



Mathematical modelling workshop: Current and Future Perspectives of micro- and macro modelling of infectious diseases: from system biology to control and dynamics

13 – 15 January 2016

AGENDA

Wednesday, 13 January 2016	
12.00 - 13.00	Registration
13.00 - 13.10	Welcome of participants Modra Murovska, MD, PhD, “Baltinfect” coordinator
	Session 1. Mathematical tools for infectious disease modeling: current state and perspectives? Session Chairs: Mihails Bariševs,
13.10 - 13.50	Natal van Riel , Assoc. Prof., Department of Biomedical Engineering, Technische Universiteit Eindhoven, Netherlands “Using mathematical and computational modelling to study human disease”
13.50 - 14.30	Sofia Johansson , Asst. Prof., Department of Microbiology, Tumor and Cell Biology, Karolinska Institutet “Natural Killer cell receptor dynamics investigated with novel quantitative techniques.”
14.30 - 15.10	Nuno Sepulveda , Dr., London School of Hygiene and Tropical Medicine, United Kingdom, and Centre for Statistics and Applications of University of Lisbon, Portugal “Serology and mathematical modelling as joint tools to inform the epidemiology of infectious diseases on the cusp of elimination”
15.10 - 15.30	<i>Coffee break</i>
15.30 - 16.10	Rimantas Eidukevicius , Asst. Prof., Department of Mathematical Statistics, Faculty of Mathematics and Informatics, Vilnius University “Estimating of Durations of Cell Cycle Phases Using a Stochastic Model and Flow Cytometry Data”
16.10 - 16.50	Yoram Louzoun , Prof., Department of Mathematics, Bar-Ilan University, Ramat Gan, Israel “Impact of bacterial load and spatio-temporal population structure on epidemiology of infectious diseases”

Thursday, 14 January 2016

	Session 2: Systems Biology and Biological Networks Session Chairs: Uldis Berķis
10.00 - 10.40	Alexander Kel, Dr, Chief Scientific Officer, GeneXplain GmbH, Wolfenbüttel, Germany
10.40 - 11.20	Vladimir Poroikov, Prof., Head of Department for Bioinformatics, Institute of Biomedical Chemistry, Moscow, Russia "Discovery of new pharmaceutical agents using in silico approaches: PASS, GUSAR, PharmaExpert and Way2Drug platform"
11.20 - 11.40	<i>Coffee break</i>
11.40 - 12.20	Juergen Borlak, Prof., Director of the Institute for Pharmaco- and Toxicogenomics, Centre of Pharmacology and Toxicology, Hannover Medical School, Germany "Immunogenomics reveals molecular circuits of diclofenac induced immune-mediated liver injury in mice"
12.20 - 13.00	Marzio Pennisi, Dr, Department of Drug Sciences, University of Catania, Italy "Coloured petri nets for modelling immune response"
13.00 - 13.40	Athina Geronikaki, Prof., Head of the Laboratory of Pharm. Chemistry, School of Pharmacy, Aristotle University of Thessaloniki, Greece "Computer-aided finding of new pharmaceutical agents with multitargeted action"
13.40 - 14.40	<i>Lunch break</i>
	Session 3: Modelling of cell interactions Session Chairs: Maria Issagouliantis
14.40 - 15.20	Olga Tikhonova, Senior Scientist, Laboratory of Systems Biology, Institute of Biomedical Chemistry, Moscow, Russia "Proteome and transcriptome analysis of retinoic acid-induced differentiation of human promyelocytic leukemia HL-60 cell"
15.20 - 16.00	Alexey Chernobrovkin, Dr., Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Sweden
16.00 - 16.40	Olga Kel-Margoulis, Dr, Director Applied Life Science informatics, GeneXplain GmbH, Wolfenbüttel, Germany

Thursday, 15 January 2016

	Session 4: Modelling platforms Session Chairs: Šimons Svirskis
10.00 - 10.40	Šimons Svirskis , Assoc. Prof., Head of Laboratory, AKMVI, Riga Stradiņš University, Latvia “Matlab as a platform for analysis and modelling in molecular biology: MBET, SBET, PGET, Simulink”, “Integrated usage of simple and advanced software tools for data analysis and mathematical modelling”
10.40 - 11.00	Vladimirs Kozlovs , Leading Researcher, AKMVI, Riga Stradiņš University, Latvia “Matlab usage in data analysis”
11.00 - 11.40	Agnieszka Kaczor , Adjunct Researcher, Faculty of Pharmacy with the Department of Medical Analytics, Medical University of Ljublin, Poland “Molecular modeling for cannabinoid receptors”
11.40 - 12.20	Juergen Borlak Prof., Director of the Institute for Pharmaco- and Toxicogenomics, Centre of Pharmacology and Toxicology, Hannover Medical School, Germany “Advanced computational biology methods identify molecular switches for malignancy in an EGF mouse model of liver cancer”
12.20 - 13.10	<i>Lunch break</i>
	Session 5. Groupworks
13.10 - 13.40	1. GeneXplain Tutors: Olga Kiel-Margulis, Alexander Kiel
13.10 - 13.40	2. Drug design Tutors: Vladimir Poroikov, Juergen Borlak
13.10 - 13.40	3. Matlab Tutors:
13.40 - 14.00	Discussion
14.00 - 14.10	Closing remarks
	Presentation title not submitted

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Submitted abstract		