possible pairs multiple times. Similar algorithms are used in communications and computer systems testing, but our algorithm must satisfy the additional need for repeated testing to deal with inter-preparation variability seen in biological systems. Our algorithm furthermore adaptively reduces the number of experiments required depending on the results obtained so far. Finally, it incorporates statistical tests to evaluate how non-linearly "unexpected" each pairwise interaction is, relative to the prediction from the linear combination of effects of the two (or more) inputs alone. The statistic ranks all of the pairwise interactions from the most to the least unexpected. The algorithm thus functions as a global screen for the most unexpected interactions in the input set. Even large numbers of inputs require only small, experimentally tractable, numbers of test sets. Altogether, our approach promises to be able to guide the experimental discovery and global mapping of interactions between inputs to a system without any knowledge of the internal structure of the system. We are testing and further refining the approach using the Luo-Rudy computational model of mammalian ventricular myocytes, and then applying it experimentally to map the interactions between the many neuromodulators of a crustacean cardiac system.

P12 Balance between efficiency and stability in a neural circuit model of the Drosophila brain

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Fruit fly (Drosophila melanogaster) is becoming a promising model animal in computational neuroscience for its small brain size, complex cognitive behavior and abundant data from genes to circuits. Although much has being learned about the functions of individual sensory systems, how do they operated and integrated at the brain-wide level in Drosophila remains poorly understood. To provide a platform for studying computation of the fly nervous system, we initiated the Flysim project with a goal to construct a full-brain neural circuit model with a single-neuron resolution based on the data obtained from the flycircuit database. Although containing only ~28,000 neurons (account for 22% of the fly brain) at the current stage, our fly brain model already exhibits unexpectedly rich dynamics. Due to the strongly recurrent excitation, the brain model is inherently unstable and epilepsy-like activity frequently arose from the baseline state. We further found that the epilepsy-like activity cannot be suppressed by solely strengthening the inhibitory synapses but can be eliminated by implementing short-term depression. However, depressed synapses strongly attenuate the propagation of signals and lead to an inefficient neural circuit. Therefore, a functioning nervous system requires fine balance between stability and efficiency. Additional analyses revealed that the epilepsy-like activity originates from a group of specific brain regions that are functionally less understood but seem to play roles in integrating signals from different sensory modules. By a large-scale screening through the inhibitory system of the brain model, we further discovered that the epilepsy-like activity can be suppressed by a small number of inhibitory neurons if they are manually activated. Interestingly, the epilepsy-suppressing ability of these neurons does not come from their inhibitory strength, but from their unique innervating patterns over the excitatory system. In conclusion, despite being in an early stage of the model development, our fly brain model has already shown its strength in providing insights into brain-wide neural dynamics which may not be revealed by analyzing the random or simple small-world neural networks.

P13 Effects of aging in Parkinson's disease: role of L – type Ca channel in dopamine neuron computational model

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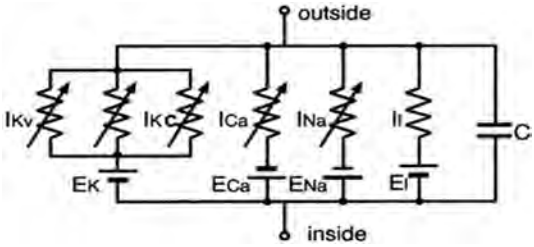
Introduction
Evidence from a number of independent studies has demonstrated that loss of the nigrostriatal dopamine neurons (DA) is one of the characteristic hallmarks of Parkinson's disease (PD). Selective deterioration of these neurons due to aging is responsible for the cognition, reward learning and motor deficits associated with PD. The ion channels, as dynamic gate keepers of membrane permeability, drive spontaneous, rhythmic firing of action potentials in these neurons. Basic biophysical characteristics of DA neurons include broad action potentials (>2 ms), a spontaneous pacemaker-like firing pattern (1–5 Hz), a "sag" in the membrane potential recorded during hyperpolarizing current pulses and bursting spike patterns. From recent experimental studies [1], it is observed that neurons from old mice exhibit slower firing rates, narrower spike widths, and more variable inter spike intervals compared with neurons from young mice due to smaller L-type calcium channel currents. Computational models can succinctly describe the interactions among various ion channels and allow the user to investigate the contribution of each ion channel to the overall observed cellular electrical behavior. The aim is here to establish a mathematical platform of sufficient biophysical detail to quantitatively simulate Ca^{2+} channels in DA neuron model and to investigate contribution of this active conductance in pathophysiological condition of these neuron with respective to PD.

The Objectives
DA neurons are autonomous pacemakers that fire action potentials even in the absence of active excitatory synaptic input. DA neuron pace making is influenced by intrinsic ion conductances, and the voltage gated calcium channels. Here we tried to address those questions. How L – type calcium channel is involved in control of spontaneous firing frequency, specifically by inducing a near-threshold depolarization? Second is how L type Ca^{2+} channel is coupled small-conductance Ca^{2+}-sensitive K^+ (SK) channel to mediate after hyperpolarization ?

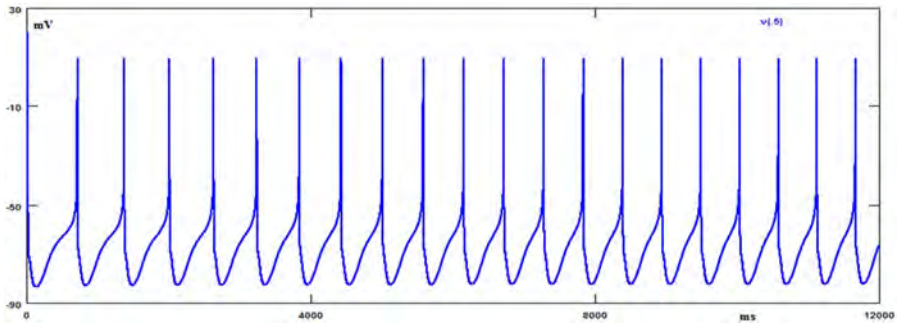
Methods
Formulation of a conceptual model, which is expressed in a mathematical form, is the first step in translation of a physical system to a computational model. Here the conceptual model is based on classical Hodgkin-Huxley (HH) approach, which endows the model with wide generality and makes it adaptable to tuning in the light of fresh experimental data. The model used in this study is based on an existing DA neuron model [2]. The set of passive properties, voltage-dependent ionic channels, and their kinetics were identical to

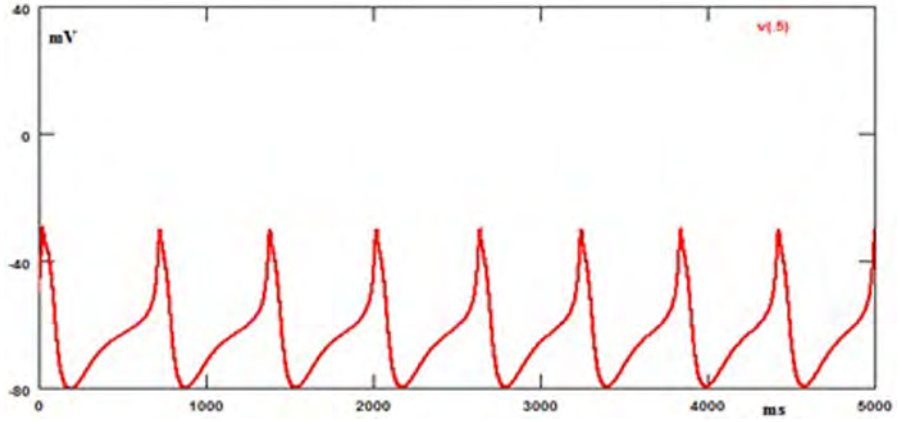


those in this model, already validated against a number of different experimental findings on electrophysiological and synaptic integration properties of DA neurons. Ionic channels such as calcium (ICa), sodium (INa), calcium activated potassium channels (IKca) and delayed rectifier potassium (IKDR)) were uniformly distributed throughout the dendrites, whereas KA and Ih conductances linearly increased with distance from soma. The major modifications were that the pace making mechanism comprised of the L-type Ca^{2+} currents and T-type Ca^{2+} currents those were modeled with borrowed parameters from recent experimental result [1].The Parallel Conductance model (shown in Figure 1) is intended to represent the flow of ions through their respective ionic channels in a small area of membrane. Every ion potential can be modeled as a variable conductance in series with respective Equivalent potential.

Results

The Spike generated in our model is shown in Figure 2. The Active conductances for rising phase are voltage gated Sodium current and voltage gated calcium current. Voltage gated Potassium current and Calcium activated potassium current are essential for repolarization phase. The L-type Ca^{2+} current ICaL first appears at V » –30 to –20 mV; the peak of the current-voltage (I–V) relationship arises at V » 0 mV. The half-activation potentials for activation is at –24.8 mV. The L-type Ca^{2+} channel maximum conductance is 200 mS/cm^2.The L-type calcium channels in other cell types have been shown to be permeable to other cations but there are no data specific to DA neuron cells. Thus, the Goldman-Hodgkin-Katz formulation commonly used in other excitable cell models is not used here; instead, Nerst potential ECaL in the model is fixed at 90 mV. The T-type Ca^{2+} current ICaL first appears at V » –80 to –60 mV; T-type activation occurs at low voltages and in DA neurons inactivates at –40 mV. The half-activation potentials for activation is at –49.6 mV. The T-type Ca^{2+} channel maximum conductance is 144 mS/cm^2. Spontaneous firing of DA neurons in brain slice preparations is almost exclusively driven by slow intrinsic conductances. In our model, small-conductance Ca^{2+}-sensitive K^+ channels is major determinants of firing rate. Figure 3 shows the spike in normal cell, depolarization without spike due to peptide accumulation.





Here the decline in L-type calcium currents due to aging eliminates the normal spike generation properties. Mean firing rates were significantly slower in Figure 3 compared with Figure 2.

Discussion

We have modeled only two voltage gated ion channels (L-type and T-type Ca^{2+} channel) according to the HH formalism, our model allowed us to take into account different experimental findings on the effects of aging, providing new insight on how the DA neuronal firing properties is altered due to aging related conductance change in L-type Ca^{2+} channel. It also shows that putative coupling between T-type Ca^{2+} channel and SK channel can affect the duration of after hyperpolarization period. Future model can provide more insights into it.

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P14 Modeling presynapse–astrocyte interactions

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Astrocytes have gained an increased interest in neuroscience due to their ability to influence synaptic transmission through gliotransmitters. Many studies and models concentrate on tripartite synapses formed by two neurons and an astrocyte. The effects of tripartite synapse on paired pulse facilitation and depression were suggested for example by De Pittà et al. [1] (PLoS Comput. Biol. 2011). In the presented work we concentrated on the pathway from the presynapse to the astrocyte and back to the presynapse. We will investigate what effect the release amount of glutamate after a spike in the presynapse has on the release amount of IP3, calcium and glutamate in the astrocyte. A version of Tsodyks-Markram presynaptic model is used as described by De Pittá et al. and astrocytic effects as described in the same paper. These effects are applied to spiking neuronal network INEX by Lenk [2] (Lecture Notes in Comput. Sci. 2011). The simulators are combined by modifying values of synaptic strengths (W) in the INEX model according to neurotransmitters released in presynaptic models attached to each synapse. At an event of spike amount U calcium enters the presynaptic terminal and binds to vesicle sensors u. There is an amount of x neurotransmitter present in the presynapse at any given time. Amount of u*x resources are released (RR). Glutamate affects the value U by modifying parameter alpha. Alpha describes the effect of presynaptic glutamate receptors to release probability. U is changed towards alpha depending on glutamate amounts released by astrocyte. INEX parameter W is used for initial U for each synapse and resources released (RR) as weight for spiking synapse. The uptake of glutamate in the synaptic cleft triggers an IP3 increase in the astrocyte which in turn triggers a release of calcium from the endoplasmic reticulum. When the calcium concentration reaches a certain threshold glutamate is released from the astrocyte. The glutamate is detected by the presynapse and the effect decays over time. The glutamate level together with the frequency of occurring spikes affects the release amount RR in the presynapse. We simulated the interaction between one excitatory presynapse and an astrocyte and applied three different spike frequencies from low to high and three different initial excitatory synaptic strengths W. Low input frequencies show no effect by the astrocytes. In the midrange spike frequencies the astrocyte gets activated and resources released become periodic. In too high frequencies the astrocyte is activated at the beginning. However, since the IP3 and calcium never fall below the threshold again, no more astrocyte effect is visible. To summarize, the results show that steady state input of spikes can lead to periodic output of the synapse. The periodical output is dependent of initial resources released level and frequency of spiking.

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P15 Workflow for mapping tracer injection studies of the common marmoset into a reference template

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Tracer injection studies provide a valuable insight into brain connectivity. However, the two dimensional nature of such data renders it difficult to make comparisons between injections performed in different animals or between tracer injection studies and those conducted with inherently three dimensional methods like resting state functional magnetic resonance or diffusion tensor imaging. In order to facilitate such comparisons, one has to bring the two dimensional data into a common, three dimensional space. In this study we propose and validate an automated workflow for mapping the common marmoset connectivity data obtained from tracer injection studies into reference template space of a stereotaxic atlas [1, 2]. Nine marmosets were injected with fluorescent retrograde tracers in the dorsolateral prefrontal cortex. These tracers label the cell bodies of neurons that send projections to the injection site, thus providing a map of neuronal inputs. Due to the limited number of distinguishable tracers, building a map of connectivity requires the registration of multiple specimens to a common atlas. The process of mapping data obtained from a single specimen into the atlas space comprises several steps. In the initial stage, the location of stained cells marked on the fluorescence sections are aligned with the neighboring Nissl sections. Afterwards, the Nissl stained sections are stacked and reconstructed into volumetric form. The reconstruction is initially performed with affine transformations followed by deformable warping. The latter step removes section specific distortions and allows for more reliable subsequent deformable mapping [3] into the atlas space. The process yields a set of transformations which are then applied to the actual cells locations. In the final step the individual cells are assigned to a particular brain structure based on the atlas parcellation. The described process was conducted for nine test cases and resulted in a database of the cell's coordinates in the atlas space. The results can be visualized on a 3D model of the marmoset brain or projected onto a cortical flat maps. The reliability of the workflow was assessed in two ways. First, by comparing the number of the cells in each cortical area indicated by the automated approach with the count determined manually by an anatomist. Second, by measuring distances between mapping-based and ground truth locations of the injection sites. The established workflow allows the processing of the additional cases to produce a spatially defined connectivity map of the marmoset cortex,

independent of anatomical parcellation scheme [4], unlike the traditional method relying on prior assignment of data to discrete anatomical structures. Additionally, it allows purely spatially based comparisons of connectivity with three dimensional imaging methods.

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P16 Macaque brainnetome atlas constructed with anatomical connectivity profiles

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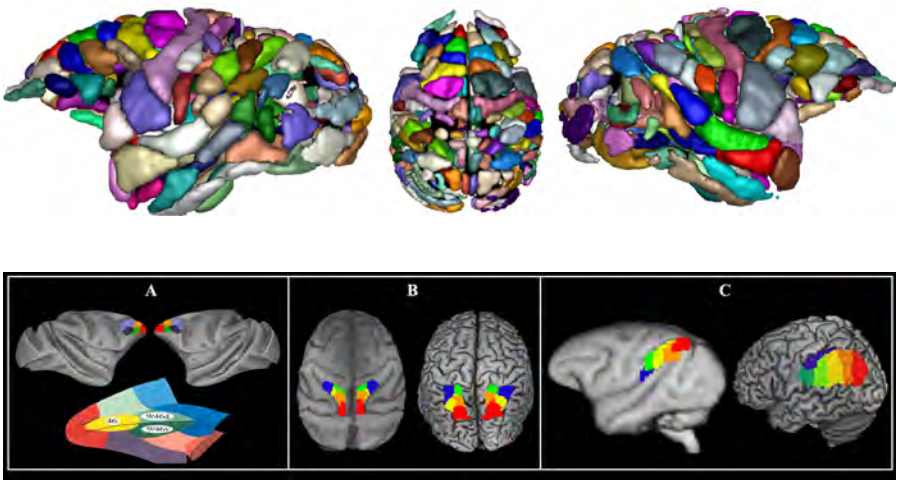
Introduction
Macaque model has been widely used to investigate the brain mechanism of specific cognitive functions and psychiatry disorder. However, because of lack of detailed functional architecture map for macaque, the present studies on macaque progress very slowly. Although many previous studies have established the cortical subdivisions based on post-mortem cytoarchitectonic technique [1, 2], the intrinsic limitations of this method made this type of parcellation cannot inform the functional segregation which was considered to be determined by its external anatomical connectivity patterns [3–6]. In this study, we aimed to construct a new macaque cortex atlas based on its anatomical connectivity profiles based on diffusion MRI *in vivo*. The newly constructed macaque cortex atlas is called macaque brainnetome atlas.

Materials and Methods
Twenty-four anesthetic macaques were scanned using Siemens 3.0 T magnet. The DTI data include 65 non-collinear volume, 1 non-diffusion-weighted images (b = 0 s/mm^2), voxel-dimensions of 1.5 ´ 1.5 ´ 1.65 mm^3 with gradients b = 1000 s/mm^2. In addition, Sagittal 3D T1-weighted images were also acquired with 224 sagittal slices, slice thickness = 0.5 mm. DTI data was preprocessed using the FSL package and voxelwise estimates of the fiber orientation distribution were calculated [7]. The macaque cortex seed areas were defined using NeuroMaps atlas which identified rough subdivisions of macaque cortex [8]. After obtained the cortex seed areas, we transformed the seed areas' masks to individual diffusion space for fiber tracking. Subsequently, the connectivity matrix and cross-correlation matrix are calculated. Cross-correlation matrix was fed into the spectral clustering [9] to segmentation to define different clusters. Finally, the maximum probability map (MPM) of each cortex area was calculated (detailed procedures seed [5, 9] for human inferior parietal lobule parcellation).

Results
The macaque cortex was parcellated into 160 subregions in both hemispheres and each hemisphere contained 80 subregions. The subregions in both hemispheres were approximately symmetrical arrangement. In each hemisphere, we identified 14 subregions in fron-



tal cortex, 9 subregions in sensorimotor cortex, 13 subregions in parietal cortex, 16 subregions in temporal cortex, 16 subregions in occipital cortex, and 12 subregions in limbic system (only including insula and cingulate cortex) (Figure 1). In the new atlas, we found three main characters: (1), the constructed macaque cortex atlas showed similar but more fine-grained subdivisions compared with cytoarchitectonic findings (Figure 2A). (2), the connectomical macaque atlas showed similar topographical patterns with human cortex subdivisions in some areas (for example superior parietal lobule in Figure 2B). (3), the new macaque cortex atlas identified different topographical organization in some brain areas compared with human cortical connectomical atlas (for example left inferior parietal lobule in Figure 2C).

Conclusion

Macaque brainnetome atlas provided detailed functional organizations for macaque cortical areas to better characterize its functions. It may facilitate the future study of macaque cortex network and provided cues to study the evolution between human and non-human primates.

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P17 Gender-specific neural circuits of emotion regulation in the centromedial amygdala

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A popular gender stereotype harbors some truth: Males have been showed to prefer cognitive coping strategies, such as reappraisal, planned and rational actions, and positive thinking, whereas females prefer emotion-focused coping solutions, such as suppression rumination [1, 2]. However, what underlies gender differences in emotional regulation is still poorly understood. In this study, we addressed this issue from a brain network perspective. Utilizing resting-state functional magnetic resonance imaging (fMRI) data and emotion regulation scores from a large sample of healthy Han Chinese subjects, we found gender-specific functional connectivity patterns associated with emotion regulation seeded in the centromedial amygdala (CM). Specifically, in males, emotion regulation ability was positively correlated with the strength of the resting state functional connectivity (rsFC) between the right CM and the medial superior frontal gyrus (SFG), and in females, emotion regulation ability was positively correlated with the strength of the rsFC between the right CM and the insula and superior temporal gyrus (STG). Moreover, we found that there is an opposite correlation pattern between the emotion regulation ability and connectivity strength in males and females. The differences in the CM modulation circuits in males and females implied that males primarily recruit areas involved with cognition whereas females strongly engage areas associated with emotion.

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P18 Brainnetome atlas: a new brain atlas based on connectivity profiles

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Brain atlas is considered to be the cornerstone of basic neuroscience and clinical researches. However, the existed atlases are lack finer grained parcellation results and do not provide the functional important connectivity information. Over the past thirty years, remarkable advances of multimodal neuroimaging techniques that are rapidly advancing our understanding of the organization and function of the human brain. The introduction of the framework for identifying the brain subdivisions with *in vivo* connectivity architecture has opened the door to neuroanatomical studies at the macro-scale brain studies. In this abstract, we present a new brain atlas – brainnetome atlas. It is constructed with brain connectivity profiles [1, 2]. The brainnetome atlas is *in vivo*, with finer-grained brain subregions, and with anatomical and functional connection profiles [3]. Here we first give a brief introduction on the history of the brain atlas development. Then we present the basic ideas of the brainnetome atlas and the procedure to construct this atlas. After that, some parcellation results of representative brain areas will be presented, which include brain areas with heterogeneous cytoarchitectures [4] and homogeneous cytoarchitecture [5, 6]. We also give a brief presentation on how to use the brainnetome atlas to address issues in neuroscience and clinical research. For example, how to determine the boundary of Wernicke's area [7], what is the organization of Broca' area across languages, and what is mechanism of visuospatial attention lateralization, and what new findings can be made with the brainnetome atlas for basic and clinical neuroscience issues.

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P19 Time scales and evolution of resting state functional connectivity

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Scientists are studying functional connectivity from resting state functional MRI as biomarkers for staging diseased and healthy states in the brain. Studies have shown that rs-fMRI connectivity evolves over time, although in practice it is usually considered as static. We have conducted a preliminary investigation of temporal evolution in rs-fMRI connectivity. Using NITRC 1000 functional connectome project datasets, we examine, the possibility of classifying networks by characteristic time scales and investigate the properties of these networks from rs-fMRI data. We also wish to discover overlapping functional networks and the network variation between groups at different ages. Investigation of functional connectivity at time scale 10 s–6 min, showed an increased correlation in timescale 38 s amidst the decay of activation at 10–26 s and 1–6 min. The connectivity increase is seen as a widely distributed network with condensed connectivity at specific cluster which were not significantly present (showed as several unconnected sub networks) in time scale 6 min. Analyzing different age-groups, the condensed network varies spatially, suggesting the presence of age-varying resting state connectivity.

P20 Higher-order interactions in macroscopic functional networks of the brain and its relation to BOLD global signal

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Introduction
Functional networks of the brain are usually studied at the macroscopic level by extracting pair-wise interactions based on BOLD signals. However, higher-order interactions (HOIs), i.e., the ones that manifest only in triplets, quadruplets, etc., could have important effects on network activities but have not been fully examined at the macroscopic level. Specifically, the relation between HOIs and the global signal (GS), which reflects the common fluctuations among all brain areas, remains unclear. To address these issues, here we first characterized HOIs in macroscopic functional networks based on resting state (rs) fMRI data with and without global signal regression (GSR), and then studied the relation between HOIs and GS, as well as other possible mechanism that can give rise to HOIs, by simulating BOLD signals in distributed brain networks.

Methods
The data set is the first and second scanning of 100 subjects in HCP Q3 (TR = 720 ms, 1200 frames in each scanning). In total, 226,000 frames (about 48 hours) of imaging data were used. Standard preprocessing was applied, including head motion correction, 0.01–0.1 Hz filtering and regressing movement. Simulated BOLD signals were generated by combining a mean-field network model with the Balloon-Windkessel hemodynamic model [1]. To quantify network activities and the strength of HOIs, we used a threshold for individual ROIs and then converted the original signals into binary time series, based on if the amplitude is above the threshold or not.

Results
We analyzed activities of the Fronto-Parietal Network (FPN, 11 ROIs) and the Default Mode Network (DMN, 12 ROIs). To measure the effect of HOIs on network activities, we separately applied a pair-wise model [Ising model, [2]] and a model with thresholding-induced HOIs [DG model, [3, 4]] to the data. We use the Jensen–Shannon (JS) divergence to estimate the accuracy of the two models. For GSR data, we found that, consistent with a recent study under GSR condition [5], the Ising model gave reasonably accurate description of probability distributions of network states, and its JS divergence was slightly larger than that of the DG model (less than 1.5 times for both networks), implying weak HOIs in the data; However,

for data without GSR, the Ising model became much worse (with 2.5 ~ 4 times larger JS divergence) than the DG model, suggesting a stronger effect of HOIs in such condition. Importantly, the DG model's performance was the same for data with and without GSR, indicating that the increased HOIs with GS can be explained as a thresholding-induced effect, rather than an intrinsic feature of brain activities. Next we tried to understand these empirical results by simulating both neuronal activities and BOLD signals in a network model with excitatory coupling between brain areas, in which the strengths of common input and pair-wise coupling were changed systemically. We found that, in both neuronal and BOLD signals, strong common input, which serves as a source for the global signal, led to significant HOIs. Consistent with our empirical results, such HOIs could also be explained by the DG model. In addition, we found that the coupling strength has very little effect on the strength of HOIs in the network. These results shed new light on understanding both weak HOIs in data with GSR and apparently strong HOIs in data without GSR.

Conclusion

We found that, although there are sizable HOIs in brain's functional networks in data without GSR, they are mainly due to the thresholding operation introduced in the data analysis. The true, intrinsic HOIs in BOLD signals are therefore weak regardless of GSR. This warrants the use of methods based on pair-wise interactions in studying functional networks. We also found that such lack of intrinsic HOIs may be resulted from the fact that brain areas usually interact with each other via pair-wise, excitatory connections, suggesting that the lack of intrinsic HOIs may be a generic property of such networks.

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P21 Sensory integration in the zebrafish brain, what are the functions of the thalamus and the cerebellum?

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The integration of sensory information across modalities occurs in all forms of life from single cells to humans. This integration can allow inputs from one modality to modify responses to another, either enhancing or depressing the magnitude of the neural activity that results from a given stimulus [1]. Integration can also reduce the lag between sensory input and motor reactions or the latency of neurons' responses [2, 3]. In the cat superior colliculus (SC), integration occurs via multisensory neurons receiving converging inputs [4]. Each of these neurons has excitatory receptive fields, one for each modality to which it responds, forming topographic maps of each modality, thus allowing spatial registration of multisensory inputs. However, recent data suggest that multimodal integration may also occur without multisensory neurons. An example can be found in zebrafish larvae, where visual input modulates an auditory escape response. The neurons driving the response, called Mauthner cells, do not receive direct visual input, but the efficacy of the VIIIth nerve afferents were increased by dopaminergic neurons from the hypothalamus [1], allowing for visual modulation of audition. Complex neural circuits such as this one may be responsible for many behavioural responses involving cross-modal integration. The optic tectum (OT) of zebrafish is the anatomical equivalent of the SC; as in the mammals, the superficial layers of the OT receive the retinal afferents and process visual input [5]. This processed information flows to the deeper layers where it is relayed to pre-motor nuclei. Furthermore, it has been shown that multimodal inputs converge on OT neurons in Xenopus tadpoles [6] and that the periventricular neurons of the rainbow trout receive multi-sensory afferents and as such may be responsible for their integration [7]. While the superficial layers of the tectal neuropil have been well characterised, the functions of the deeper layers remain elusive, and the mechanisms by which they may mediate multimodal integration are unknown. The same applies to the thalamus, which is well known as a crossroads for a wide array of sensory information, but which is poorly understood at the level of cellular circuits. Although the cerebellum is generally viewed as a motor processing centre, evidence also suggests functions in sensory integration [8, 9]. Recent work has shown that cerebellar lesions disrupt pitch discrimination in human patients [10], and this has been corroborated by PET imaging showing an increase of activity in the lateral cerebellum during pitch discrimination exercises [11]. In rats, cerebellar Purkinje cells respond to whiskers stimulation and present a topographical map of the inputs [12]. In summary, while numerous brain regions have been shown to process sensory information, and while the interconnectedness of these regions must underlie sensory integration, we still have a poor appreciation for how different modalities are integrated, and how resulting behaviours are produced. The details of these relationships can only be described if the circuits can be characterised

at the cellular level, both in terms of their anatomy and their activity. As a transparent animal and with the rise of powerful light-based tools to monitor and manipulate the brain, the larval zebrafish offers a perfect window into functioning neural circuits. The system is particularly promising given the similarities that exist in the key sensory processing centres between zebrafish and mammals. Recent work in the host's lab has shown cerebellar outputs to the deep layers of the tectal neuropil and to the thalamus [13] and robust projections also exist from the thalamus to the tectal neuropil (Scott lab, manuscript in preparation). This establishes, at least at an anatomical level, the necessary components for complex cross-modal integration, with two important sensory-processing structures sending converging information into a third structure, the OT, which itself has been implicated in sensory integration. It also parallels closely the connectivity of the homologous mammalian brain structures in what may be an evolutionarily conserved integration mechanism. To clarify these relationships, we use transparent zebrafish larvae, in combination with transgenics and optogenetics, to study the functional links among cerebellum, optic tectum and thalamus in a way that has been previously unapproachable. We are using optogenetic neuromodulation [14] of the regions of interest using channelrhodopsin (ChR) by a Spatial Light Modulator (SLM) [15]. The SLM allows us to project holograms to precisely activate selected brain regions. Combined with the genetically encoded calcium sensor GCaMP6 [16] and single plane illumination microscopy (SPIM), we are mapping out the functional connectivity among the thalamus, cerebellum, and tectum, describing the scheme of functional separation and overlap in tectal cells receiving thalamic and cerebellar input. This will reveal the "code" within the tectal circuitry that integrates streams of information for different brain regions and sensory modalities. Outside of the OT, not much is known regarding the brain regions involved in sensory processing in zebrafish and how they are connected. We are using a pan-neuronal GCaMP6 [16] to identify, in an unbiased fashion, other brain regions involved in sensory integration, focusing on visual, auditory and lateral line input. To that end we are imaging the whole brain while we play sensory stimuli of each studied modality. This will allow us to identify the compartments of each brain regions that are responsive to each modalities, and register these patterns to identify how the inputs from different modalities may be combined or kept separate. For the data analysis, we are using the Thunder library [17] running on the NECTAR cluster. We are using simple correlation and non-negative matrix factorization that we found to be more robust and informative than principal component analysis. In our preliminary unbiased screen, we observed visual response in the thalamus and cerebellum, which confirms our interest in those brain regions. Interestingly, the thalamic response appeared tuned to a moving spot moving caudo-rostrally. Using genetically targeted expression of GCaMP in the thalamus, we further investigated the response profile of the thalamic response to changing polarity and size of the spot. Smaller spots or large bright spots on a dark background did not elicit any response. The thalamic response appears tuned to bigger, fast spots known to elicit hunting behaviour. By expressing ChR in either the thalamus or the cerebellum, we were able to use the SLM to specifically activate those brain regions and look for neural responses in the OT. We found that activating the cerebellum triggered responses in the optic tectum.

Activating the thalamus, which is inhibitory, triggered rebound firing in the optic tectum. These experiments show that functional connectivity exists between the cerebellum, thalamus and optic tectum. We plan to investigate how those feedback may be involved in the filtering of sensory information to trigger specific behavioural responses. This work will pave the way for further studies into the integration of multimodalities inputs, and the possible mechanisms by which they influence behavioural outputs. As a future direction, hopefully in my own independent research group, I would aim to identify the behavioural relevance of this integration in a stationary rheotaxis preparation. Such a preparation would allow me to present conflicting stimuli (flow and visual, for instance) to study their impacts on integration, and to activate or silence brain regions or circuits implicated in the above work.

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P22 Soma detection in *Drosophila* brain using machine learning

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To compute the neuronal structure in the Drosophila Melanogaster's brain is important to study the behaviors and gene function. Images of neurons are obtained by three dimensional confocal microscope. Two tasks in computing the neuronal structure are finding the cell-body and construct the neuronal structure. We present an automatic method to determine the cell-body by applying machine learning technique. Data set consists of raw data containing noises. The size of the image is 1024 ´ 1024 ´ 150. There could be more than one soma in the volume and the number of soma is not known. Data set consists of 100 volume images. These images are divided into 5-fold for cross validation. Proposed method starts with some candidate voxels that could be the center of the soma. These points are obtained by the distance transform of the image of the neuron. A regression model is then constructed based on the features that are voxel intensity, coordinate of the voxel, and density and balance factor around the candidate voxel. The result shows that sensitivity is more than 80% and true positive rate is near 90%.

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P23 Precise predictions of intelligence and personality traits from brain structure

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The recent surge of interest in the relationship between brain structure and cognitive function has revealed numerous correlations between regional morphometric properties of the brain such as grey matter volume and cognitive traits such as cognitive abilities and personality traits [1]. While consistent results across multiple studies [e.g., [2–4]] suggest the presence of personal information in structural MRI data, it remains unknown to what extent such brain-behaviour correlations allow us to make predictions about an individual's traits. In the present study, we used a machine-learning approach to predict an individual's age, gender, intelligence, and big five personality traits from high-resolution T1 weighted MRI images (1mm isotropic). One of the challenges to construct a predictive model from MRI data is the dimensionality of features (i.e., the number of voxels), which is typically much higher than sample size (i.e., the number of participants). In our current study, we used a relatively large sample for a study of this sort (n = 470), but there is still a 100-folds difference to the number of voxels corresponding to grey matter (i.e., ~450,000). To address this issue, we applied the regularization method called the elastic net, which has been shown to outperform other approach when the number of features is much larger than the number of samples [5]. Our results indicate that this approach can successfully construct highly accurate prediction models for age, gender, intelligence and all the five components in the Big Five Model of personality traits. This is in stark contrast with the conventional, univariate voxel-based morphometry (VBM) approach which shows only weak correlations between particular brain regions and traits. In summary, our study demonstrates the richness of the information we can extract from an individual's brain MRI scan, and suggests that possibility that we can create highly precise predictions models for intelligence and personality traits.

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P24 Harnessing cloud computing for high capacity analysis of neuroimaging data from NDAR

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Introduction
The National Database for Autism Research (NDAR, http://ndar.nih.gov) and other NIH/NIMH data repositories are amassing and sharing thousands of neuroimaging datasets. With the availability of this deluge of data and the development of the NDAR infrastructure for its organization and storage, the bottleneck for applying discovery science to psychiatric neuroimaging has shifted to the computational challenges associated with data processing and analysis. Maximizing the potential of these data requires automated pipelines that can leverage high-performance computing (HPC) architectures to achieve high throughput computation without compromising on the quality of the results. A disadvantage of this approach is that it requires access to HPC systems that are not always available, particularly at smaller research institutions, or in developing countries. Cloud computing resources such as Amazon Web Services (AWS) Elastic Compute Cloud (EC2) offers a "pay as you go" model that might be an economical alternative to the large capital costs and maintenance burden of dedicated HPC infrastructures. Realizing this need, the developers of the Laboratory of Neuro Imaging (LONI) Pipeline, the Neuroimaging Informatics Tools and Resources Clearinghouse (NITRC) Computational Environment (CE) and the Configurable Pipeline for the Analysis of Connectomes (C-PAC) have implemented pipelines in EC2 that interface with NDAR. Each pipeline was used to perform a benchmark analysis of 2,000 structural images from the NDAR database to establish the feasibility of this approach.

Methods
Each of three pipelines were installed into Amazon Machine Images (AMIs) and customized to perform structural preprocessing on NDAR data. The LONI Pipeline (http://pipeline.loni.usc.edu) was enhanced to permit direct access to NDAR collections for workflow-based data processing [1]. Workflows can be created from a combination of commonly available neuroimaging processing tools represented as Pipeline Modules. With respect the benchmark analysis, specifically developed Pipeline Modules captured the results from FreeSurfer and FSL FirstAll, updated the NDAR with the results and returned them back to the NDAR Amazon Cloud storage server. C-PAC (http://fcp-indi.github.io) is a configurable pipeline for performing comprehensive functional connectivity analyses that was extended to include the Advanced Normalization Tools (ANTs) cortical thickness methodology

[2] and to interface it with NDAR (https://github.com/FCP-INDI/ndar-dev). Results of this workflow include 3D volumes of cortical thickness and regional measures derived from the Desikan-Killiany-Tourville atlas (http://mindboggle.info/faq/labels.html). NITRC-CE (http://www.nitrc.org/projects/nitrc_es/) is an AMI that is pre-installed with popular neuroimaging tools. A series of scripts were developed for NITRC-CE to interact with NDAR, calculate a series of quality assessment measures on the data, perform structural imaging analysis using FreeSurfer and FSL FirstAll results, and to write the results back to NDAR (https://github.com/chaselgrove/ndar).

Results

Speeds obtained for processing structural data in EC2 were consistent with those obtained for local multi-core processors. For example, using an EC2 instance with 4 processors and 15 GB of RAM (m3.xlarge), the C-PAC pipeline was able to complete the ANTS cortical thickness pipeline in 8.5 h per subject, in comparison to 9 h on a local workstation with 12 processors and 64 GB of RAM. EC2 processing cost $1.94 per image for on demand instances and an estimated $0.26 per image when using spot instances.

Conclusion

Analyzing data using cloud computing is an affordable solution, with low hardware and software maintenance burdens; this can be beneficial for smaller laboratories and when data is already in the cloud. Further reductions in cost can be obtained using lower costs spot instances, which fluctuate in price and may get shut down if demand gets too high.

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P25 An attempt to correlate the activation of resting state network with behavioral data during virtual object transfer task performance

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Introduction
Resting state networks (RSN) are detected as functional connectivity of spontaneous low frequency fluctuations (<0.1 Hz) in the BOLD signal during "rest status," i.e., the subjects are not performing any task but they are awake. Several RSNs, which are supposed to be analogues of task related networks, have been identified, such as default mode network (DMN), motor network, somatosensory network, auditory network, language network, and so on [1]. Several studies reported dependency of activation in resting state networks on aging [2–4]. Given that a population of older adults will provide more variability and heterogeneity due to differences in physical and cognitive status as the results of their backgrounds and histories, it will be pertinent to examine if we can obtain a more sensitive index with specific RSN map corresponding to the neurological target of interest. One approach to extract age-related change of RSN will be classification of the subjects by using some behavioral data. In this study, we evaluated the effect of different phases of behavioral performance data included in one complex processing on the RSN activity detection.

Material and Methods
Neurologically healthy 24 older (61–75, 12 females) and 23 young (20–36, 12) adult volunteers who gave written informed consent participated in this study. The older volunteers were recruited from a community club. As the reference behavioral data, a virtual bean transfer task using turnkeys [5], which simulates one of the physical batteries for older adults was used. This task consisted of three serial operations; (1) a small, round object (bean) on the left (Lt) side of the visual field appears and the subjects hold them with two sticks, (2) the object is moved with the sticks toward a red round target (a pot) on the right (Rt) side, (3) finally, it is dropped into the target by releasing the sticks. The subjects repeated this operation for 6 minutes. For resting state fMRI, the subjects kept their eyes open and fixed their eyes to the cross hair displayed on the LCD monitor for 7 minutes. The functional magnetic resonance imaging (fMRI) data were obtained using a GRE-EPI sequence (3T, TR 3000 ms, TE 30 ms, 39 axial slices, 3 mm slice thick, 0.75 mm inter slice gap, matrix 64 × 64, FOV 192 mm). T1 weighted 3D images were obtained for anatomical reference. The functional images were pre-processed (slice-time adjusted, realigned, normalized and smoothed) with SPM8 (Wellcome Trust Centre for Neuroimaging, UCL, London). For RSN analysis, 25 independent components (ICs) were obtained using GIFT toolbox. Behavioral data were obtained from the turnkey log during the steps described above. The success

rate of holding the object and transferring it throughout the session was obtained as an index representing difficulty of task performance for each subject. The resultant *T*-statistics maps of the ICS for each subject were processed using SPM8 for 2nd level analysis ($p < 0.001$, uncorrected).

Results

The correlation between the success rate of holding and that of transfer were $r = 0.56$ in the older adults and $r = 0.71$ in the young adults group. The following differences of RSN were detected by employing the success rates of these two operations as covariates in the 2nd level analysis of IC maps. (1) Dorsal default mode network (DMN): Lt caudate head ($T = 5.5$) by holding covariate (HC); Lt BA7 ($T = 4.8$) by transfer covariate (TC) in the contrast of older–younger (E–Y). Lt caudate body (4.4) by TC, but no significant differences by HC for the contrast of young vs elderly (Y > E). (2) Ventral DMN: Lt BA40 ($T = 6.1$) and Lt Putamen ($T = 4.7$) by HC; Lt caudate body ($T = 5.2$) and Rt caudate tail ($T = 4.5$) in E > Y. Rt BA7 ($T = 4.4$) by HC; Lt BA7 ($T = 4.7$) by TC in Y > E. (3) Sensorimotor network (SMN): Rt caudate head ($T = 4.6$) and Rt BA6 ($T = 4.1$) by HC; Rt BA31 ($T = 4.8$) and Rt BA33 ($T = 4.5$) by TC in Y > E. Rt BA39 ($T = 4.5$) and Rt Putamen ($T = 4.4$) by HC; Lt BA3 ($T = 5.7$) and Rt BA4 ($T = 4.9$) by TC in Y > E. (4) Posterior DMN: No significant differences.

Conclusion

In this analysis, we focused on the RSNs of DMN and SMN. It was suggested that the activity of these RSNs may partially correlate with segmented behavioral data. Although the functional structure of DMN is considered to be heterogeneous and its role is still controversial, its relationship with attention and executive function has been suggested [6]. Since the trials were randomly started after a short rest, which was modulated by jittering, this task demands both attention for starting the operations and serial switching among the 3 operations. Therefore, we hypothesized that age-related decline of these functions may be reflected to the analogue RSN activity. The age-related decline observed in the DMN and increase in SMN was compatible with previous reports [3]. By introducing covariates representing performance level of different cognitive steps but continuously performed towards one goal, age-related change of RSN activity could be differentially characterized in several nodes, although such difference was not detected in the posterior node of DMN. Although this study was cross-sectional in nature, it potentially suggested that classification of RSN activity in the older adults may reflect the performance level.

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P26 Tracts discovery using the skeleton representation of neurons in the drosophila brain and application to connectome study

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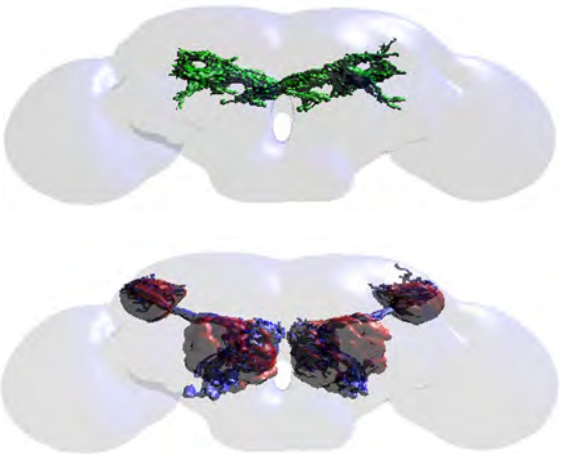
We present a method to compute the tracts in the brain of Drosophila. This method uses the skeleton representation of neurons that are obtained by the neuron tracing method first published in ISBI 2008. Purpose of the tracts discovery is to understand the connectome of neurons in the fly brain. An assumption for a tract is that it consists of a long enough branchless part of neuron called path. The proposed method cluster the paths according to the length, the location, and orientation of the paths. 16,000 neurons are in the database. 146 tracts (length greater than a given threshold) were discovered; some of them were not reported in the previous literatures, including a pair of crossing tracts. Each tract has a ring shaped structure at one end. We demonstrate a connectivity analysis using the crossing tracts. We can see that the ring structure grasps an arm of the mushroom body and a tract connecting AL and LH in the fly brain.



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P27 Development of the neurodata without borders: neurophysiology file format

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In this study, we examined the network model of our co-expressed gene groups, to study regulation mechanism, hierarchical structure and achieved function. One of our point of these analysis is connection characteristics of highly clustered and sparsely connected co-expression gene nodes. We will show the result of our investigation of the network measures and models concerning 3D expression map.

P28 Data management and license policy in EEGBase

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EEGBase (http://eegdatabase.kiv.zcu.cz) is a web repository of Electroencephalography (EEG) and Event-Related Potentials (ERP) experiments. These experiments produce large amounts of heterogeneous data. To give these data meaning they are described by accompanying metadata. We have tested several approaches to express metadata. As an initial step we defined an ontology [1] describing data produced in our laboratory. Because EEGBase had initially stored data only in a common relational database and we had needed to transfer them to Semantic web technologies, we designed and implemented a Semantic Framework software tool [2]. Semantic Framework maps data from common technologies (relational database, object-oriented model) to semantic web languages as Resource Description Framework (RDF) and Web Ontology Language (OWL). The usage of the Semantic Framework enables semantic web readers to access data stored in EEGBase using the RDF and OWL output directly. Moreover, the data produced in the RDF/OWL format enabled the registration of EEGBase repository as a data source within the NIF registry [3]. Despite benefits that the usage of Semantic Framework brought we were facing difficulties with inflexibility of the relational data model and user interface (UI) as collaborative researchers expressed their interest to use the system for various experiments. In addition, we also extended the scope of the laboratory for different experiments including electrocardiogram (EKG), muscle activity, motion abilities measurements, etc. As a result, we changed/extended the used terminology and ontology, data repository and user interface. The NoSQL database Elasticsearch was deployed to store experimental metadata. The relational database stayed for the data such as user accounts, where a relational integrity is required. Combination of the relational database and NoSQL database ensures both stability and data integrity of the system core and sufficient flexibility for experimental metadata. Efforts to provide a standard description of electrophysiology domain resulted e.g., in definition of odML terminologies [4], the Neuroscience information exchange format (NIX) (https://github.com/G-Node/nix) and in the development of the Ontology for Experimental Neurophysiology (OEN) [5]. Because OEN is not finished yet, we extended odML terminologies by metadata used in EEGBase and integrated odML into EEGBase. The resulted terminology containing almost 60 terms then describes almost any electrophysiological experiment. To facilitate the use of this terminology when entering metadata we decided to implement a system of user templates varying for different users and experiments. The described terminology then serves as a set of default terms offered to the user in the user interface. Moreover, the user can modify this set according to the needs in specific experiments. Such a modified set of terms can be saved as a template and used repeatedly. With rising interest in downloading experimental data a suitable license policy has to be implemented. The data produced in our laboratory are usually provided under "Creative Commons Attribution-Non-Commercial-ShareAlike 4.0 International License." The EEGBase

users who would like to provide their own experiments have two following options. They can create a free account but all uploaded data must accept a "free" data license policy. If the user wants to provide his/her data for a fee, he/she must pay for the account. The paid account is active for a restricted time period only. When this period expires, the user is asked to pay for a new period. If the user does not prolong the paid account, the license for the data is changed to a free license until the paid account is restored. Once data are downloaded under a free license, the license policy for their users who downloaded them is not changed even if the data owner changes the license by paying for the account later.

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P29 Metadata collection framework for consistent storage, analysis and collaboration

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Recent progress in neuroscience leads to increasingly complex protocols, experimental approaches, and variety in experimental metadata. Availability of tools for reliable metadata consolidation, as well as for effortless data and metadata access becomes crucial for efficient and reproducible research. In this work we present a framework targeted to improve metadata collection, storage, access and exchange, as important ingredients of experimental electrophysiology. The framework comprises a set of tools [1] for consistent metadata management in a single database. Metadata are always kept aligned to the same object model, relevant for a particular domain of neuroscience. To account for the huge diversity of experimental settings, we use modern resource description framework techniques [RDF, [2]], which provide the required flexibility in data annotation while enabling consistent organization and machine-readability. A common data scheme is provided by a core ontology with generally used terms that can be extended and customized to fit the specific requirements of an individual lab or project. A flexible plugin system enables including tools to extract metadata from proprietary file formats for automated metadata collection. Data storage is file based, supporting distributed storage and integration from multiple users and versioning using popular tools like git [3]. In addition, the usage of RDF enables integration of standards for provenance tracking [4] into the metadata collection workflow. A graphical interface provides key functions to create, manage, search and query metadata and annotations, but one can also directly access the stored metadata in files. Metadata is saved using standard RDF formats accessible with open source RDF libraries from Python, C/C++, Matlab and other languages. Moreover, the framework provides Java-based application access (API). These options enable integrating metadata and data management seamlessly within the data analysis workflow, fostering scientific progress through neuroinformatics.

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P30 Kernel electrical source imaging – spatial source localization from ECoG and SEEG recordings

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In epilepsy patients with pharmacologically intractable epileptic seizures surgical treatment may be the only solution. Often, non-invasive methods do not sufficiently localize epileptogenic foci and invasive methods of presurgical evaluation are necessary. These may include recordings of extracellular electric potential with depth electrodes, which is called stereoencephalography (SEEG), or with subdural electrodes placed directly over the cortex (electrocorticography, ECoG). Given these recordings one needs to estimate the spatial location of the sources in the brain that are to be lesioned. Improving the precision of localization of these sources from ECoG and SEEG recordings, which is termed electrical source imaging, is a major challenge of the field [1]. Here we propose a new method, kernel Electrical Source Imaging (kESI), which takes into account realistic brain morphology and spatial variations in brain conductivity. The method can localize multiple sources, and is flexible to arbitrary electrode positions and so it can be used effectively for a specific patient's case. The core of the method is in the construction of kernel functions requiring computation of the potentials generated in the brain by numerous basis functions covering the probed volume, which is an extension of our previous work [2]. To show the proof-of-concept we generated dipolar ground truth data inside a simplified spherical brain model with uniform conductivity. We assumed the electrodes on the surface of the sphere and inside the spherical volume emulating ECoG and SEEG style recordings, respectively. The potentials generated at these electrodes were computed using Finite Element Methods (FEM) in FEniCS software, the mesh was generated in gmsh. In kESI, this FEM model was used to compute the potentials generated by the basis functions, and hence obtain the reconstructed sources. We could show how different distributions of electrodes affect the quality of reconstruction. This may lead to a procedure for prescribing optimal distributions of electrodes depending on available prior knowledge (e.g., dysfunction of specific brain structures) and clinical resources (availability of specific electrodes, etc).

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P31 Corticostriatal circuits and their role in disease

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The basal ganglia (BG) represent subcortical structures considered to be involved in action selection and decision making [1]. Dysfunction of the BG circuitry leads to many motor and cognitive disorders such as Parkinson's disease (PD), Tourette syndrome, Huntington's disease, obsessive compulsive disorder and many others. Therefore, we simultaneously recorded local field potentials (LFPs) in primary motor cortex and sensorimotor striatum to study features directly related to healthy versus pathological states such as Parkinson disease and levodopa-induced dyskinesia [2, 3]. The striatum, the input stage of the basal ganglia (BG), is an inhibitory network that contains several distinct cell types and receives massive excitatory inputs from the cortex. Cortex sends direct projections to the striatum, while striatum can affect cortex only indirectly through other BG nuclei and thalamus. Firstly we analyzed spectral characteristics of the obtained signals and observed that during dyskinesia, the most prominent feature was a relative power increase in the high gamma frequency range around 80 Hz, while for PD it was the beta frequency range. Secondly our preliminary results have shown that during both pathological states effective connectivity in terms of Granger causality is bidirectional with an accent on striatal influence on cortex. In the case of dyskinesia we have also found a specifically high increase in effective connectivity at 80 Hz. In order to further understand the 80-Hz phenomenon we have performed cross-frequency analysis across all states and both structures and observed characteristic patterns in the case of dyskinesia in both structures but not in the case of PD and healthy state. We have seen a large relative decrease in the modulation of the amplitude at 80 Hz by the phase of low frequency oscillations (up to ~10 Hz). It has been suggested that the activity of local neural populations is modulated according to the global neuronal dynamics in the way that populations oscillate and synchronize at lower frequencies and smaller ensembles are active at higher frequencies Our results suggest unexpectedly a lack of coupling between the low frequency activity of a larger population and the synchronized activity of a smaller group of neurons active at 80 Hz.

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P32 Network analysis of 3D gene expression pattern, using microtomy based transcriptomic data sets in ViBrism DB

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We have succeeded to examine the three dimensional expression patterns of wide varieties of RNA molecules in the whole anatomical context of the brain by the development of microtomy techniques, and created a database, ViBrism DB, in which measured expression densities are used for three dimensional (3D) expression map reconstructing with the microtomy techniques, and disclosed various spatial expression patterns concerning mouse brain. By the use of our expression maps, we also have created co-expression network graphs of genes of interest.

P33 An ontology-based semantic question complexity model and its applications in neuroinformatics

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Neuroscience is an important field of study because of the huge number of neurological disorders [1] and the quest scientists have for solving brain mysteries [2]. Enormous datasets containing large images are commonly produced in this field [3]. Usually, data are gathered using different methods in different labs and data resources are scattered. Also, ordinary methods of searching might not be enough to resolve the semantics of scientific questions properly. Therefore, scientists are always looking for better tools to handle and search the data. Data structures and schemas such as ontologies [4] have evolved to assist managing the bulk of information in this field and ontology-based (or enhanced) applications have been developed to assist neuroscientists in handling the information. Ontology-based applications have practiced different approaches [5] including using ontologies for question answering both in restricted (closed) domains with the approach discussed in [6] and open domains such as the approach used in PowerAqua [7]. There have been few efforts in question answering in neuroscience and a limited range of question types have been addressed in them. Current approaches do not use the full potential of ontologies, mostly use basic relationships such as "is_a" and most of applications have limited capability of query expression [7]. For example, they can answer queries asking for "volume" or "inferior parietal lobule," but are not able to understand and answer questions such as "what is the volume of inferior parietal lobule of the brain?." Therefore, an approach which addresses question answering in a systematic manner and considers the complexity of questions and their structure seems necessary. This way, shortages of the field and the scope of the research will be clearer; also, more complex questions can be identified and answered. In this research, an ontology-based model is proposed which has the ability to track changes and helps in answering conditional questions. To build this model, sample questions sourced from experts and literature are analyzed, tokenized and then clustered until a state known as theoretical saturation [8] is reached. The outcome of this process is 8 clusters which are called dimensions. These eight dimensions are: relationships such as partOf and subClassOf; concepts involved such as hippocampus and Precentral Gyrus; domain-specific phrases that specify scientific processes or attributes such as curvature, activation, volume and thickness; changes such as extra or time (temporal changes); summary or statistical phrases such as summary, total number; data resources such as ontologies or data-files; conditions such as connected and finally indeterminate phrases such as elderly. Relationships, concepts and domain-specific phrases are loaded

from ontologies in neuroscience such as NIFSTD [9] and this, makes the model an ontology-based one. The model has some unique features such as the potential to cover temporal changes. The evaluation of the model was done via a different set of sample questions from a different expert team of neuroscientists. After proposing the model, its applications including capability of inferring information, question classification, and interface design are investigated. At the lowest level, dimensions can be individually used to infer or enquire information. For example, questions containing indeterminate phrases can be marked as "unanswerable" as more information is needed to resolve them. This information can be either enquired using user interaction processes or guessed through applying methods such as fuzzy logic. Another example is that in many cases, the type of the answer can be known by looking at the dimensions present in the question. For example, when the value of the domain-specific phrase dimension is volume, it means that the question is looking for the volume which is a number. Using the model and techniques such as ontology-based query expansion [10], a range of question can be answered which were not answerable without the ontologies. A question classification or taxonomy can be shaped using model dimensions. Question classification is the task of assigning categories to questions [11]. Individual or multiple dimensions can be used to build this classification. For example, considering the number of resources as the core dimension of the classification, level 1 would be questions using only one ontology as the resource. Level 2 would have two ontologies as the resource and possible ontology mapping would be needed to map the two ontologies. This goes on and at the highest level (level *n*) the classification would have *n* ontologies. The question answering system which is built in response to this question classification will be a mediator system that integrates resources in order to answer a question. Another use of the model is in interface design; also dimensions can be seen as frame semantics [12] of complex questions. Dimensions can be fields of a keyword-based (concept based) interface [13] where they are categories (or drop down lists) and related values are loaded from ontologies, data resources and other pre-defined lists into them. Doing this, the user will be guided through posing a scientifically valid question and the cost of query translation will be omitted. TAMBIS [14, 15] is an example of keyword-based interface. It worth mentioning that the model can also be used to build faceted search interfaces [16] or text-based ones [13].

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P34 CARMIN: a common web API for remote pipeline execution

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Introduction
Web platforms are changing the practice of neuroinformatics by enabling transparent, remote access to computing infrastructures (clusters, grids, and clouds) and to federated databases. However, their interfaces sometimes lack documentation and they remain non-uniform, which is detrimental to wider adoption and sustainability. We describe the on-going efforts of the France Life-Imaging national infrastructure [1] to define CARMIN (Common API for Research Medical Imaging Network), a common API for pipeline execution on the web that will allow a greater integration between image data repositories and image processing workflows for both Push and Pull data streams.

API Concepts
Our API manipulates objects that contain mandatory or optional attributes and functions. Function calls return a response envelope containing the status code returned by the function (0 in case of success), an optional message, and possibly the object returned by the function. The API is modular so that platforms may support only consistent functionality subsets, defined by a list of objects. Object functions referring to objects of a different module must be optional. Platforms advertise their list of supported modules and other presets through a GlobalProperties object.

API Definition
Our API currently manipulates the following objects that are part of a Processing module: (1) Pipeline describes the input and output parameters of a pipeline, the pipeline name and version, and optional error codes and messages associated to the pipeline. Pipelines have two functions allowing to get the attributes of a specific pipeline, and to list pipelines available in the platform. (2) Pipeline Parameter defines the input and output of a pipeline. It has a name, a type (File, String, Boolean, Int64, Double, or List), and two booleans that specify whether the parameter is optional, and whether it is an input or an output. It may also have a default value and a description. (3) Execution is the object associated to a pipeline execution. It has a name, a status (Initializing, Ready, Running, Finished, Initialization Failed, Execution Failed, Unknown, or Killed), a timeout after which the execution is killed, a list of input values associated to pipeline parameters, and a list of returned values. An execution

may also contain an error code, standard output and error, and a start and end date. Executions functions include get, update, init, play (launch), kill, delete, and get Results.

Authentication
Two authentication functions are available but only one of them must be supported by the platforms. Authenticate HTTP implements basic HTTP authentication, i.e., the user name and password are passed in the HTTP header. Authenticate Session works at a higher level, i.e., it leave it up to the platform to check the user's credentials and set a session.

Implementation
The API is being implemented in the CATI [2], FLI-IAM WS, and VIP [3] execution platforms. We use SOAP Web-Services to ensure compatibility with other services in France Life-Imaging. Our API specification and on-going implementation are publicly released and available at https://github.com/fli-iam.

Future Work
We are working on a Data module for data transfers, and on a Management module to interact with users and groups. A restful implementation is also under study. Furthermore, we are considering extensions to support other platforms, in particular CBRAIN [4]. We welcome any collaboration to further extend and improve this API specification.

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P35 Boutiques: an application-sharing system based on Linux containers

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Porting applications to computing platforms is a costly and error-prone process which is often replicated several times while sharing applications would enable repurposing and facilitate interoperability. Existing application-sharing systems are usually bound to a particular infrastructure or execution environment, which makes applications hardly transferable between platforms. Recently, the wide spreading of Linux containerization, in particular through the Docker system, has enabled the sharing of virtual appliances at an unprecedented scale. We present the Boutiques application-sharing system based on Docker containers. Applications described in Boutiques consist of (1) a JSON descriptor stored in a Git repository and (2) a Docker image containing the application and all its dependencies. We implemented software tools to create Boutiques applications and to import them to CBRAIN [1], VIP [2], and Pegasus [3]. Using this framework, we were able to import 11 applications from Boutiques to our three platforms in a few hours only. This proves the concept of Boutiques which we plan to extend to other computing platforms and to more complex application descriptions, including pipelines.

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P36 Multidisciplinary approach to identify gene-environment interplay triggering autism

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Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder characterized by deficits in social communication and interaction, restricted interests and repetitive behaviours. Many ASD patients suffer of comorbidities including epilepsy, sleep problems, metabolic conditions and gastrointestinal disorders (GID) [1]. Although causative mutations have been found in ~30% of autistic children, for most of the patients the cause of the disease is still unclear. Recent findings suggest that gene-environment interaction plays an important role in the aetiology of the disorder. Among environmental factors, gut microbiota are now receiving great attention as possible triggering agent of autism. Metagenomics analyses of gut microbioma of ASD children with GID and intestinal permeability have found dysbiosis [2] that correlates with disease risk and severity probably through a microbiota-gut-brain axis [3, 4]. Indeed, intestinal pathogens lead to impairment of immune system, to production of toxins and neurochemical compounds and to leaky gut causing the adsorption of many xenobiotics [5]. In addition to gut pathogens, a genetic predisposition and an alimentary factor increasing intestinal permeability were also found. The genetic risk was imputed to haptoglobin gene (HP), that plays a key role in the regulation of intestinal tight junction. This gene has 2 common co-dominant alleles whose distribution is different between several immune-mediated diseases, including schizophrenia, and healthy population [6]. The alimentary cause is imputed to gliadin (a component of gluten), that binds to the chemokine receptor CXCR3 that, in turn, activates haptoglobin [7] thus enhancing gut permeability. On the other hand, circulating microRNAs are a promising class of biomarkers for many diseases, including autism [8], and for their prognosis definition. Recently, among circulating human microRNAs, exogenous RNAs (xenomiRs) from plants (diet-derived), bacteria and fungi were found as part of a circulating RNA homeostasis [9, 10]. In this scenario, we have recruited 222 ASD patients and 100 controls and collected biological samples and clinical data as well as the alimentary diary. We are performing a multidisciplinary analysis in order to identify the genetic risk factor(s) and the environmental cause(s) triggering the disease. To this purpose high-density genotyping analysis, by "HumanOmni1S-8 v1.0 DNA Analysis BeadChip," has been carried out on both patients and controls and bioinformatics GWAs is in progress. HP genotype will be also analyzed in the same samples. Parallel, circulating total RNAs have been isolated from the serum of a subgroup of 25 ASD patients and 25 controls and the

quantification of a set of human microRNA is nearing completion. In serum samples food intolerances have been analyzed too. Neuroinformatics integration of the obtained results with the available gene list of corresponding anatomical structure(s) and with data available from Allen Human Brain Atlas [11, 12] will be performed in the frame of the INCF Digital Atlasing Program Further ASD patients suffering from GID and healthy controls will be recruited and samples of blood, serum and feces collected as well as clinical data and dietary diary. GWAs, circulating RNAseq and stool metagenomics analyses will be performed on biological samples in order to identify the endogenous (genetic risk and human circulating microRNAs) and exogenous (microbiota and xenomiRs) profile of ASD patients and controls. All the data obtained will be submitted to a neuroinformatics integration and systems biology analysis to find a possible gene-environmental cross-talk via epigenetic mechanisms.

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P37 Development and usage of odML based OpenEHR archetypes in electroencephalography

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Electroencephalography (EEG) as a non-invasive brain waveforms measurement is being used even outside laboratories or hospital environment. Behaviour of our brain during daily mental activities could be an interesting subject of a long term recording and analysing. Affordable headsets (e.g., Mindwave, Brain link, one-purposed-like devices as Mindflex games etc.) are good examples of home EEG peripherals to BCI (Brain-Computer Interface) applications. Neurofeedback can be used not only to handle BCI apps or games, but even for brain training itself (e.g., software home-of-attention comes with the idea of virtual coach for brain). A user can train intentional evocation of his/her alpha and lower beta waveforms (meditation, concentration) and improve his/her attention. Another situation is, e.g., when a sport shooter wants to know a relation between the waveforms produced by his/her brain during various mental and physical states (training, competition, illness, stress etc.) and his/her shot score. Such results can be very useful, but to make this a reality, standardized data description (a proper set of metadata included) and suitable application are crucial. An electrophysiology metadata set is a frequently debated topic. EEGBase [1] presents a metadata set designed besides others by domain experts from Pilsen University Hospital. OdML [2] provides a metadata format and also well described and respected set of metadata (definitions, datatypes, restrictions etc. included). The NIX project [3] implements odML terminology within the universal data format for electrophysiological data. Last but not least OEN [4] (Ontology for Experimental Neurophysiology), which is currently under development, extends the scope of metadata set and increases its expressive power. Nevertheless, the metadata set can never be finite. If the above mentioned shooter wants consider data from other domains as well (e.g., diet), the data becomes a metadata for the current domain (electrophysiology in that example). For that reason an idea of personal electronic health record system was proposed [5]. It is a system, where the user will be able to store "any" bio data for which a particular domain description (in form of a module) exists. The modules would extend the system with new domains, analytic functions etc. An openEHR concept was chosen to solve this modularity. Its idea is to describe various domains (or their pieces) by three layers: (1) generic reference model (RM) (general data properties and structure); (2) specific domain archetype (concrete data structure, ontology bindings, and data restrictions); (3) data input templates (solves problems of specific cases like complementary restrictions, archetype subset, archetype composition etc.). Since reference models are immutable and templates are very specific for each implementation, archetypes are the core of a well described

domain. Currently, no archetypes for electrophysiology exist in the public openEHR archetype repositories (so called Clinical Knowledge Managers, CMKs). A first set of our electrophysiology archetypes was designed according to EEGBase metadata, which was merged with the odML metadata subset. Terms binding with any ontology was not considered in the solution. Current version is proposed as fully based on odML. Because odML is not full-fledged ontology its terms do not have the URIs. This issue had to be solved as well as "odML to openEHR archetypes" transformation technique. There are three transformation proposals – automatic, semiautomatic and manual. Automatic approach considers that all archetypes are based on cluster reference model. Cluster RM provides loose tree structure of attributes (so-called datapoints) without any mandatory parts or restrictions (like, e.g., protocol or history in case of Observation RM). It means that one archetype is created for one odML root section). Subsections are represented by nested clusters. OdML attributes can be mapped directly to the archetype datapoints, where complex data types (non-primitive data types) are substituted by slot datapoints (reference to other archetype, which represents complex data type). An explicit mapping between odML and openEHR data types is necessary. Absence of specific RMs can be solved by semi-automatic approach. An odML section is manually mapped to a specific RM. Its subsections and attributes have to be assigned to a proper part of archetype (e.g., if the experiment is classified as an observation RM, than its protocol must be specified). This process could be non-trivial because odML attributes, crucial for a given RM, may be absent. This has to be fixed manually. The rest of the attributes can be mapped as in the previous approach. Manual design of archetypes starts from scratch and uses odML only for its list of terms and definitions. This approach presupposes new description of the electrophysiology domain. The process is similar to the development of a new ontology. Therefore, an already existing ontology could simplify the development process. While the first way limits the openEHR power, the third approach in connection with already existing and well-designed ontology could bring more benefits. Semi-automatic approach provides suitable solution for most cases. As it was mentioned before, each datapoint in the archetype should be bound to a particular ontology/terminology term using a public unique ID/URI. Since single terms (properties) from odML terminologies do not have their own IDs, for that reason, their identification was proposed. It consists of the URL to the (root) section of odML repository (e.g., http://portal.g-node.org/odml/terminologies/v1.0/experiment/electrophysiology.xml) and XPath to the given term (e.g., /odML[@version=1]/section/property/name[text()=Type]/./value[-text()=EEG] for property of type "EEG"). For the next version, OEN is expected to be used. Before archetypes will be published in public CKM, their draft forms are available at https://github.com/NEUROINFORMATICS-GROUP-FAV-KIV-ZCU/sehr/tree/master/CKM.

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P38 Usefulness of a neural network having the logistic function as the activation function of its output unit

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Posterior probabilities are used as Bayesian discriminant functions. It is well known that a neural network can learn a posterior probability [1]. In the two category case, the logit transform of a posterior probability is a log ratio of two probability measures shifted by a log ratio of two prior probabilities. Since the logit function is monotone, the logit transform of a posterior probability is also a Bayesian discriminant function [see Ref. [2]]. Though there is no simple way of obtaining a Bayesian discriminant function of the latter type as an output of a neural network, it can be obtained as the inner potential by training a neural network. If a neural network has the logistic function as the activation function of the output unit, the inner potential of the unit is the logit transform of the output. If the two probability distributions are from the exponential family and the network outputs the posterior probability, the inner potential has thus a simple form. Using this simplicity, Funahashi [3] has proposed a neural network which may approximate a Bayesian discriminant function, where he has supposed that the probability distributions are normal. We have shown that a network based on the algorithm given in [4] can in fact learn Bayesian discriminant functions [5], though Funahashi has not shown that his network can learn a Bayesian discriminant function. We have also shown that the network can be extended to multi-category cases [6]. We show that the neural network with the output unit having the logistic activation function is versatile, mainly because the inner potential of the output unit of a trained neural network is approximately a log ratio of two probability measures. The network has a capability of converting a Bayesian discriminant function to the corresponding Mahalanobis discriminant function. If the probability distributions are normal, the conversion can be done simply by shifting the inner potential of the output unit by a constant, because the logarithm of the p.d.f. of a normal distribution is a linear function of the square of the Mahalanobis distance. The network can also estimate the constant, the size of the sift [7]. Even if the distributions of the teacher signals are not normal, their distributions can be converted to normal individually, by applying the law of large numbers and the central limit theorem, in a way that keeps the means and variances of the distributions. Hence, the network can be used to obtain a Mahalanobis discriminant function, even when the distributions of the original teacher signals are not normal [8]. Furthermore, the network can realize the algorithm of Khasminskii et al. [9] for estimating Markov chains because the posterior probabilities at the respective steps can be obtained by shifting the inner potential of the output unit. These algorithms can be extended to multi-category cases, if several neural networks are simultaneously used [6, 8].

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P39 Closing the feedback loop: experiences from community driven development of a file format

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Modern science is evolving towards a multidisciplinary and highly collaborative endeavor in which it is not necessarily the same person that records and analyzes the data. Therefore a unique, non-proprietary and open format capable of storing many different types of data and allowing sufficient metadata for data annotation is needed to allow easy and efficient use of data sharing, archiving and reuse. Here we review technical difficulties and solutions, the need for community input, and the role the INCF played and could play in community-driven neuroinformatics software development, using the example of the NIX file format for electrophysiological data. The NIX project started in the context of the Electrophysiology Task Force of the INCF Data Sharing Program [1]. Initially, it was intended to be a proof of concept but soon evolved in many iterations into a seriously pursued project with more than 3000 commits into three different repositories [2] and extensive documentation [3, 4]. Today the project includes a well defined data model [5] as the foundation of a file format specification based on HDF5 [6]. A C++ I/O library was implemented, allowing users to read and write NIX files without having to care about the exact format specification. Language bindings in Python and Matlab ensure availability in multiple environments. In this process we encountered challenges at technical, logistical, and sociological levels. One aspect, probably common to many such projects, is that resources are limited and development for the greater part relies on a small group of contributors with diverse backgrounds residing at different locations. Improving communication, collaboration, and code quality management is therefore essential. Second, software that is intended to be useful to a broader community poses substantial demands on cross-compiling and cross-platform support, deployment, and packaging. In these technical demands, the NIX development benefited strongly from tools freely available to open-source projects that support unit testing, coverage estimation, code review, and continuous integration. Further, it is crucial to guide development by multiple use cases and feedback from scientists. While several labs participated in the process, engaging the wider community proved difficult because scientists, even those that are interested in the developed software, have to focus on their research and do not immediately profit from participating in the development. Given time constraints and publication pressure, how can we give experts an incentive to invest themselves into such projects? We will discuss experiences and perspectives regarding this challenge, as well as the role organizations like the INCF could play in helping to bring together developers and scientists and thus to close the feedback gap. In addition to the

issues raised above, defining a file format that fulfills the needs of the neurosciences is, on its own, a demanding task that strongly depends on expert feedback. In this presentation, we want to share our experiences and seek fruitful discussions on both community-driven software development in a scientific working environment and the file format itself, which probably leaves room for improvements and more effective design in future versions.

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P40 Synapse transmission between neurons in different systems of dimension

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Synapse transmission between neurons in different systems of dimension *n* Math and Music Physiological Base. The physiological substantiation on the application of the digital system for coding and decoding of a melody is the following: children begin their contact with digits already in preschool age, when they are taught to count, and this system is learned by children quite firmly, since it is often used in their daily life. But the generally accepted music grammar is new for them and, naturally, requires some additional period of time to be acquired by children. It is for that reason that in the initial period of musical teaching, children inevitably spend a lot of time and efforts to read a melody written down in music signs. Naturally, it slows down rate of training, causes psychoemotional discomfort, lowers the child's interest to music. Therefore, in the initial stage of teaching, besides work with generally accepted music grammar, will be useful to replace it with a digital system for a certain period. This does not mean that we want to do without standard music grammar, but at the initial stages of musical education, the system of digital coding and decoding of music sounds is undoubtedly useful, as it speeds up teaching of children. Neurophysiological Aspect. It is well known that the difficulties in the perception of any information, including musical one, cause strain of the main functional systems in the child's organism. The developed digital technology of musical training is perspective, has a practical result, but it requires the physiologic and psychology researches devoted to studying of an influence of a recommended method to psychoemotional status and to a condition of the main functional systems of the child's organism: the central nervous system, the muscular system and others. For this purpose, the experimental researches are to be performed, namely: ENG, EMG ,EEG – tests to study the degree of mental load that the child has received in perception of the information recorded in different systems of dimension. Test Electronystagmography allows us to investigate eyeshot, positional nystagmus and also to determine the quantity of fluctuations of the eyeballs during the perception of melody written in the music marks and digital symbols. Electromyography test, allows us to investigate the threshold of muscular irritability (min – max)and amplitude of muscle tension, depending on effort and accuracy of pressing of a key on the keyboard of the instrument. The method of ENG and EMG joins the visual analyzer with neuromotor function of the hands and explains, on the scientific point of view, the ratio between the load on muscles of eyes and muscles of hands, and also it proves the possibility of development of muscular fatigue in hands depending on the quantity of eyeballs' fluctuations. EEG – test allows us to make up the comparative diagrams of dynamics of the proceeding neurophysiological processes, and also it offers an opportunity to investigate the functional activity of neurons during the synthesis both of music and digital patterns. The realization of the described scientific researches in this direction will allow us to approach closer to

understanding of more subtle mechanisms of the child's mental activity and to detect the physiological factors in the promotion to the enhancement of the speediness, quality and efficiency of musical education. Parallel Description In practice, using the generally accepted music grammar, the child connects the definition of the location of the melody to the pitch i.e., to the system of dimension, which is written down in the form of an expanded construction, both on x – the horizontal and on y – the vertical. By reading the music information, the direction of eyeballs' movements is spasmodic, and it has a multistep combination both on y – the vertical, from the G – key up to the F – key, and on x – the horizontal often with a return of eyesight to the starting point of support. For an integration, synthesis and the modification of the complex pattern of the received information the structures of the central nervous system require an additional period of time. It is a neurophysiological process proceeding in an interval of time between the moment of perception of the music information from the sheet and the moment of the hands' response on the keyboard of an instrument. A great number of irregular nervous impulses are transferred to the central nervous system per unit of time and, as the consequence of this, the fatigue of hand muscles is considerably increased [1]. An amplitude of muscle tension is directly dependent on the frequency of innervation, where each subsequent nervous impulse coincides with the phase of increased excitability of the muscle [2]. At the level of the synaptic terminal we can see untimely synthesis of the neurotransmitter, deep and stable depolarization of the postsynaptic membrane and, as a result, the convulsive reflexes are thus formed. An important neurophysiological moment has been marked: within a short time interval the contracture, that is, constantly high muscular tension is formed, which in turn, is harmfully reflected on the content and character of the melody. In practice, using the method of the digital key, the child connects the definition of digital melody to the system of dimension which is written down in the form of an integral construction both on x – the horizontal and on y – the vertical. Reading the digital information the trajectory of eyeballs' movements on y– the vertical is projected to the exact determinant (digit, sign, symbol), the trajectory of eyeballs' movements on x – the horizontal is projected in one direction, forward. In the given system of dimension the integration of the digital information proceeds instantly, its realization on an instrument proceeds in reflexive time – ratio. The paradoxical phenomenon is revealed: the time interval between the moment of perception of the digital information and the moment of the hands' response on the keyboard of an instrument, is contracted to the minimum. We achieve a reduction of load on hand muscles at the expense of decreasing of an amplitude between muscle tension and the resulting movement and, consequently, the time intervals between effort and accuracy of pressing of a key are considerably shortened. At the level of the synaptic terminal we can see an allocation of neurotransmitter directly proportionally to the frequency of generated impulses by neurons and, as a result, the coordinated reflexes are thus formed. An important neurophysiological moment has been marked: the reciprocal muscular innervation is formed, that is, the rational distribution of the manual technique on the keyboard of an instrument, which in turn, is considerably reflected on the content and character of the melody. Grain of truth lies in the fact that at the expense of perception of melody by means of digits its

realization becomes faster and easier, which in turn, is positively reflected on the psychoemotional status of the child and enables him to dynamically realize the potential music abilities in psychosomatic action as a result. Statistics and practice show that the period of learning by standard music grammar is delayed for several years. At early stage of learning at Children's Music School, within of two – three months, up to thirty percent of children lose their interest to music subject and leave the study. This phenomenon is explained by the study overload arising at the first contact of the child to difficult format of adopted note coding and decoding of music information.\ Kids of new generation should have different methods of training. They are capable to perceive information faster, with cross-modal processing, activating all senses at once: visual perception, audio analyzers, neuromotor functions. http://reflectionmusic.ucoz.com/by Stepanov S. M., Ukraine

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P41 Butterfly: a paradigm towards stable bio & neuro informatics tools development

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Particularly in life science, with the front runner fields Bioinformatics and Neuroinformatics, the world has been changed by small, efficient, fast, logical, embedded and intelligent software, databases and management systems. Software design and its engineering are essential for bio and neuro informatics software impact. We propose a new approach "Butterfly" (1, 2), for the betterment of modelling of scientific software solutions by targeting key developmental points: intuitive, graphical user interface design, stable methodical implementation and comprehensive output presentation.

The focus of research was to address following key points:

(1) Differences and different challenges required to change from traditional to scientific software engineering.
(2) Scientific software solution development needs feedback and control loops following basic engineering principles for implementation.
(3) Software design with new approach which helps in developing and implementing a comprehensive scientific software solution.

Conscious adaptation of Scientific Software Engineering (SSE) principles as exemplified here by the suggested butterfly design and its multilayered architecture (Figure 1) might look like an increase in developmental work load in comparison to many current bioinformatics programming methods. However, on the long run, it will reduce the burden by making the scientific application well designed, flexible, structured and reusable. It allows a product line development, is analytical and allows qualitative software improvement. Furthermore, Human Computer Interaction (HCI) concepts make it user friendly, easy to learn and to deploy.

We validated the approach by comparing old and new bio and neuro informatics software solutions. Moreover, we have successfully applied our approach in the design and engineering of different well applied and published Bioinformatics and Neuroinformatics tools including DroLIGHT (3–5), LS-MIDA (6), Isotopo (7), Ant-App-DB (8, 9), and Lipid-Pro (10).

Keywords: Neuroinformatics, Bioinformatics, Butterfly Paradigm, Human Computer Interaction, Scientific Software Solutions

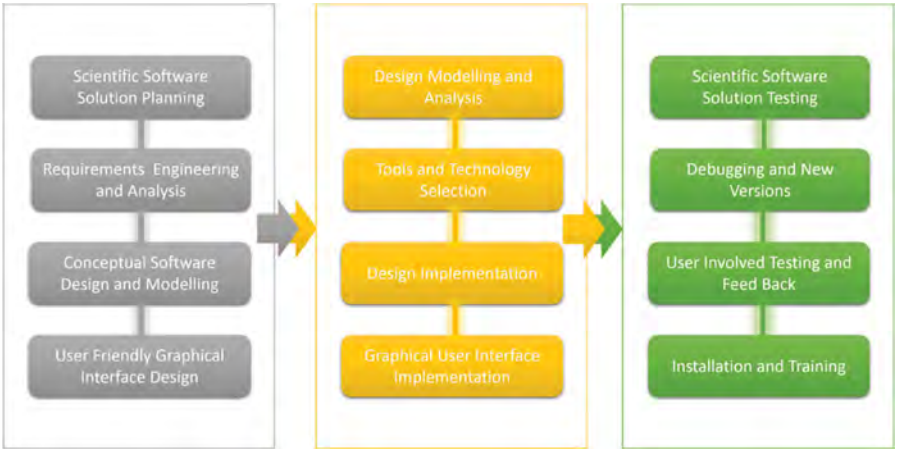

Figure 1. **Butterfly three layer model.** Shown in grey is the abstract layer, the basis for design and development (yellow), followed by implementation and testing by the user (green) so that the software is released including installation and training.

Acknowledgements
The authors would like to thank German Research Foundation (DFG- TR34/Z1) for funding on this research. The authors thank to the University of Wuerzburg Germany, University of Massachusetts USA and The Jackson Laboratory USA for support in this publication. Authors also thank to all interested colleagues for critical input on the approach and anonymous reviewers for helpful comments.

Conflict of Interest
The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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P42 Increased levels of FFA during heat stress after a 2-week repeated heat stress

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The purpose of this study was to determine whether repeated heat stress is closely related to circulating levels of free fatty acids (FFA) during repeated heat stress, defined as immersion of the lower body up to an umbilical level in hot water, 42 ± 0.5°C (three times/week, 30 min/day) for 2 weeks. There were significant correlations between mean body temperature and FFA before and after repeated heat stress ($p < 0.001$, respectively), and the level of FFA was significantly higher after repeated heat stress during heat stress ($p < 0.01$). The threshold of mean body temperature for lipolysis was lowered by repeated heat load and enhanced lipolysis during heat stress. However, caution is needed for diabetic individuals.

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P43 Caffeine links dopamine and serotonin release during passive heat loading

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The aim of this study was to investigate the serum serotonin (5-HT), prolactin (PRL) and plasma dopamine (DA) levels in humans with and without caffeine ingestion during and after passive heat loading (half immersion in 42°C hot water). Eleven male volunteers participated in the randomized experiment (CON, $n = 15$, 200 mL of tap water vs. CAFF, $n = 15.3$ mg•kg^{-1} and 200 mL tap water). After 60 min, passive heat loading was conducted for 30 min. Blood samples were collected and assessed for 5-HT, DA and PRL with and without caffeine during and after passive heat loading. 5-HT was significantly lower in the CAFF group compared to the CON group after passive heat loading for 30 min (Post) ($p < 0.05$) and also after 60 min of resting ($p < 0.01$). DA and PRL were significantly higher in the CAFF group than in the CON group at the Post time point ($p < 0.001$). In conclusion, 3 mg•kg^{-1} caffeine ingestion prior to passive heat loading can alter central serotonergic and dopaminergic activity, which may contribute to reduced central fatigue and subsequently, to reduced general fatigue. Prolactin responses during passive heat loading were also significantly related to caffeine ingestion in this study. However, the inhibitory effects of DA on PRL by caffeine remain to be elucidated.

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P44 Neuroprotective effects of α-mangostin against scopolamine-induced cognitive deficits

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Cholinergic neurons, particularly in the basal forebrain, are markedly depleted in Alzheimer's disease (AD) which is associated with cognitive deficits. Muscarinic antagonist scopolamine (SCO)-induced cognitive deficits is commonly used as a model for AD. The extract from the fruit rind of mangosteen (*Garcinia mangostana* L.) was recently reported to improve spatial memory in SCO-induced amnesic rats. α-Mangostin (α-MG) is an aprenylated xanthone derivative from the fruit rind of mangosteen. The effects of α-MG on learning and memory performance were thus investigated in SCO-induced amnesic rats. Eight groups (n = 8 each) of 8-weeks-old male Wistar rats were i.p. injected with normal saline solution (1 ml/kg), donepezil (2 mg/ml/kg; positive control), α-MG (50 mg/ml/kg), or α-MG (100 mg/ml/kg) followed by i.p. injected with SCO (2 mg/ml/kg) or normal saline solution (1 ml/kg) an hour later. Thirty minutes later, the learning and memory performance were assessed using Morris water maze test. All rats received four trials per day. These procedures were repeated for 7 days. On day 7, all rats were tested in the probe trial. We found that donepezil and α-MG (50 and 100 mg/ml/kg) given to rats before SCO administration could ameliorate adverse effects of SCO by decreasing time to find platform on training session and increasing both time spent and number of entries into the target quadrant in probe trial session when compared to their control group. These findings indicated that donepezil and α-MG could improve spatial memory impairment. Pretreatment with donepezil and α-MG provided neuroprotective effects against SCO-induced memory deficits and neuronal impairment in rat brain. Future work will be required to determine whether the effects of α-MG on cholinergic system in hippocampus, cerebral cortex, and basal forebrain are related with an amelioration of the SCO-induced memory deficits.

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P45 Brain transcriptome database (brainTx, formerly CDT-DB) – profiling of spatio-temporal gene expression during postnatal development of mouse brain

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The mouse brain develops into functional circuits and architectures during the first few weeks of postnatal life through a series of developmental events that are genetically programmed. To decipher the underlying genetic basis, we have analyzed and systematized the spatiotemporal gene expression profiles during the postnatal mouse brain development, and have created a database named Brain Transcriptome Database (BrainTx) The BrainTx is a neuroinformatics database for sharing and mining large amounts of gene expression data in terms of developmental time-series patterns, brain regional and cellular patterns, and tissue distribution patterns obtained by microarray analyses, *in situ* hybridization analyses, etc. By using the BrainTx, we could *in silico* identify many genes that are specifically expressed in time and space during brain development. Collectively, our results indicated that the postnatal development of the mouse brain is programmed by thousands of different genes, which exhibit differential expression patterns in time and space in developing mouse brain. Moreover, the BrainTx is a valuable bioinformatics tool for elucidating the molecular basis of brain development. This research was supported by funding from Neuroinformatics Japan Center, RIKEN BSI to INCF Japan Node BrainTx Platform Committee. BrainTx URL: http://www.cdtdb.brain.riken.jp

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P46 Infrastructure for neuroscience ontologies bridging between experimental data in 3D atlas, computational modeling and analytical tools: a basement approach of dynamicbrain platform (DB-PF) toward inter-platform coordination in the J-node

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Neuroscience ontologies have been discussed energetically in the International Neuroinformatics Coordinating Facility (INCF) and related international nodes [1]. Ontologies in general is convenient for readers who are interested in items of the database or website, offering sophisticated accesses based on the Web Ontology Language (OWL) [2] to increase accessibility. Neuroinformatics platforms of the INCF Japan-Node are organized in the XooNIps system [3], which needs to design an additional module to access with OWL based queries like a form that Linked Open Data (LOD) offers [4]. For example, a J-Node platform, ViBrism (Virtual Brain with 3D-ISM) is a 3D-map database of endogenous gene expression in a virtual whole mouse brain produced with an original sampling-device [5], which is expected to connect to other J-Node platforms effectively. We DynamicBrain Platform (DB-PF) have cooperated with Physiome.jp [6], which is a part of the Worldwide Integrative Biomedical Research Cooperation to promote Physiome and Systems Biology and organize the PHML Model Database, and PhysioDesigner and Garuda alliance [7], which is an open platform that supports multilevel modeling of physiological systems in the field of integrated life sciences and systems biology including physiology and neuroscience. In this approach, we tried to connect between the XooNIps database and PHML Model Database by using a Java client application, as the preparation to link between the 3D-map database such as ViBrism and XooNIps model database. A code to represent 3D positions and supplemental information on the linked data is possible to embed into the description property of the XooNIps database, which enhances a potential of the current XooNIps and provides an opportunity to consider on the next generation and possible cross communications in J-Node platforms.

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P47 Abstract field: a python module for neural field modelling

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In this work we present two main contributions: the first one is a Python implementation of the discrete approximation of the Laplace-Beltrami operator (LBO) [1] allowing us to solve Robinson's neural field model [2] on a curved (cortical) surface; the second contribution is a generalised implementation of the aforementioned neural field model which we call Abstract Field Representation (AFR). With this simplified dynamical model one can also express the spatially homogeneous case presented in previous work [3, 4] where various brain states and diseases are studied (e.g., rest, sleep and epilepsy). Many other variants may be defined with the AFR thanks to vector operations and spatialization of parameters. These two components constitute an open-source module for neural field modelling that can be seamlessly integrated in the multiscale hierarchy of The Virtual Brain (TVB) simulator [5, 6], which is an established user-ready software [7]. From a systems neuroscience point of view, our contribution favours the integration of multiple approaches to large-scale brain modelling that may lead to more biophysically realistic explanations of how our brains work and interact with the world. From a neuroinformatics perspective, we think this is a valuable addition to the ecosystem of software for meso- and macroscopic brain modelling. Indeed, having different computational models under the same numerical framework is, mildly put, desirable. In simple words, this module represents a way to compare and validate a range of computational models for large scale brain modelling in a systematic way. Lastly, we hope it will assist in the creation of very much needed standard tests in computational neuroscience [7].

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Neuro Informatics 2015

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