Signalling Networks: From data to modelling

TGAC
The Genome Analysis Centre™
**BBSRC** Greater Norwich Development Partnership

Trainers Biographies

Laurence Calzone, Institut Curie, France

Dr Laurence Calzone is a research scientist at Institut Curie. She has already published mathematical models using several formalisms including nonlinear ordinary differential equations and, more recently, Boolean formalism to address specific biological questions such as: the timely organization of the budding yeast cell cycle, the description of syncytial cycles in drosophila, cell fate decision processes in response to cell death signals, interplays between MAPK pathways, metastasis process, etc.

She has very good experience in constructing these models based on published articles and in analysing patient data using these models. She has also participated in developing methods to improve the simulations of the mathematical models she builds.

Tamas Korcsmaros, TGAC, UK
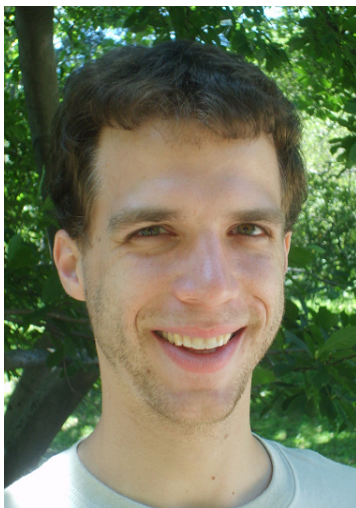
Tamas Korcsmaros was born in Budapest, Hungary. He started his research work as a high-school student in a biochemist laboratory at Semmelweis Medical University. He graduated as a biologist at the Eötvös Lorand University in Budapest. During his PhD studies Tamas developed a gap-filling signalling network database (http://SignaLink.org) and established the NetBiol- Network Biology research group (http://netbiol.elte.hu). Currently, his group is focusing on signalling and regulatory networks. They develop novel databases and webservices as well as perform systems-level analyses. Tamas established a bioinformatics course for Master students in biology. He teaches 450 university students per year and has been participated as an external faculty member of the Pathways and Networks course at EMBL-EBI in 2012. Since 2001, Tamas is participating as a volunteer in talent support organizations. He is the Chairman of the Research Student Foundation supporting 5000 high-school research students. In 2009, Tamas received the FEBS Young SysBio Investigator award. In 2012, his research and talent support work were acknowledged by the Pal Juhasz-Nagy Talent Support Award, the Bolyai Research Scholarship of the Hungarian Academy of Sciences and by the prestigious Junior Prima Award for outstanding Hungarian young scientists.

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Pablo Porras, EMBL-EBI, UK

Pablo started his career in the University of Córdoba, Spain, doing research about trans-membrane protein translocation and redox homeostasis. After that, he moved to Berlin to work in the Neuroproteomics group of the Max Delbrueck Center, getting involved in projects dealing with interactomics, neurodegenerative diseases and the ubiquitin-proteasome system. During this postdoc, he faced the problem of how to represent and analyze molecular interactions data, an experience that led him to join the EBI to work as a scientific curator in the molecular interactions database IntAct, where he deals with representation, integration and basic analysis of large interaction datasets. He has been heavily involved in training and research collaborations since arriving to the EBI in 2011.

Julio Saez-Rodriguez, RWTH University Medical Hospital, Germany

Julio Saez-Rodriguez is Professor of Computational Biomedicine at the Joint Research Center for Computational Biomedicine at the RWTH University Medical Hospital in Aachen, Germany (www.combine.rwth-aachen.de) and a visiting group leader at the European Bioinformatics Institute (EMBL-EBI). He is an affiliated member of Sage-Bionetworks and a director of the DREAM initiative to catalyze the development of methods in systems biology (www.dreamchallenges.org).

He studied Chemical Engineering at the Universities of Oviedo and Stuttgart, and obtained his PhD at the University of Magdeburg and the Max-Planck-Institute with E. D. Gilles in 2007. After this, he was a postdoctoral fellow at Harvard Medical School with Peter Sorger and Doug Lauffenburger at M.I.T., and a Scientific Coordinator of the NIH-NIGMS Cell Decision Process Center. From 2010 until 2015 he was a group leader at EMBL-EBI with a joint appointment in the EMBL Genome Biology Unit in Heidelberg, as well as a senior fellow at Wolfson College (Cambridge).

His group develops and applies computational methods to acquire a functional understanding of signaling networks and their deregulation in disease, and to apply this knowledge to develop novel therapeutics. To this end, his group collaborates closely with experimental groups and pharmaceutical companies.

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Jean-Marc Schwartz, University of Manchester, UK

Jean-Marc Schwartz is a Lecturer in Systems Biology at the University of Manchester. He previously completed a PhD in Computer Engineering at Laval University and a postdoc at the Kyoto University Bioinformatics Center. His group works on the development of mathematical and computational models of biological systems using a range of methods, including network analysis, constraint-based, logical and kinetic modelling. In close collaboration with experimental biologists these projects address important biomedical and biotechnological topics, including cancer research, bone diseases, circadian rhythms and biofuel production. He leads the systems biology component of the European Commission funded SYBIL consortium on skeletal diseases.

Denes Turei , EMBL-EBI, UK

Dénes Türei studied biology at Eötvös Loránd University Budapest, Hungary, doing research about community ecology of freshwater mesocosms. After he did his PhD at Semmelweis University Budapest and Eötvös Loránd University Budapest, constructing SignaLink 2, Autophagy Regulatory Network and NRF2ome, 3 databases of cellular signaling. From 2014 in EMBL-EBI he developed a combined literature curated signaling network accompanied by a software tool for analysing pathways. He also contributed in the analysis of lipidomics mass spectrometry data. Since 2011 at Eötvös Loránd University Budapest and later in EBI he has been involved in teaching various topics in bioinformatics.