CNS*2019 WORKSHOP Petra RITTER | Julie COURTIOL

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VIRTUALBRAINCLOUD

PROGRAM

July 16, morning session, Room S3

09.30 - 10.00	The Virtual Brain simulation platform and Virtual Brain Cloud
	Petra Ritter, Charité Universitätsmedizin Berlin, Germany

- **10.00 10.30** Modeling brain dynamics in brain tumor patients Hannelore Aerts, *Ghent University, Belgium*
- **10.30 11.00** Ethical and legal aspects of personalized brain simulation and data sharing Mariana Rissetto, University of Vienna, Austria
- 11.00 11.30 Coffee break*
- **11.30 12.00** Terminologies, ontologies and data curation Sumit Madan, *Fraunhofer SCAI, Germany*
- 12.00 12.30 Cloud and HPC solutions Alexander Peyser, Forschungszentrum Jülich, Germany
- **12.30 13.00** Enriching big data analytics by computational modeling Oleksandr Popovyh, *Forschungszentrum Jülich, Germany*

July 17, afternoon session, Room S2

14.50 - 15.20	BrainX3: a tool for multi-modal data integration, analysis, visualization and
	interaction
	Riccardo Zucca, Universitat de Barcelona, Spain
15.20 - 15.50	Machine-learning tools for large-scale data
	Hugo Richard, Paris-Saclay University, France
15.50 - 16.20	Linking spiking neural networks to TVB
	Gianluca Susi, Technical University of Madrid, Spain & University of Rome "Tor
	Vergata", Italy
16.20 - 16.50	Coffee break*
16.50 - 17.20	Interfacing TVB with a digital atlas
	Anastasia Brovkin, University Medical Center Hamburg-Eppendorf, Germany
17.20 - 17.50	The Virtual Epileptic Patient
	Julie Courtiol, Charité Universitätsmedizin Berlin, Germany
17.50 - 18.20	The Neurodegenerative Virtual Brain
	Randy McIntosh, University of Toronto, Canada
18.20 - 18.30	Final discussion & closing remarks



ABSTRACTS

The Virtual Brain simulation platform and Virtual Brain Cloud Petra Ritter^{1,2}

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We introduce here VirtualBrainCloud - a EU project - that integrates existing software tools and platforms to provide access to high quality clinical multi-disciplinary data to integrate them via computational brain models and to make them useful in clinical practice. Central to this project is The Virtual Brain (TVB) simulation platform. It allows connectome-based modelling of human and mouse whole brain dynamics, and enables the "integration" of brain dynamics at different levels: from cellular to whole brain. This computational modeling system is tailored to the individual, and bridges multiple scales to identify key mechanisms that predict disease progression and serves as Precision Decision Support System. The workshop will provide insight in the interdisciplinary work and related challenges that range from computational and clinical neuroscience to infrastructure and legal and ethical matters.



Modeling brain dynamics in brain tumor patients

Hannelore Aerts¹

¹Ghent University, Faculty of Psychology and Educational Sciences, Dept. of Data Analysis, Ghent, Belgium

Brain tumor patients scheduled for tumor resection often face significant uncertainty, as the outcome of neurosurgery is difficult to predict at the individual patient level. Recently, computational modeling of brain activity using so-called brain network models has been introduced as a promising tool for this purpose. However, brain network models first have to be validated, before they can be used to predict brain dynamics. As a first step, we optimize individual brain network model parameters in brain tumor patients to maximize the fit with empirical brain activity. Subsequently, we extend this line of research by examining the stability of fitted parameters before and after tumor resection, and compare it with baseline parameter variability using data from healthy control subjects. Based on these findings, we perform the first "virtual neurosurgery" analyses to evaluate the potential of brain network modeling in predicting brain dynamics after tumor resection.



Ethical and legal aspects of personalized brain simulation and data sharing

Mariana Risseto¹

¹Vienna University, Dept. of Innovation and Digitalization in Law, Vienna, Austria

The aim of presentation is to provide an overview of the most relevant legal provisions contained in the General Data Protection Regulation (GDPR), as well as ethical considerations, in relation to data processing taking place during the course of the Virtual Brain Cloud project (VBC project). In particular, it focuses on the definition of personal data in the context of health data processing. In this regard, an essential question is whether brain images can be deemed personal data within the meaning of the GDPR. Furthermore, the presentation analyses the most relevant and appropriate legal basis for processing activities of personal data by partners of the VBC project. Special attention is paid to the factors to be taken into account when assessing the lawfulness of further processing of personal data. Moreover, but equally as crucial as the legal bases, personal data processing activities must comply with the fundamental principles embedded in the GDPR. On the same line, the presentation identifies potential risks of data sharing and storage of personal data on the cloud, and provides a legal analysis thereof. In addition to the data protection legal analysis, it highlights the ethical implications of employing an artificial intelligence system trained with personal data, given the sensitive nature of the information being processed. Finally, the presentation focuses on the requirements to ensure that data sharing within the VBC project complies with the GDPR, particularly concerning the need to identify the origin of the data.



Terminologies, ontologies and data curation

Sumit Madan¹

¹Fraunhofer Institute for Algorithms and Scientific Computing, Dept. of Bioinformatics, Germany

In translational research, controlled bio-medical vocabularies such as terminologies, ontologies, taxonomies play a vital role as they provide a mean to model domain representations. Their features such as definition of concepts and their relationships, the use of standard identifiers and labels, textual definitions enhance the usage and the acceptance of vocabularies by scientific community. Access to semantics through bio-medical vocabularies further facilitates integration and interoperability of heterogenous data that is scattered across departments and institutions. In this talk, we will take a functional perspective on bio-medical vocabularies focusing on how they can be used for data curation, data annotation, semantic data integration and their application in text and data mining.



Cloud and HPC solutions

Alexander Peyser¹

¹SimLab Neuroscience, Institute for Advanced Simulation, Jülich Supercomputing Centre, Jülich Research Centre, Jülich, Germany



Enriching big data analytics by computational modeling

Oleksandr V. Popovych^{1,2}

¹Institute of Neuroscience and Medicine, Brain and Behaviour (INM-7), Research Centre Jülich, Jülich, Germany ²Institute of Systems Neuroscience, Medical Faculty, Heinrich Heine University Düsseldorf, Düsseldorf, Germany

Investigation of the origin and properties of the brain dynamics at rest as reflected by the dynamics of the blood oxygen level-dependent (BOLD) signals measured by the functional magnetic resonance imaging (fMRI) requires an essential involvement of multimodal imaging and modeling approaches. The latter include whole-brain mathematical dynamical models derived from empirical data, where the structural connectivity (SC) extracted from diffusion weighted MRI data can be used to construct the underlying network of coupled neuronal models of local dynamics. The obtained models of neuronal networks can be validated against the functional neuroimaging data to obtain the best correspondence between simulated and empirical neuronal dynamics. The validation process can strongly be influenced by used empirical data, where the algorithms and parameters of data processing and signal extraction may shape the results of model fitting. However, the estimation of the ground truth for the extracted structural and functional brain data is still unknown, and there are many approaches and parameters of the data processing involved in the reconstruction of SC and BOLD signals, whose values are largely conjectured. Here we investigate the impact

of the data parameters on the outcome of model validation. We in particular consider different anatomical and functional brain atlases used to parcellate the cortex into a set of brain regions that define the nodes of the model brain networks. We also consider different frequency bands for filtering of the empirical BOLD signals used to extract the natural frequencies of coupled oscillators. Such models are compared with those where the natural frequencies are drawn from random distributions from the same frequency bands. We show that the variation of the considered parameters of the data processing can indeed cause a significant impact on the model fitting outcome, when the simulated model dynamics is compared with functional and structural empirical data. Differentiating and explaining such an impact of the data processing on the parameters and dynamics of the validated models can enhance the model fitting procedure for deriving realistic models of the brain dynamics as well as contribute to selection of the most appropriate parameters of the data processing for big data analytics.



BrainX3: a tool for multi-modal data integration, analysis, visualization and interaction

Riccardo Zucca¹

¹SPEC, Institute for Bioengineering of Catalonia, Barcelona, Spain

We present BrainX3, a publicly available interactive software platform for three-dimensional visualization, analysis and simulation of multi-modal neuroimaging, electrophysiological and semantic data. BrainX3 provides a mean to organize and visualize these different data types and combine them to extract meaningful insights about brain structures and pathways. BrainX3 works seamlessly with the BIDS data standards and store the derivative results in a way that can be easily shared.

In this talk, we will present the most recent advances that have been integrated into the platform. Specifically, we will focus on the visualization of intracranial recordings and how to generate multi-modal visualizations from these data. The integration of BrainX3 within the VBC platform aims to bring powerful processing and visualization tools to the large community of physicians, researchers and the general public.



Machine-learning tools for large-scale data

Hugo Richard^{1,2}

¹Parietal team, Inria, NeuroSpin, CEA, Gif-sur-Yvette, France ²Paris-Saclay University, Gif-sur-Yvette, France

Thanks to the advent of functional brain-imaging technologies, cognitive neuroscience is accumulating maps of neural activity responses to specific tasks or stimuli, or of spontaneous activity. In this presentation, we consider data from functional Magnetic Resonance Imaging (fMRI), for which we propose a machine learning-based analysis framework: how to learn a model of brain activity that should generalize on unseen data. We give different illustrations of this concept tailored to different data anlaysis problems. Most of the solutions we present are available in the Nilearn library.



Linking spiking neural networks to TVB

<u>Gianluca Susi</u>^{1,2}

¹UPM-UCM, Center for Biomedical Technology, Madrid, Spain ²University of Rome "Tor Vergata", Rome, Italy

The Virtual Brain (TVB) is a brain simulator based on mean-field models, which embraces novel concepts from computational, cognitive and clinical neurosciences in order to drastically reduce the model's complexity while still keeping it sufficiently realistic. On the other hand, Spiking Neural Network (SNN)-based simulators are often characterized by limitations dictated by computational complexity, but they allow us to introduce region-specific alterations of neurophysiological parameters and to explore the long-term effect of plasticity, bringing added value in understanding the temporal course of some neurodegenerative diseases (NDDs). The talk will focus how SNNs can be used for NDD progression models to be implemented in TVB.



Interfacing TVB with a digital atlas

Anastasia Brovkin¹

¹Institute of Computational Neuroscience, Universitätsklinikum Hamburg-Eppendorf, Hamburg, Germany

Fundamental relations between architecture, connectivity and function of the cerebral cortex still remain elusive. This is partly due to a lack of detailed, quantitative cytoarchitectonic data for the human brain. Currently, the only comprehensive source of such information is the classic work of von Economo and Koskinas (vEK), which, however, is only available in a paper-based 2D atlas in non-standard space. Our project is aimed at constructing an extensive virtual 3D model of the vEK atlas in stereotactic space (i.e., MNI-152, Colin-27).

Recent efforts manually mapped the vEK parcellation onto the FreeSurfer Desikan-Killiany atlas based on the textual description and 2D drawings. To overcome related problems, we aimed at explicitly defining a virtual 3D vEK model independent of existing reference geometries –which became possible by 3D scanning 2 individual, well-preserved 3D plaster models of the cortical parcellation of manufactured in the era of von Economo. We will present our progress in reconstructing the 3D model and illustrate the integration of the extracted atlas into the BigBrain atlas –and by extension– its inclusion into The Virtual Brain (TVB) neuroinformatics platform which is currently being merged with the Human Brain Project infrastructure as a comprehensive, complementary tool for large-scale brain network modelling.

This data, comprising systematic quantitative macroscopic as well as microscopic anatomical descriptors, such as layer thickness, cell density and cell sizes, is essential for linking fundamental aspects of macroscopic and microscopic cortical organization and connectivity. The inclusion of the vEK atlas into the aforementioned, open-source, infrastructure offers the prospect of reliably mapping human cytoarchitectonic information into common cortical parcellation schemes, enabling and advancing the enrichment of the human connectome.



The Virtual Epileptic Patient

Julie Courtiol¹

¹Charité Universitätsmedizin Berlin, Dept. of Neurol, Brain Simulation Section, Berlin, Germany

The identification of the epileptogenic zone (EZ), a subsets of brain regions generating seizures in patients with refractory partial epilepsy, is crucial for neurosurgery and requires unambiguous criteria for the degree of epileptogenicity of brain regions. Patient-specific brain network models in conjunction with latest machine-learning approaches allow an optimal estimation of the EZ using The Virtual Brain (TVB) neuroinformatics platform. These results provide guidance in the presurgical evaluation of epileptogenicity based on electrographic signatures in intracerebral electroencephalograms (iEEG) validated in small-scale clinical trials. A non-invasive alternative approach based on functional signatures in functional Magnetic Resonance Imaging (fMRI) allows the characterization of the EZ outside the seizures (i.e., during the interictal period), and provides a mechanistic explanation to resting epileptic brain. These results are a first step toward a new method for a preoperative estimate of the EZ without relying on ictal epileptiform activity. The example of epilepsy nicely underwrites the predictive value of personalized large-scale brain network models, and opens the way to larger clinical applications such as neurodegenerative diseases, targets of the Virtual Brain Cloud.



The Neurodegenerative Virtual Brain

Randy McIntosh^{1,2}

¹Rotman Research Institute, Baycrest, Toronto, Ontario, Canada ²Department of Psychology, University of Toronto, Toronto, Canada

Neurodegenerative brain diseases, such as Alzheimer's and Parkinson's disease, are characterized by gradual decline in brain structure that eventually leads to overt cognitive and behavioural deficits. While many single biomarkers have been suggested, there is potential for integrative modeling approaches to make meaningful progress is early diagnosis and prognosis. We have used The Virtual Brain to integrate brain structure and function measured from individual patients and yielded personalized computational models that provide more sensitive means to characterize patients at different stages of disease progression and cognitive capacity. Additional modeling efforts will focus on integration slower timescale processes represented by transmission of toxic proteins early in neurodegenerative disease.