

SCHEDULE FOR METABOLIC PATHWAY ANALYSIS 2019

12.-16. August 2019, Riga, Latvia

Monday, 12th of August

From 08:00	1st floor	Registration	
10:00 - 17:30	3rd floor	Tutorials	
17:30 - 18:00		Coffee break	
18:00 - 18:45	Room 106 I1	Opening lecture: Harald H. H. W. Schmidt	The end of medicine as we know it
19:00 - 21:00	2nd floor	Welcome reception	

Tuesday, 13th of August

From 08:30	1st floor	Registration	
09:00 - 09:20	Room 106	Opening of the conference	
	Room 106	Session 1.1 - Systems Medicine, Chair Egils Stalidzans	
09:20 - 09:55	I2	Invited speaker - Adil Mardinoglu	The use of systems biology in treatment of liver diseases
09:55 - 10:15	T1	Silvio Waschina, Johannes Zimmermann, Julia Pagel and Christoph Kaleta	Elucidating the metabolic processes within the gut microbiome that precede sepsis in preterm infants and remission in IBD patients
10:15 - 10:35	T2	Germán Andres Preciat Gonzalez, Luojiao Huang, Emma Schymanski, Thomas Hankemeier and Ronan Fleming	Atom mapping data for genome-scale metabolic network reconstructions; Application in human dopaminergic neuronal metabolism
10:35 - 11:00	2nd floor	Coffee break	
	Room 106	Session 1.2 - Systems Medicine, Chair Adil Mardinoglu	
11:00 - 11:35	I3	Invited Speaker - Kathrin Thedieck	Systems approaches to metabolic signalling
11:35 - 11:55	T3	Jean-Marc Schwartz and Zita Soons	Fluxomics reveals cellular and molecular basis of increased renal ammoniogenesis
11:55 - 12:15	T4	Darta Zake, Egils Stalidzans, Linda Zaharenko and Janis Klovins	Physiologically based metformin pharmacokinetics model for estimation of therapeutic concentrations in various tissues
12:15 - 12:35	T5	Thomas Sauter, Tamara Bintener, Dominik Ternes, Dagmar Kulms, Serge Haan, Elisabeth Letellier and Maria Pires Pacheco	Identifying and targeting cancer-specific metabolism with network based drug target prediction
12:35 - 14:00	2nd floor	Lunch	
	Room 106	Session 2.1 Fundamentals of metabolic network structure, Chair Stefan Schuster	
14:00 - 14:35	I4	Inv. speaker - Athel Cornish - Bowden	Modern Theories of Life
14:35 - 14:55	T6	Stefan Mueller, Georg Regensburger and Juergen Zanghellini	Flux tope analysis: which combinations of reaction directions are (thermodynamically) feasible?
14:55 - 15:15	T7	José P. Faria, Filipe Liu, Janaka N. Edirisinghe, Samuel M.D. Seaver, James G. Jeffryes, Qizh Zhang, Pamela Weisenhorn, Boris Sadkhin, Nidhi Gupta, Tian Gu and Christopher S.	High Throughput Genome-Scale Metabolic Model Reconstruction and Reconciliation with Tn-seq Data
15:15 - 15:35	Room 106	Open MPA 2019 organising committee meeting	
15:35 - 16:00	2nd floor	Coffee break	
	Room 106	Session 2.2 Fundamentals of metabolic network structure, Chair Isabel Rocha	
16:00 - 16:20	T8	Tin Yau Pang and Martin Lercher	Natural selection on the extent of intracellular crowding
16:20 - 16:40	T9	John Barrett and Friedrich Srienc	Statistical Thermodynamics of Metabolic Reaction
16:40 - 17:00	T10	Filipe Liu, Samuel M.D. Seaver, José P. Faria, Janaka N. Edirisinghe, James G. Jeffryes, Tian Gu and Christopher S. Henry	Validation and Curation of Biochemical Networks through thermodynamics and visualization
17:00 - 17:20	T11	Nima Saadat and Ovidiu Popa	Impact of prophage encoded enzymes on the metabolic capacity of the hosts.
17:45 - 19:30	2nd floor	Poster session beginning with Lightning poster talks	

Wednesday, 14th of August

	Room 106	Session 3.1 Reconstituted Systems and Synthetic Biology, Chair Cong Trinh	
09:00 - 09:35	I5	Invited speaker - Herbert Sauro	A Menagerie of Systems Biology Standards With a Special Focus on the Synthetic Biology Open Language
09:35 - 09:55	T12	Ashley Beck, Tomas Gedeon, Jeffrey Heys and Ross Carlson	Surface area is a cellular resource that can be used to predict and design competitive biological organization
09:55 - 10:15	T13	Marian Breuer, Tyler Earnest, Chuck Merryman, Kim Wise, Lijie Sun, Michaela Lynott, Clyde A. Hutchison Iii, Hamilton Smith, John Lapek, David Gonzalez, Valerie De Crecy-Lagard, Drago Haas, Andrew D. Hanson, Piyush Labhsetwar, John Glass and Zaida Luthey-Schulten	Essential metabolism for a minimal cell
10:15 - 10:35	T14	Mikk Õun, Nikita Rom, Raivo Vilu, Vassili Kiritsenko, Kristo Abner, Taivo Lints and Maria Bubina	A Novel Tool for Metabolic Model Optimisation and Result Visualisation
10:35 - 11:00	2nd floor	Coffee break	
	Room 106	Session 3.2 Applied metabolic systems analysis and engineering, Chair Kathrin Thedieck	
11:00 - 11:35	I6	Invited speaker - John Wain	Changing Culture in Microbiology
11:35 - 11:55	T15	Steffen Klamt, Simon Boecker and Ahmed Zahoor	Extending the Scope of Enforced ATP Wasting as a Tool for Metabolic Engineering in Escherichia coli
11:55 - 12:15	T16	Debolina Sarkar and Costas Maranas	SNPeffect: Identifying Functional Roles of SNPs using Metabolic Network Information
12:15 - 12:35	T17	Stefan Schuster, Maximilian Fichtner and Severin Sasso	How to cope with the combinatorial complexity of fatty acids?
12:35 - 13:00		Collection of lunch packages	
13:00 - 19:00		Field trip	

Thursday, 15th of August

	Room 106	Session 4.1 Pathways of primary and secondary metabolism, Chair Hyun-Seob Song	
09:00 - 09:35	I7	Invited speaker - Uwe Sauer	Metabolic Coordination Through Metabolite-Protein Interactions
09:35 - 09:55	T18	Esther M. Sundermann, Martin J. Lercher and David Heckmann	In silico exploration of paths toward C4 metabolism
09:55 - 10:15	T19	Leonor Guedes Da Silva, Sergio Tomás Martínez, Mark C. M. van Loosdrecht and Aljoscha Wahl	The environment selects: Modeling intracellular energy allocation in microbial communities under dynamic environments
10:15 - 10:35	T20	Fernando Cruz, Catarina Ribeiro, Miguel Silva, Isabel Rocha, Ahmad A. Zeidan and Oscar Dias	What Can Multiple Genome-Scale Metabolic Models Unveil About the Same Organism? A Case Study of the Dairy Bacterium Streptococcus thermophilus
10:35 - 11:00	2nd floor	Coffee break	
	Room 106	Session 4.2 Pathways of primary and secondary metabolism, Chair Sabine Peres	
11:00 - 11:35	T21	Jorgelindo da Veiga Moreira, Laurent Schwartz and Sabine Peres	Modulating mitochondria horsepower for biotechnological applications
11:35 - 11:55	T22	Martin H. Rau, Paula Gaspar, Maiken L. Jensen and Ahmad A. Zeidan	Genome-scale metabolic modeling of Streptococcus thermophilus uncovers the signature of milk adaptation
11:55 - 12:15	T23	Ross Carlson, Michael Henson, Luke Hanley and Matthew Fields	In silico and Multi-omics analysis of Reverse Diauxie in Pseudomonas aeruginosa
12:15 - 12:35	T24	Jürgen Zanghellini and Bianca Buchner	Comprehensive elementary mode analysis of Mycoplasma mycoides JCVI-syn3.0.
12:35 - 14:00	2nd floor	Lunch	
	Room 106	Session 5.1 Applied metabolic systems analysis and engineering, Chair Herbert Sauro	
14:00 - 14:35	I8	Invited speaker - Dong-Yup Lee	Model-guided design and engineering of probiotic LAB system with host and microbiome interactions

14:35 - 14:55	T25	Egils Stalidzans, Agris Pentjuss and Atis Elsts	Automation of constrained kinetic metabolic model optimization by COPASI wrapper SpaceScanner
14:55 - 15:15	T26	Philipp Schneider and Steffen Klamt	Characterizing and Ranking Computed Metabolic Engineering Strategies
15:15 - 15:35	T27	Hyun-Seob Song, William Nelson, Joon-Yong Lee, Christopher Henry, Janaka Edirisinghe, Filipe Liu, James Stegen, Emily Graham, Kelly Wrighton, Kewei Chen, Xuehang Song, Jianqiu Zheng, Glenn Hammond, David Moulton, Xingyuan Chen and Tim Scheibe	Multimics-based Metabolic Network Reconstruction and Pathway Analysis for Predictive Biogeochemical Modeling
15:35 - 16:00	2nd floor	Coffee break	
	Room 106	Session 5.2 Applied metabolic systems analysis and engineering, Chair Dong-Yup Lee	
16:00 - 16:20	T28	Katharina Nöh and Axel Theorell	A Critical View on Ockham's Razor as Criterion for Model Selection in Systems Biology
16:20 - 16:40	T29	Oliver Hädicke	In silico profiling of Escherichia coli and Saccharomyces cerevisiae as cannabinoid factories.
16:40 - 17:00	T30	Sean Mack, Eric Hill, Young-Mo Kim, Lye-Meng Markillie, Teresa Palazzo, Karl Weitz, Robert Young, Ganesh Sriram and Daniel Dwyer	Integrated Flux Analysis of Susceptible and Resistant Escherichia coli under Antibiotic Stress
17:00 - 17:20	T31	Sophia Santos, Sara Correia and Isabel Rocha	Inferring optimal minimal media for genome-scale metabolic models using evolutionary algorithms
17:45 - 19:30	2nd floor	Poster session beginning with Lightning poster talks	
20:00		Conference dinner in restaurant "Rozengräls"	

Friday, 16th of August

	Room 106	Session 6.1 Methodology and mathematical algorithms and software, Chair Oliver Ebenhoeh	
09:00 - 09:35	I9	Invited speaker - Anne Siegel	Using automated reasoning to explore unconventional organisms: a first step to explore host-microbial interactions
09:35 - 09:55	T32	Alon Stern, Tomer Shlomi, Boris Sarvin, Won Dong Lee and Elina Aizenshtein	Inferring subcellular compartmentalized flux in cancer cells: A new approach integrating isotope tracing with thermodynamic analysis
09:55 - 10:15	T33	Mattia G. Gollub and Jörg Stelling	Probabilistic Integration of Flux Constraints and Thermodynamic Data in Metabolic Models
10:15 - 10:35	T34	Roland Sauter and Ines Heiland	Estimating the Impact of Cofactor Concentration Changes in Genome-scale Models
10:35 - 11:00	2nd floor	Coffee break	
	Room 106	Session 6.2 Methodology and mathematical algorithms and software, Chair Ross Carlson	
11:00 - 11:20	T35	Johann Rohwer, Carl Christensen and Jan-Hendrik Hofmeyr	PyScEStoolbox: providing deeper insight into the regulatory behaviour of kinetic models
11:20 - 11:40	T36	Sergio Garcia and Cong Trinh	Solving the Modular Cell Biocatalyst Design Problem with Multi-objective Evolutionary Algorithms
11:40 - 12:00	T37	Ana Bulović, Stephan Fischer, Edda Klipp, Vincent Fromion and Anne Goelzer	Automated creation of bacterial resource allocation models
12:00 - 12:20	T38	Christian Lieven, Moritz Beber and Nikolaus Sonnenschein	Memote: A community-driven effort towards a standardized genome-scale metabolic model test suite
12:20 - 12:40	Room 106	Closing remarks	
12:40 - 14:00	2nd floor	Lunch	
14:00 - 19:00		Departures	