



Cri iCS WORKSHOP

*“The challenges of
multi-scale integration in Biology”*

Keynote Speakers





Luonan CHEN is Director of the Key Laboratory of Systems Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences. Chen and his group established a dynamical network biomarkers (DNB) framework, which can be used to track changes in gene regulatory networks, anticipating the occurrence of a critical transition. DNB was found to be particularly effective when applied to data from state-of-the-art technologies such as RNA-seq and microarray data. Through the DNB approach and time-course mRNA-sequencing data analysis, Chen and his group theoretically identified DNB alterations that play key roles in drug resistance in cancer therapy.

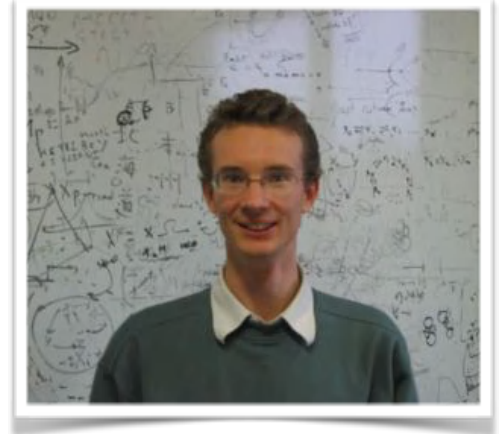
More about Luonan Chen [here](#).

Mirjana EFREMOVA, after her PhD in Computational Cancer Immunology at the Medical University of Innsbruck, joined Sarah Teichmann's Lab at the Wellcome Trust Sanger Institute in Cambridge, where she has a position as Postdoctoral Fellow. She is combining single-cell technologies and computational approaches in order to investigate the cellular diversity in different tissues. Moreover, she is currently working on the development of computational methods for inferring cell-cell communication networks, with a focus on the interactions between cancer and immune cells in a tumour microenvironment; in particular, she significantly contributed in the improvements of CellPhoneDB, an accurate repository of ligands, receptors and their respective interactions, which has recently been integrated with a statistical framework that allows predictions of enriched cellular interactions between different cell types from single-cell transcriptomic data.

More about Mirjana Efremova and her team [here](#).



Didier GONZE is Assistant Professor at Université Libre de Bruxelles, where he focuses on biological oscillatory and synchronization mechanisms within the research Unit of Theoretical Chronobiology. The core of his interdisciplinary interests is the modeling of temporal dynamics for biological rhythms, for which he made significant contributions in bridging theoretical and computational modeling and experimental validation. He is author of more than 100 publications about molecular mechanisms of circadian clocks, genetic circuits and cell differentiation, to cite some. In addition, he recently organized a Summer School on “Microbial Community Modeling” in Leuven. More about Didier Gonze [here](#).



The physicist and neuroscientist **Viktor JIRSA** is Director of the Institut de Neurosciences des Systèmes (INS) and Director of Research at the Centre National de la Recherche Scientifique (CNRS) in Marseille. He has made significant contributions to the understanding of the link between brain function and network dynamics. By using methods from nonlinear dynamical system theory and computational neuroscience, he investigated how network structure constrains the emergence of functional dynamics. He is the curator of “The Virtual Brain” platform. Furthermore, Jirsa and colleagues developed a mathematical model called “The Epileptor” which allowed to model epilepsy phenomenologically using the first principles rooted in mathematics and bifurcation theory to derive a taxonomy of seizures. More about Viktor Jirsa [here](#).

On the interface between mathematical modeling and biology, **Philip MAINI** is Statutory Professor of Mathematical Biology in Oxford. He has over 300 publications in the field and has held visiting positions at a number of universities worldwide. In 2014 he was listed in "The World's Most Influential Scientific Minds 2014" (Thomson Reuters). His present research projects include the modelling of avascular and vascular tumors, normal and abnormal wound healing, and a number of applications of mathematical modelling in pattern formation in early development, as well as the theoretical analysis of the mathematical models that arise in all these applications.

More about Philip Maini [here](#).



Anupam SENGUPTA joined the University of Luxembourg in May 2018 as an ATTRACT Fellow, kicking off experimental biophysics research activities within the Physics and Materials Science Research Unit. Anupam heads the Physics of Living Matter Group, interfacing research activities between the Physics and Materials Science Research Unit (PHYMS), the Luxembourg Centre for Systems Biomedicine (LCSB) and the Luxembourg Institute of Health (LIH). Using a cross-disciplinary approach, Anupam's team studies biological processes and systems under changing environments, with a particular focus on the role of geometry, order and topology in living matter. More information about Anupam Sengupta [here](#).



Internal Speakers



Rudi BALLING is the Director of the Luxembourg Centre for Systems Biomedicine in Luxembourg. He studied Nutrition at the Universities of Bonn and Washington State University, USA and received his PhD in Human Nutrition from the University of Aachen, Germany. After completing research posts at the Samuel Lunenfeld Research Institute in Toronto, Göttingen and Freiburg, he became Director of the Institute of Mammalian Genetics at the GSF in Munich (1993-2000) and of the Helmholtz Centre of Infection Research in Braunschweig (2001-2009). During this time Rudi Balling has coordinated the German Human Genome Project (1996-2000), the European ESFRI-Project EATRIS (European Advanced Translational Medicine Research Infrastructure) (2008-2010) and the Bill & Melinda Gates Grand Challenges Consortium on the development of Vaccine Animal Models (2005-2009). In 2009, he founded the Luxembourg Centre for Systems Biomedicine (LCSB), an interdisciplinary Research Centre at the University of Luxembourg dedicated to the analysis of neurodegenerative diseases through computational and system biology oriented approaches.

Alexander SKUPIN studied Physics at the Humboldt University in Berlin and graduated in 2004 under supervision of Lutz Schimansky-Geier with a work on noise-induced effects in neuronal networks. In 2008, he obtained his PhD in theoretical biophysics at the Humboldt University for his interdisciplinary work on calcium signalling with Martin Falcke. After his first postdoc focused on metabolism with Oliver Ebenhöf at the Max-Planck Institute for Molecular Plant Physiology in Potsdam, he spent 2 years at the Institute for Systems Biology in Seattle (USA) where he continued his interdisciplinary work with Aimee Dudley on Systems Genetics, with Sui Huang on cell fate dynamics and with David Galas on information flow in biological systems. In 2014, he started his interdisciplinary “Integrative Cell Signalling” research group at the Luxembourg Centre for Systems Biomedicine where his team combines microscopy and single cell analysis techniques with theoretical concepts from physics to investigate principles of living matter and their implications for health and disease. He is also heading the LCSB imaging platform and is co-coordinator of the CriTICS DTU.





Since Mar. 2015, **Feng HE** is a principal investigator and leads the junior group of immune systems biology (GISB) from the Department of Infection and Immunity (DII) at LIH. He pursued his PhD (cumulative thesis) in experimental systems biology from Technical University of Braunschweig, Germany and Helmholtz Centre for Infection Research (HZI) with Prof. An-Ping Zeng and continued a 2-year postdoc training in Prof Klaus Schughart's lab. Afterwards, during his postdoctoral training (2010-2015) at Luxembourg Centre for Systems Biology in Prof. Rudi Balling's lab and as a visiting researcher in University of Cambridge and Institute for Systems Biology, Seattle, Feng has developed various systems biology approaches to computationally predict and experimentally validate novel key gene candidates and gene networks from dynamic/time-series 'omics' datasets. Feng was originally trained in chemistry and biochemical engineering (MSc. degree, Department of Biochemical Engineering, Tianjin University, China, 2004). His network-guided experimental approaches have led to the discoveries of several novel key genes in immune cell functions.

Jorge GONCALVES leads the Systems Control group at LCSB. The group aims to understand the source of diseases and find new therapies and cures. This is accomplished by building mathematical models and tools that pinpoint the exact location of diseases. The predictive power of these models comes from mimicking the most important feature of biological systems: the fact that they are dynamic in nature, as molecular numbers change over time in response to internal or external stimulus. When pushed from their comfort zone, systems respond by activating a number of elements that try to restore their initial state. This transient behaviour is essential to an understanding of how components in the system interact. Hence, time-series data offer a window into complex biochemical systems. Theoretically, the group is developing tools to model and analyse time-series data. Examples are tools to infer causal networks between measurements, to find differential expressed systems, and systematic engineering control tools for synthetic biology design. The group collaborates with experimental biologists to generate mathematical models that can subsequently be tested experimentally. Examples include the understanding the molecular details of circadian rhythms to learn about the sources of Parkinson's Disease.

