



sbv IMPROVER Symposium 2013 – Workshop Speakers and Presenters

Leonidas Alexopoulos, Ph.D.

Assistant professor, National Technical University of Athens,
Co-founder and chief scientific advisor, ProtATonce Ltd Assistant



Leo Alexopoulos received his PhD in Biomedical Engineering from Duke University (2004) and then became a postdoctoral scientist in the Department of Biological Engineering at MIT and the Department of Systems Biology at Harvard Medical School.

He returned to Greece in 2008 where he is currently an Assistant Professor at the National Technical University of Athens (NTUA) and the director of the Systems Bioengineering Group.

He is also co-founder and chief scientific advisor of ProtATonce, a startup company that specializes on multiplex assays. His research group at NTUA focuses on the design of high throughput medical devices including multiplex systems and on computational and experimental aspects of systems pharmacology. He has received several international awards, authored more than 40 scientific publications in leading journals, and he has collaborated with leading pharmaceutical companies including Pfizer, Vertex, and Boehringer Ingelheim.

Theodore Sakellaropoulos, MSc

Research Assistant, Bioengineering Group NTUA and ProtATonce Ltd.



Theodore received his MSc in Mechanical Engineering from the National Technical University of Athens (NTUA) in 2012.

He immediately joined the Bioengineering Group of NTUA as a research assistant focusing on the development of proteomic assays and the interpretation of proteomic data. In the same year he also joined ProtATonce Ltd, a newly founded startup providing support in multiplexed assays, as a research assistant.

His work there focuses on the modeling of protein data for hypothesis generation and testing in human diseases.



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Vincenzo Belcastro, Ph.D.

Assistant Investigator, Telethon Institute of Genetics and Medicine (TIGEM)



Vincenzo Belcastro is a Computer Scientist, graduated with top 5% performance. The topic of his thesis was the evaluation of reverse-engineering algorithms for gene network inference from gene expression data. This work resulted in a joint first author publication, which is one of the most cited reviews in the field.

Vincenzo then successfully passed the entry exam for the Ph.D program in Human Genetics under the UK Open University training scheme. The topic of his research was the development of an Information Theoretic approach for gene network inference in human and mouse species.

At the end of the Ph.D. program, Vincenzo joined Philip Morris International (PMI) where he spent almost 3 years as computational biologist in the Research and Development department. At PMI Vincenzo focused on the development and application of computational tools for the analysis and interpretation of biological experiments. During his period in PMI Vincenzo was honoured of an Excellence and an ABCD award.

Vincenzo was then selected to cover the position of Assistant Investigator at the Telethon Institute of GENetics and Medicine (TIGEM).

The aim of his research project at TIGEM is the design and development of Systems Biology approaches to gain insight into dis-regulated signaling and regulatory pathways involved in genetic diseases.



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Alexander Klenner, Dr. phil. nat.

Scientist, Fraunhofer Institute for Scientific Computing and Algorithms (SCAI)

Title of Talk: “BEL Networks Derived from Qualitative Translations of BioNLP Shared Task Annotations – BioNLP in the context of the Network Verification Challenge”



Alexander is a bioinformatician by training with years of experience in rational drug design and virtual screening. Before joining Fraunhofer Institute for Scientific Computing and Algorithm he worked in academia in Germany and Switzerland at the University of Frankfurt and the ETH Zurich.

He obtained his PhD in Bioinformatics from the University of Frankfurt and is now a scientist at SCAI facilitating the dialogue between chemists, biologists and computer scientists. He is responsible for coordination of all relation extraction activities at SCAI and an expert for biomedical text-mining and natural language processing in English and German language.

He is involved in managing national and international projects with various partners from industry and academia and author of several research publications.



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Monica Munoz-Torres, Ph.D.

Biocurator and Bioinformatics Analyst, Genomics Division, Lawrence Berkeley National Laboratory

Title of Talk: “Web Apollo- Lessons learned from community based bio-curation efforts”



Monica Munoz-Torres is a member of the Berkeley Bioinformatics Open-Source Projects group (BBOP) in the Joint Genome Institute (JGI) at LBL, where she provides evolutionary and biologically relevant perspectives to the development of genome annotation editing tools.

Monica arrived at LBL after lending her expertise to the Steering Committee of the Biodiversity Genomics Initiative at Smithsonian Institution, as she completed postdoctoral work in computational genomics at Georgetown University. At Georgetown she was the curator of Hymenoptera Genome Database and occupied her time creating more effective ways to share genomic information with the research community, as well as generating more intuitive ways of annotating and curating genes in a community-based environment. She received a PhD in Genetics at Clemson University (2009) working on developing genomic resources for, and conducting molecular evolutionary studies in insect species of the order Hymenoptera.

Her earlier work was focused on orchestrating manual annotation efforts for over 300 insect genomics researchers, which granted her a unique perspective on the relevance of biocuration to the advancement of scientific knowledge for the genomics community. Currently, Monica is part of the Development Team for Web Apollo - a web-based annotation editor designed to support community-based curation of genomes - and a member of the Gene Ontology Consortium. She leads the Community Curation Group within the global initiative to sequence and annotate the genomes of 5,000 arthropods (i5K Initiative), and is a member of the Executive Committee of the International Society for Biocuration (ISB).



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Yukiko Matsuoka, B.A.

Senior Researcher, The Systems Biology Institute
Researcher, ERATO Kawaoka infection-induced host response project, Japan Science and Technology Agency

Title of Talk: “Weaving Knowledge into Biological Pathways in Collaboration”



Yukiko Matsuoka leads the platform development for systems biology such as CellDesigner (biochemical, gene regulatory pathway editor), and Payao (online pathway curation platform).

She has been an active member of the standardization of SBGN (=systems biology graphical notation). Working with biologists, Yukiko Matsuoka has been engaged in the pathway modeling with CellDesigner, including comprehensive EGFR, mTOR, and disease-specific maps such as Alzheimer disease, Parkinson's disease, and most recently Influenza virus infection.

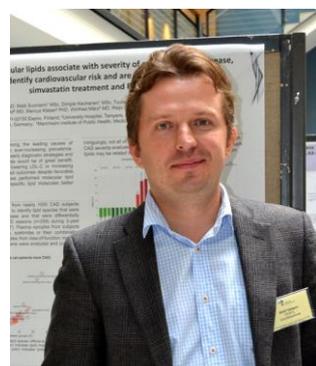
Her research interests include the area of systems biology, modeling, visualization, and traditional medicines.

She received the B.A. in liberal arts from International Christian University, Japan. She worked in the software/IT industry for over ten years such as Lotus and worked as chief administrative officer for RoboCup.

Kirill Tarasov, MS.S

Bioinformatics specialist, Zora Biosciences

Title of Talk: “The need for mechanistic models for lipid metabolism – The future after Lipidmaps”



Kirill Tarasov is a bioinformatics specialist leading data analysis group at Zora Biosciences.

Kirill is specialized in developing complete informatics solutions for supporting high-throughput studies from raw data processing to integration and interpretation of results.

His background in biophysics and bioinformatics combined with experience in experimental biochemistry led to a number of successful publications in such journals as Science, PNAS and Genome Biology.

Kirill holds a MS.S degree in biophysics from Saint Petersburg State Polytechnic University. Kirill is finalizing his PhD thesis in Biochemistry at Université de Montréal and Clinical Pharmacology at University of Helsinki.



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Prof. Heinz Koeppel

Assistant Professor at ETH Zurich

Title of Talk: “Bayesian network reconstruction from dynamic signaling data ”



Heinz is an assistant professor for Systems Theory in Biology at ETH Zurich, Department of Electrical Engineering and Information Technology since 9/2010 and holds a co-appointment as a group leader at IBM Zurich Research Labs since 01/2013.

He was trained in theoretical physics and electrical engineering and spent postdoc periods at UC Berkeley (Erwin Schrodinger fellow), Ecole Polytechnique Federale de Lausanne (EPFL) and Harvard Medical School. He received the Fred Margulies best PhD thesis award of the International Federation of Automatic Control (IFAC).

He is program committee member of several computer science conferences and associate editor of the journal for Nonlinear Theory and its Application, the EURASIP Journal on Bioinformatics and System Biology and technical committee member at the IEEE Circuits and Systems Society and holds four patents. He is part of the organizing team of this year's prediction challenge DREAM8.

His computational lab is dedicated to mathematical modeling and analysis of signal transduction and gene expression. In particular, he works on Bayesian inference of stochastic models, optimal experimental design and the quantification of cell-to-cell variability. He lately worked on network reconstruction algorithms.