International Conference on Systems Biology 2008

Friday August 22, 2008

1000-1800 Tutorial Programme (Chalmers University of Technology, Mathematical Sciences)

Time/Room	Presenters	Affiliation	Title
1000-1300 MV-F33	Frank T Bergmann, Kyung Hyuk Kim	University of Washington and Keck Graduate Institute, USA	Systems Biology Workbench
1000-1300 KA	Henning Schmidt, Simone Frey	University of Rostock, Germany	Systems Biology Toolbox 2 for MATLAB
1000-1300 MV-H12	Jasmin Fisher	Microsoft Research, Cambridge, UK	Executable Biology
1100-1300 MV-H11	Christopher Southan	EMBL-EBI Hinxton, UK	An introduction to open small-molecule resources of high utility for Systems Biologists
1200-1600 Pascal	Matthias Machacek, Luca Finelli, Antoine Soubret	Novartis Pharma AG, Basel, Switzerland	Drug development with a systems perspective
1400-1600 MV-F31	Yiannis Kaznessis	University of Minnesota, USA	Computational Synthetic Biology
1400-1600 MV-H11	Paul D. Thomas	SRI International, Menlo Park CA, USA	The Panther Software System
1400-1600 MV-H12	Chris J. Myers, Nathan Barker, Hiroyuki Kuwahara, Curtis Madsen, Nam-Phuong D. Nguyen	University of Utah and Southern Utah University, USA; University of Trento, Italy	iBioSim: A tool for the analysis and design of genetic circuits
1400-1600 MV-F33	Stuart Moodie, Anatoli Sorokin	University of Edinburgh, UK	EPE2 Take advantage of the new features of Edinburgh Pathway Editor
1500-1600 MV-F23	Max Flöttmann, Jörg Schaber, Edda Klipp	Max Planck Institute for Molecular Genetics, Berlin, Germany	Automatic model generation and discrimination with ModelMage
1400-1815 MV-F26	Nicolas Le Novere	EMBL-EBI Hinxton, UK	Systems Biology resources at the European Bioinformatics Institute
1615-1815 MV-F31	Corrado Priami	CoSBi, Trento, Italy	Process algebra modelling of biological systems
1615-1815 MV-H11	Andreas Weidemann, Martin Golebiewski	Bioquant at University of Heidelberg, EML Research, Germany	Database supported modeling: SYCAMORE and SABIO-RK
1615-1815 MV-F33	T. M. Murali	Virginia Polytechnic Institute and State University, USA	Host pathogenic networks
1615-1815 Pacal	Akira Funahashi, Akiya Jouraku, Yukiko Matsuoka, Norihiro Kikuchi, Hiroaki Kitano	The Systems Biology Institute; Keio University; Mitsui Knowledge Industry, Japan	Cell Designer 4.0
1615-1815 MV-H12	Ion I. Moraru	University of Connecticut Health Center, USA	From quantitative microscopy to spatial simulations of kinetic models

Saturday August 23, 2008

0900-1430 Tutorial Programme (Chalmers University of Technology, Mathematical Sciences)

Time/Room	Presenters	Affiliation	Title
0900-1100 MV-H12	Steffen Klamt	Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany	Structural and functional analysis of cellular networks with CellNetAnalyzer
0900-1100 MV-H11	Jean Peccoud	Virginia Bioinformatics Institute, USA	Linguistic methods to design and verify synthetic genetic constructs
0900-1100 MV-F23	Fedor Kolpakov	Institute of Systems Biology, Novosibirsk, Russia	New possibilities of the BioUML workbench
0900-1100 MV-F31	Pedro Mendes, Stefan Hoops, Sven Sahle, Ralph Gauges	Virginia Bioinformatics Institute, USA, University of Manchester, UK, University of Heidelberg, Germany	Introduction into parameter estimation with COPASI
0900-1100 Pascal	Nataša Pržulj, Tijana Milenković	University of California Irvine, USA	Biological networks: Analyses, models, functions, and disease
0900-1100 MV-F33	Mats Jirstrand	Fraunhofer-Chalmers Centre, Gothenburg, Sweden	Component based modeling of biochemical networks using PathwayLab
1130-1330 MV-F23	Thomas Maiwald	University of Freiburg, Germany	Dynamic modelling and multi-experiment fitting with PottersWheel
1130-1330 Pascal	Jörg Stelling, Carsten Conradi	ETH Zürich, Switzerland; Max-Planck-Institute Magdeburg Germany	Reaction network theory for Systems Biology
1130-1330 MV-H11	Rod Smallwood, Simon Coakley, Salem Adra, Susheel Varma	University of Sheffield, UK	FLAME – a Flexible Large-Scale Agent Modelling Environment
1130-1330 MV-F26	Arthur Goldsipe, Jeremy Muhlich, Julio Saez-Rodriguez, Douglas A. Lauffenburger, Peter K. Sorger	MIT and Harvard Medical School, Boston, USA	Linking models to data and experimental prediction via Systems Biology Pipeline
1130-1330 MV-F31	Eva Balsa-Canto, Julio R. Banga	IIM-CSIC, Madrid, Spanish Council Scientific Research	Advanced model identification using global optimization
1130-1330 MV-F33	Mikael Benson, Jesper Tegnér, Pablo Villoslada	The Queen Silvia Children's Hospital and Karolinska Institute, Sweden; University of Navarra, Spain	What good is systems biology for clinical research and practice? An introduction
1130-1330 MV-H12	Nicolas Le Novère (The SBGN-team)	EMBL-EBI Hinxton, UK	The process diagrams of the Systems Biology Graphical Notation

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Saturday August 23, 2008			
1500-1800	**Opening session (Congress Hall)**		
	Chairperson: Stefan Hohmann (University of Gothenburg)		
1500-1530	Opening speeches	Stefan Hohmann, Gothenburg, Sweden	Chairman of the ICSB2008 organising committee
		Hiroaki Kitano, Tokyo, Japan	Chairman of the International Society for Systems Biology
		Karin Markides, Gothenburg, Sweden	President, Chalmers University of Technology
		Pam Fredman, Gothenburg, Sweden	Vice-Chancellor, University of Gothenburg
		Jan Törnell, AstraZeneca, Mölndal, Sweden, UK	Platinum sponsor official
		Pierre de Meyts, Novo Nordisk, Denmark	Platinum sponsor official
1530-1615	**Chris Sander**	Sloan-Kettering Institute, New York, USA	Networks from experiments: combinatorial perturbation of cancer pathways (P-01)
1615-1700	**Wolfgang Baumeister**	Max Planck Institute of Biochemistry, Martinsried, Germany	Cryoelectron tomography: From molecules to systems (P-02)
1700-1720	Frederick Marcus	European Commission, Brussels, EU	Systems Biology in Europe
1720-1730	Edda Klipp	Max Planck Institute for Molecular Genetics, Berlin, Germany	ENFIN - Enabling Systems Biology
1730-1740	Boris Zhivotovsky	Karolinska Institute, Stockholm, Sweden	APO-SYS - Apoptosis systems biology applied to cancer and AIDS
1740-1750	Wolfgang Schamel	Max Planck Institute of Immunobiology, Freiburg, Germany	SYBILLA - Systems biology of T-cell activation
1750-1800	Stefan Hohmann	University of Gothenburg, Sweden	UNICELLSYS - Eukaryotic unicellular organism biology
1800-2000	**Opening reception (Lobby)**		
2000-2300	Visit to Liseberg amusement park (optional, entry free - attractions on own costs)		

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Sunday August 24, 2008

0830-1030	Plenary session 1: Network biology (Congress Hall)		
	Chairperson: Mats Jirstrand (Fraunhofer-Chalmers Center for Industrial Mathematics, Gothenburg)		
0830-0900	Frank Holstege	University of Utrecht, Netherlands	Understanding regulatory circuitry through expression-profile phenotypes (P-03)
0900-0930	Charlie Boone	University of Toronto, Canada	Global mapping of the yeast genetic interaction network (P-04)
0930-1000	Rune Linding	Institute of Cancer Research, London, UK	Casting a net for kinases - systematic discovery of In vivo phosphorylation networks (P-05)
1000-1030	Eran Segal	Weizmann Institute, Rehovot, Israel	Cracking the regulatory code: Predicting expression patterns from DNA sequence (P-06)
1030-1100	Coffee		
1100-1300	**Dedicated session 1-1: Cell-regulation - metabolism (Congress Hall)**		
	Chairpersons: Jacky Snoep (Stellenbosch) and Matej Oresic (Espoo)		
1100-1120	Jacky Snoep	University of Stellenbosch, South Africa	Predicting flux control distributions in metabolic networks for which limited kinetic information is available (DS-1-1-01)
1120-1140	Matej Oresic	VTT Espoo, Finland	Reconstruction of lipid pathways at cellular and systemic level (DS1-1-02)
12min	Sarah-Maria Fendt	ETH Zürich, Switzerland	Limited number of transcription factors control metabolic fluxes in yeast (DS1-1-03)
12min	Michael Ederer	Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany	Thermodynamically-consistent reduced-order modeling of the oxygen response of Escherichia coli (DS1-1-04)
12min	Balazs Papp	Biological Research Center, Szeged, Hungary	Plasticity of genetic interactions in yeast metabolism (DS1-1-05)
12min	Natal van Riel	Eindhoven University of Technology, Netherlands	Modeling the glycolytic pathway in human skeletal muscle tissue; understanding the regulation of its hundredfold dynamic range (DS1-1-06)
12min	Rawisara Ruenwai	King Mongkut's University of Technology Thonburi, Bangkok, Thailand	Genome-wide regulation of <gamma>-linolenic acid biosynthesis in Saccharomyces cerevisiae (DS1-1-07)
12min	Brendan O'Malley	Unilever R&D Colworth, Sharnbrook, United Kingdom	Mathematical model of low density lipoprotein (LDL) endocytosis by hepatocytes (DS1-1-08)
1100-1300	**Dedicated session 1-2: Standards and repositories (Room J1)**		
	Chairpersons: Nicolas Le Novère (Hinxton) and Alan Ruttenberg (Cambridge MA)		
1100-1120	Nicolas Le Novère	EMBL-EBI Hinxton, UK	MIASE - The minimum information about a simulation experiment (DS1-2-01)
1120-1140	Alan Ruttenberg	Science Commons, Cambridge MA, USA	Sharing biological data and knowledge on the semantic web (DS1-2-02)
15min	Jean Peccoud	Virginia Bioinformatics Institute, Blacksburg VI, United States	Targeted development of registries of biological parts (DS1-2-03)
15min	Esther Schmidt	EMBL-EBI, Cambridge, United Kingdom	Reactome - a knowledgebase of human biological pathways (DS1-2-04)
15min	Martin Golebiewski	EML Research GmbH, Heidelberg, Germany	Annotating experimental kinetic data for quantitative modelling: The SABIO-RK database (DS1-2-05)
15min	Susanna-Assunta Sansone	EMBL-EBI, Cambridge, United Kingdom	Reporting standards for omics data - synergistic efforts (DS1-2-06)
1100-1300	**Dedicated session 1-3: Drug discovery (Room G3)**		
	Chairpersons: Hans Westerhoff (Manchester)		
1100-1120	Hans Westerhoff	University of Manchester, UK, and Free University of Amsterdam, Netherlands	Targeting the networks and their fragilities (DS1-3-01)
10min	Mark Davies	Astra Zeneca, Macclesfield UK	Systems Biology in drug safety assessment (DS1-3-27)
10min	Phillip Hundeshagen	German Cancer Research Center, Heidelberg	A novel approach to screen for regulators of autophagic activity (DS-1-3-22)
10min	Klaus Maier	University of Stuttgart, Institute of Biochemical Engineering, Germany	Parameterization of a large-scale, autonomous network model of the hepatic metabolism from transient metabolite data (DS1-3-03)
10min	Lars Kuepfer	Bayer Technology Services GmbH, Systems Biology, Leverkusen, Germany	Using physiology-based pharmacokinetic modelling to dissect mechanisms in hepato-biliary transport (DS1-3-04)
10min	David Orrell	Physiomics plc, Oxford, United Kingdom	A systems biology approach to cancer chronotherapy (DS1-3-05)
10min	Mohammed Atari	University of Warwick, School of Engineering, Coventry, United Kingdom	Compartmental modelling of the breast cancer resistance protein (BCRP/ABCG2) in drug transport (DS1-3-06)
10min	Max von Kleist	Hamilton Institute, Dublin, Ireland	Physiologically based pharmacokinetic modelling in the context of drug discovery: Melding pharmacokinetics with host-virus dynamics (DS1-3-06)
10min	Barbara Bakker	Vrije Universiteit Amsterdam, Netherlands	A domino effect in drug action: From metabolic assault via gene expression to parasite differentiation (DS1-3-07)
10min	Elmar Heinzle	Saarland University, Saarbrücken, Germany	Metabolic flux analysis in Hep G2 cells indicates effects of drugs in subtoxic range (DS1-3-08)
1100-1300	**Dedicated session 1-4: Plant systems (Room G2)**		
	Chairpersons: Mark Stitt (Golm) and Przemyslaw Prusinkiewicz (Calgary)		
1100-1120	Mark Stitt	MPI Golm, Germany	Systems Biology in *Arabidopsis* and *Chlamydomonas:* linking experiments with previous knowledge and with theory (DS1-4-01)
1120-1140	Przemyslaw Prusinkiewicz	University of Calgary, Canada	From molecules to whole plants: Towards an integrative model of Arabidopsis thaliana (DS1-4-02)
12min	Florian Geier	University of Freiburg, Germany	Theoretical modelling reveals competitive complex formation as the core of an activation-depletion framework (DS1-4-03)
12min	Erim Solmaz	Max Planck Institute of Molecular Plant Pysiology, Potsdam, Germany	Kinetic modeling of the Calvin cycle (DS1-4-04)
12min	Karen Halliday	Edinburgh University, United Kingdom	Integration of light temperature signalling (DS1-4-05)
12min	Pawel Krupinski	Lund University, Sweden	Growth patterns - modeling of morphogenesis in shoot apical meristem (DS1-4-06)
12min	Achuthanunni Chokakthukalam	Oxford Brookes University, United Kingdom	Construction and analysis of a model of plant carbon metabolism (DS1-4-07)
12min	Leila Kheibarshekan	Ghent University, Belgium	Stomatal development in Arabidopsis leaf development (DS1-4-08)

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1300-1600	**Lunch break and coffee with specific activities**		
1400-1530	Industry needs in systems biology (Room G3)		
	Chairpersons: Hans Westerhoff (Manchester) and Jens Nielsen (Gothenburg)		
10min	Andy Hargreaves	AstraZeneca, Manchester, UK	The Life Sciences: what is needed in industry
10min	Jens Nielsen	Fluxome, Lyngby, Denmark	Systems Biology as input for cell factory design
10min	Birgit Schoeberl	Merrimack, Cambridge MA, USA	Merrimack Pharmaceuticals: a biotech company designed around a systems biology approach to R&D
10min	Bernhard Palsson	University of California San Diego, USA	To be announced
10min	Preston Hensley	Pfizer Biotherapeutics and Bioinnovation Center, Croton CT, USA	An academic-pharma collaboration to understand insulin resistance using an unbiased phosphoproteomic approach
10min	Pierre de Meyts	NovoNordisk, Copenhagen, Denmark	Systems Biology and Diabetes Mellitus
30min	Panel discussion and questions from audience		
1400-1600	Speakers' corners: morning speakers and previous day afternoon speakers available to meet		
1400-1445	Sander, Baumeister, Marcus, Klipp, Zhivotovsky		
1500-1545	Schamel, Hohmann, Holstege, Boone, Linding, Segal		
1300-1600	Posters, arenas, exhibition		
1600-1800	**Plenary session 2: Understanding and curing diseases (Congress Hall)**		
	Chairperson: Mikael Benson (University of Gothenburg)		
1600-1630	Douglas Lauffenburger	MIT, Cambridge MA, USA	A quantitative systems approach to understanding how signaling networks govern cell behavior (P-07)
1630-1700	Michael Snyder	Yale University, New Haven CT, USA	Mapping functional elements, regulatory circuits and variation in yeast and humans (P-08)
1700-1730	Jesper Tegner	Karolinska Institute, Stockholm, Sweden	Understand disease networks in Atherosclerosis
1730-1800	Douglas Kell	University of Manchester, UK	The cellular uptake of pharmaceutical drugs: A problem not of biophysics but of systems biology (P-10)
1800-2000	**Free viewing posters, arenas, exhibitions**		

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Monday August 25, 2008

0830-1030	**Plenary session 3: Cell regulation (Congress Hall)**		
	Chairperson: Sven Nelander (University of Gothenburg)		
0830-0900	Sunney Xie	Harvard University, Cambridge MA, USA	Single-molecule approach to molecular biology in living bacterial cells (P-11)
0900-0930	Kwang-Hyun Cho	Korea Advanced Institute of Science and Technology (KAIST), Daejeon	From topology to dynamics and function: coupled feedback loops in signaling networks (P-12)
0930-1000	Uwe Sauer	ETH, Zürich, Switzerland	Genetic and environmental control of yeast metabolism (P-13)
1000-1030	Bela Novak	Oxford University, UK	Irreversibility of mitotic exit in budding yeast (P-14)
1030-1100	Coffee		
1100-1300	**Dedicated session 2-1: Cell-regulation - signalling (Room G3)**		
	Chairpersons: Ursula Klingmüller (Heidelberg) and Michael White (Liverpool)		
1100-1120	Ursula Klingmüller	German Cancer Research Center, Heidelberg	Linking dynamic properties of signaling networks with cellular decisions (DS2-1-01)
1120-1140	Michael White	University of Liverpool, UK	Spatial and temporal information encoding by the NF-kappaB system (DS2-1-02)
12min	Jörg Schaber	MPI Molecular Genetics Berlin, Germany	Modelling yeast osmo-adaptation: Integration of two signalling branches (DS2-1-03)
12min	Reut Shalgi	Weizmann Institute of Science, Rehovot, Israel	Shared transcription programs for miRNAs and their targets is a common feature in the mammalian regulatory network (DS2-1-04)
12min	Tetsuya Yomo	Osaka University Japan	Cellular fluctuation in protein concentration and its role on adaptive response (DS2-1-05)
12min	Julio Saez-Rodriguez	Harvard Medical School/MIT, Boston MA, United States	Interrogation of the topology of signaling networks with large-scale data within a boolean framework uncovers mechanistic differences between primary and cancerous hepatocytes (DS2-1-06)
12min	Kirouac Dan	University of Toronto, Toronto, Canada	Predictive modulation of human blood stem cell fate by the systematic manipulation of cell-cell interaction networks (DS2-1-07)
12min	Judit Zamborszky	CoSBi, Trento, Italy	Computational analysis of effects of DNA damage response on circadian rhythms (DS2-1-08)
1100-1300	**Dedicated session 2-2: Modelling approaches (Congress Hall)**		
	Chairpersons: Edda Klipp (Berlin) and Jens Timmer (Freiburg)		
1100-1120	Edda Klipp	MPI Molecular Genetics Berlin, Germany	Construction of biochemical pathway models has to cope with nested uncertainties (DS2-2-01)
1120-1140	Jens Timmer	University of Freiburg, Germany	Modelling with identifiable models (DS2-2-02)
12min	Michael Ederer	Max Planck Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany	Thermodynamic-kinetic modeling of complex formation in signal transduction (DS2-2-03)
12min	Carsten Wiuf	University of Aarhus, BiRC, Aarhus, Denmark	Analysis of biological network data using likelihood and likelihood-free inference techniques (DS2-2-04)
12min	Eva Balso-Canto	IIM-Spanish Council Scientific Research, Process Engineering Group, Vigo, Spain	An optimal identification procedure for model development in systems biology (DS2-2-05)
12min	Masashi Tachikawa	Japan Science and Technology Agency, ERATO, Complex Systems Biology Project, Tokyo, Japan	Evolutionary simulation of cell differentiation under phenotypic noise (DS2-2-06)
12min	Mark Musters	Wageningen University, Laboratory of Microbiology, Netherlands	Kinetic modeling and analysis of nonlinear biochemical networks with no quantitative information (DS2-2-07)
12min	Joachim Almquist	Fraunhofer-Chalmers Centre, Göteborg, Sweden	System identification from spatiotemporal cell population data (DS2-2-08)
1100-1300	**Dedicated session 2-3: Diagnostic markers and complex diseases (Room J1)**		
	Chairpersons: Mikael Benson (Gothenburg) and Jesper Tegner (Stockholm)		
1100-1120	Mikael Benson	University of Gothenburg, Sweden	Clinical systems biology to personalize medication (DS2-3-01)
1120-1140	Jesper Tegner	Linköping University and Karolinska Institute, Sweden	Understanding networks of Atherosclerosis (DS2-3-02)
12min	Palle Villesen	University of Aarhus, Denmark	Ultra short tandem repeats: A target for disease mutations (DS2-3-03)
12min	Wen-Hui Su	Chang Gung University, Taoyuan, Taiwan	Discovery of cancer genes through comparative oncogenomic analysis of hepatocellular carcinoma (DS2-3-04)
12min	Avi Orr-Urtreger	Tel Aviv Sourasky Medical Center, Israel	Transcriptional variations associated with Parkinson's disease (DS2-3-05)
12min	Stanley Shaw	Massachusetts General Hospital, Boston MA, United States	Placing disease mutations in context: Chemical genomics and synthetic interaction screens in human cells (DS2-3-06)
12min	Sara Hägg	Karolinska Institute, Stockholm, Sweden	Multi-organ expression profiling uncovers transendothelial migration of leukocytes and a transcription factor as potential targets in coronary artery disease (DS2-3-07)
12min	Reza Mobini	University of Gothenburg, Sweden	Identification of an IRF4 regulated module by combined ChIP-chip and gene expression analysis (DS2-3-08)
1100-1300	**Dedicated session 2-4: Microbial systems (Room G2)**		
	Chairpersons: Igor Stagljar (Toronto) and Yoshi Ohya (Tokyo)		
1100-1120	Igor Stagljar	University of Toronto, Canada	From membrane proteins to their interactomes: Lessons from yeast and humans (DS2-4-01)
1120-1140	Yoshi Ohya	University of Tokyo, Japan	Quantitative morphological analysis of heterozygous mutants of yeast essential gene (DS2-4-02)
12min	Brenda Andrews	University of Toronto, Canada	A genomic approach to map transcription factor and kinase pathways in budding yeast (DS2-4-03)
12min	Richard Yu	The Molecular Sciences Institute, Berkeley, CA, United States	MAPK-dependent negative feedback in pheromone response regulates information transmission (DS2-4-04)
12min	Jean-Baptiste Michel	Harvard Medical School, Boston MA, United States	Drug interactions modulate the potential for evolution of resistance (DS2-4-05)
12min	Vladimir Titorenko	Concordia University, Montreal, Canada	The spatiotemporal dynamics of a modular network that regulates longevity in yeast and is controlled by a novel class of anti-aging small molecules (DS2-4-06)
12min	Albert Gevorgyan	Oxford Brookes University, United Kingdom	Identification of minimal net stoichiometries and minimal substrate sets in metabolic models (DS2-4-07)
12min	Lei Yang	Technical Univestity of Denmark, Lyngby, Denmark	Longitudinal study of pseudomonas aeruginosa isolates from Cystic Fibrosis lungs (DS2-4-08)

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Monday August 25, 2008			
1300-1500	**Lunch break and coffee with specific activities**		
1330-1500	Funding needs and opportunities (Room G3)		
	Chairperson: Patrik Kolar (Brussels)		
10min	Patrik Kolar	European Commission, Brussels, Belgium	FP7: Responding to the emerging needs in systems biology research on the European level
10min	Frank Laplace	Federal Ministry of Education and Research, Berlin, Germany	Funding of Systems Biology by the German Federal Ministry of Education and Research
10min	Gabriela Pastori	Biotechnology and Biological Sciences Research Council, Swindon, UK	BBSRC funding activities in Systems Biology
10min	Lena Gustafsson	Swedish Governmental Agency for Innovation Systems, Stockholm, Sweden	From research to innovation in systems biology - a VINNOVA outlook
10min	Daniel VonderMuehll	SystemsX, Zürich, Switzerland	SystemsX.ch: The Swiss initiative in Systems Biology in a nut shell
10min	John Marks	European Science Foundation, Strasbourg, France	From Forward Look to action, the role of ESF in Systems Biology
30min	Panel discussion and questions from audience		
1330-1500	Speakers' corners: morning speakers and previous day afternoon speakers available to meet		
1400-1445	Lauffenburger, Snyder, Kishone, Kell, Xie, Cho, Sauer, Novak		
1300-1500	Posters, arenas, exhibition		
1500-2300	Excursion to Marstrand and Viking Dinner (requires separate booking - otherwise free evening)		

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Tuesday August 26, 2008

0830-1030	**Plenary session 4: From cell to organ to organism (Congress Hall)**		
	Chairperson: Bernt Wennberg (Chalmers University of Technology)		
0830-0900	Roel van Driel	University of Amsterdam, Netherlands	Composite kinetics of in vivo assembly and functioning of multi-protein complexes controlling genome function (P-15)
0900-0930	Francois Nedelec	EMBL Heidelberg, Germany	The asymmetric dance of the microtubules in mitosis (P-16)
0930-1000	Eileen Furlong	EMBL Heidelberg, Germany	Deciphering cis-regulatory networks (in Drosophila) (P-17)
1000-1030	Peter Hunter	University of Aukland, New Zealand	Developments in computational physiology (P-18)
1030-1100	Coffee		
1100-1300	**Dedicated session 3-1: Cell-to-cell variation (Room J1)**		
	Chairpersons: Johan Elf (Uppsala) and Alejandro Colman-Lerner (Buenos Aires)		
1100-1115	Johan Elf	Uppsala University, Sweden	Transcription factor search kinetics in bacterial cells (DS3-1-01)
1115-1130	Alejandro Colman Lerner	University of Buenos Aires, Argentina, and Molecular Science Institute, Berkeley CA, USA	Activation of mating response converts the HOG pathway from a transient to a sustained response (DS3-1-02)
12min	Serge Pelet	ETH Zürich, Switzerland	Quantifying Hog1p MAPK signaling at the single cell level (DS3-1-03)
12min	Pieter Rein Ten Wolde	FOM Institute AMOLF, Amsterdam, Netherlands	Regulatory control and the costs and benefits of biochemical noise (DS3-1-04)
12min	Gustavo Pesce	The Molecular Sciences Institute, Berkeley CA, United States	Genetic mechanisms that regulate the precision of signaling in different regions of dose and time axes of the yeast pheromone response (DS3-1-05
12min	Johan Paulsson	Harvard University, Boston, United States;	Fundamental limits on noise suppression (DS3-1-06)
12min	John Burnett	University of California, Berkeley CA, United States	Control of stochastic gene expression by host factors at the HIV promoter (DS3-1-07)
12min	Paul Choi	Harvard University, Cambridge MA, United States	Single-cell analysis of the Escherichia coli proteome with single-molecule sensitivity (DS3-1-08)
12 min	Sabrina Spencer	Harvard Medical School, Boston MA, United States	Origins of cell-to-cell variability in the life-or-death decision (DS3-1-09)
1100-1300	**Dedicated session 3-2: Synthetic biology (Room G2)**		
	Chairpersons: Jörg Stelling (Zürich) and Mark Isalan (Barcelona)		
1100-1120	Jörg Stelling	ETH Zürich, Switzerland	Computational engineering of synthetic circuits (DS3-2-01)
1120-1140	Mark Isalan	Center for Genomic Regulation, Barcelona, Spain	Gene network engineering: Scaffolds for evolution (DS3-2-02)
12min	Uri Shabi	Weizmann Institute, Rehovot, Israel	Towards large designed DNA libraries (DS3-2-03)
12min	Grzegorz Kudla	University of Edinburgh, United Kingdom	Coding sequence determinants of gene expression (DS3-2-04)
12min	Terence Hwa	UC San Diego, La Jolla CA, United States	De novo evolution of promoters in bacteria (DS3-2-05)
12min	Nicolas Buchler	Rockefeller University, New York, United States	Molecular titration: A simple mechanism to generate large ultrasensitivity (DS3-2-06)
12min	Yiannis Kaznessis	University of Minnesota, Minneapolis, United States	Model-driven synthetic biology (DS3-2-07)
12min	Giovanni Russo	University of Naples Federico II, Italy	How to build a network of synthetic biological oscillators that synchronize (DS3-2-08)
1100-1300	**Dedicated session 3-3: Software tools (Congress Hall)**		
	Chairpersons: Attila Csikasz-Nagy (Trento) and Mats Jirstrand (Gothenburg)		
1100-1120	Attila Csikasz-Nagy	CoSBi, Trento, Italy	Challenges for computational systems biology (DS3-3-01)
12min	Chris Myers	University of Utah, Salt Lake City UT, United States	iBioSim: A tool for the analysis and design of genetic circuits (DS3-3-02)
12min	Pedro Mendes	University of Manchester, United Kingdom	Advanced simulation and analysis of biochemical models using COPASI (DS3-3-03)
12min	Mats Kvarnström	Fraunhofer-Chalmers Centre, Göteborg, Sweden	Automated image analysis for quantification of protein localization in budding yeast (DS3-3-04)
12min	Ion Moraru	University of Connecticut Health Center, Farmington, United States	Building new experiment-oriented simulation tools (DS3-3-05)
12min	Thomas Maiwald	University of Freiburg, Germany	Dynamic modeling and multi-experiment fitting with PottersWheel (DS3-3-06)
12min	Franco Du Preez	University of Stellenbosch, South Africa	JWS Online: A web-accessible model database, simulator and research tool (DS3-3-07)
1240-1300	Mats Jirstrand	Fraunhofer-Chalmers Centre, Gothenburg, Sweden	Software tools - a survey from a theoretical perspective (DS3-3-08)
1100-1300	**Dedicated session 3-4: Model driven experimental planning (Room G3)**		
	Chairpersons: Fritz Roth (Boston) and Roland Eils (Heidelberg)		
1100-1120	Fritz Roth	Harvard University, Cambridge MA, USA	Mouse gene function prediction and complex disease (DS3-4-01)
12min	Torbjörn Nordling	KTH - Royal Institute of Technology, Stockholm, Sweden	Inference of interampatte gene regulatory networks - with application to apoptosis signalling (DS3-4-02)
12min	Bree Aldridge	Massachusetts Institute of Technology, Boston, MA, United States	Quantitative analysis of the mitochondrial-pathway requirement for receptor-mediated apoptosis in single cells (DS3-4-03]
1145-1205	Roland Eils	German Cancer Research Center, Heidelberg	Model-based study of life and death pathways diverging from the CD95 Death Receptor (DS3-4-04)
12min	Jan Schellenberger	UC San Diego, La Jolla CA, United States	Optimizing 13C labeling experiments for flux elucidation (DS3-4-05)
12min	Jason Shoemaker	University of California, Santa Barbara CA, United States	Fathead minnow steroidogenesis- in vitro modeling and experimentation reveals global regulation of sex hormone synthesis (DS3-4-06
12min	Jens Keienburg	University of Heidelberg, Bioquant, Heidelberg, Germany	Parameter estimation for a circadian clock model in neurospora using optimal experiment design (DS3-4-07)
12min	Amanda Clare	Aberystwyth University, United Kingdom	Model driven experiment planning for the Robot Scientist (DS3-4-08)

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Tuesday August 26, 2008

1300-1600	**Lunch break and coffee with specific activities**		
1400-1530	Education in interdisciplinary biology (Room G3)		
	Chairpersons: Anders Blomberg (Gothenburg) and Hans Westerhoff (Manchester/Amsterdam)		
10min	Hans Westerhoff	University of Manchester, UK	Doctoral Training: twinning the challenges of inter- and transdisciplinarity
10min	David Botstein	Princeton University, USA	Undergraduate Science Curriculum for the 21st Century
10min	Olle Nerman	Chalmers University of Technology, Gothenburg, Sweden	Experiences from interdisciplinary master programmes in bioinformatics and systems biology in Gothenburg
10min	Anders Blomberg	University of Gothenburg, Sweden	Experience from pair-student projects - graduate multidisciplinary training within the National Research School in Genomics and Bioinformatics
10min	Stefan Hohmann	University of Gothenburg, Sweden	Developing the International Course for Yeast Systems Biology
30min	Panel discussion and questions from the audience		
1400-1600	Speakers' corners: speakers of Aug 26 and 27 available to meet		
1400-1445	van Driel, Nedelec, Furlong, Hunter, Schoeberl, Nielsen, Serrano, Shapiro		
1500-1545	Omholt, Wagner, Elowitz, Yvert, Botstein, Kitano, Hood		
1300-1600	Posters, arenas, exhibition		
1600-1800	**Plenary session 5: New approaches to biotechnology (Congress Hall)**		
	Chairperson: Devdatt Dubashi (Chalmers University of Technology)		
1600-1630	Birgit Schoeberl	Merrimack, Cambridge MA, USA	Computational modeling and simulation lead to the development of MM-121, a human monoclonal antibody ErbB3 antagonist (P-19)
1630-1700	Jens Nielsen	Chalmers, Gothenburg, Sweden	Industrial systems biology: Yeast and filamentous fungi as cell factories for sustainable production of chemicals (P-20)
1700-1730	Luis Serrano	Center for Genomic Regulation, Barcelona, Spain	Evolvability and hierarchy in rewired bacterial gene networks (P-21)
1730-1800	Ehud Shapiro	Weizmann Institute, Rehovot, Israel	Why not edit DNA the way we edit text? (P-22)
1800-2000	**Free viewing posters, arenas, exhibitions**		

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Wednesday August 27, 2008

0830-1030	**Plenary session 6: Genetic variation and evolution (Congress Hall)**		
	Chairperson: Olle Nerman (Chalmers University of Technology)		
0830-0900	Stig Omholt	Centre for Integrative Genetics, Ås, Norway	Causally cohesive genotype-phenotype models - systems biology meets genetics (P-23)
0900-0930	Andreas Wagner	University of Zürich, Switzerland	On the relationship between robustness and evolvability (P-24)
0930-1000	Michael Elowitz	CalTech, Pasadena CA, USA	Noise, penetrance, and cell fate in bacterial development (P-25)
1000-1030	Gael Yvert	Ecole Normale Supérieure de Lyon, France	Genetic diversity in gene expression stochasticity and chromatin epigenetic states (P-26)
1030-1100	Coffee		
1100-1300	**Plenary session 7: Future challenges (Congress Hall) Sponsored by Novozymes**		
	Chairperson: Anders Blomberg (University of Gothenburg)		
1100-1145	David Botstein	Princeton University, USA	Genomics, computation, and the nature of biological understanding (P-27)
1145-1215	Hiroaki Kitano	Systems Biology Institute, Tokyo, Japan	Systems Biology for global climate and energy solutions (P-28)
1215-1300	Leroy Hood	Institute for Systems Biology, Seattle WA, USA	Systems medicine, transformational technologies and the emergence of P4 medicine (P-29)
1300	Stefan Hohmann	University of Gothenburg, Sweden	Closing remarks and invitation to ICSB2009
1300-1400	Lunch packages		
1330-2030	**Workshop Programme (Wallenberg Conference Centre Medicinarberget)**		
1330-1830 Ljusvågen	Ewan Birney, Pascal Kahlem	EMBL-EBI Hinxton, UK	Integrative research on the TGF-beta pathway (WS-1)
1330-1830 Ljudvågen	Christine Petit, Laurent Charvin, Tobias Moser	Institut Pasteur, France; University of Göttingen, Germany	Systems biology of hearing (WS-7)
1430-1800 Lyktan	Michael Hucka	California Institute of Technology, USA	The Systems Biology Markup Language (SBML) - continues 28/8 (WS-4)
1430-2030 Radiovågen	Ursula Klingmüller, Jens Timmer	German Cancer Research Center Heidelberg; University of Freiburg, Germany	Systems Biology of the Liver (WS-8)
Detailed programme on respective workshop website via www.icsb-2008.org			

Thursday August 28, 2008

0830-1800	**Workshop Programme (Wallenberg Conference Centre Medicinarberget)**		
0830-1700 Radiovågen	Stefan Hohmann, Martin Markström, Dina Petranovic	University of Gothenburg; Chalmers University of Technology, Sweden	Yeast Systems Biology (WS-5)
0900-1500 Mikrovågen	Grace S. Shieh	Institute of Statistical Science, Taiwan	Inferring networks for Disease (WS-2)
0900-1700 Ljusvågen	Ralf Herwig	Max Planck Institute for Molecular Genetics, Germany	Web services in Systems Biology (WS-3)
0900-1800 Lyktan	Michael Hucka	California Institute of Technology, USA	continued - The Systems Biology Markup Language (SBML) (WS-4)
22/8 0900-1700 and 23/8 0900-1300 Workshop by invitation only (Wallenberg Conference Centre Medicinarberget)			
Ljusvågen	Douglas Kell, Dieter Weichart	Manchester Centre for Integrative Systems Biology, UK	Human Metabolic Network Jamboree (WS-6)
Detailed programme on respective workshop website via www.icsb-2008.org			