

Poster Programme

Metabolic Systems		
Nr.	Authors	Poster Title
1.1	J. Zobeley, EML Research gGmbH, Heidelberg/D; J. Kammerer, D. Lebiedz, University of Heidelberg/D; U. Kummer, EML Research gGmbH, Heidelberg/D	Dynamical complexity reduction in biochemical reaction networks
1.2	M. Henson, University of Massachusetts, Amherst/USA	Modeling the synchronization of yeast respiratory oscillations
1.3	S. Rossell, Vrije Universiteit, Amsterdam/NL; C.C. van der Weijden, DSM Food Specialities, Delft/NL; A. Lindenbergh, Vrije Universiteit, Amsterdam/NL; A.L. Kruckeberg, Gothia Yeast Solutions, Gothenburg/S; B.M. Bakker, H.V. Westerhoff, Vrije Universiteit, Amsterdam/NL	Understanding Fermentative Capacity: An integrative Approach
1.4	K. Bettenbrock, A. Kremling, S. Fischer, E.D. Gilles, MPI für Dynamik komplexer technischer Systeme, Magdeburg/D	Analysis of EIACrr phosphorylation state during diauxic growth of Escherichia coli K-12: New insights into catabolite repression by lactose
1.5	W.H. Hunag, F.S. Wang, National Chung Cheng University, Chai-yi/RC	Simultaneous maximization of production rate and minimization of number of enzymes in metabolic systems via mixed-integer hybrid differential evolution
1.6	J.R. Weimar, S. Eckstein, Technical University Braunschweig/D	Modularization of systems biology markup language using hierarchical UML models
1.7	S. Fischer, A. Kremling, K. Bettenbrock, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	How detailed must a model be? Carbohydrate uptake in Escherichia coli K-12 as an example.
1.8	A. Kowald, H. Lehrach, E. Klipp, MPI for Molecular Genetics, Berlin/D	Alternative pathways as mechanism for the negative effects associated with overexpression of superoxide dismutase
1.9	W. Liebermeister, MPI for Molecular Genetics, Berlin/D	Frequency-dependent metabolic response coefficients
1.10	A. Lavrova, Moscow State University/RUS; S. Mironov, Physico-Technical Institut, Dolgoprudnyi/RUS; O. Demin, A.N. Belozersky, Institute of Physico-Chemical Biology, Moscow/RUS	Kinetic modelling of lysine biosynthetic pathway
1.11	J.R. Haanstra, A. van Tuijl, E. Veraar, Vrije Universiteit Amsterdam/NL; M.-A. Albert, de Duve Institute for Cellular Pathology, Brussels/B; C. Francke, Vrije Universiteit Amsterdam/NL; P.A.M. Michels, de Duve Institute for Cellular Pathology, Brussels/B; H.V. Westerhoff, B.M. Bakker, Vrije Universiteit Amsterdam/NL	Synergy and antagonism of glycolysis inhibitors against Trypanosoma brucei: From model to experiment
1.12	H. Schmidt, E.W. Jacobsen, KTH, Stockholm/S; K.-H. Cho, University of Ulsan/ROK	Identification of feedback loops in metabolic pathways
1.13	O. Demin, G. Lebedeva, A. Kolupaev, E. Zbova, T. Plyusnina, Moscow State University/RUS; A. Lavrova, E. Goryacheva, N. Gizzatkulov, A.N. Belozersky Institute of Physico-Chemical Biology/RUS	Strategy to develop large-scale kinetic models
1.14	O.H. Sendin, IIM-CSIC, Vigo/E; J. Vera, N.V. Torres, University La Laguna, Tenerife/E; J.R. Banga, IIM-CSIC, Vigo/E	Multi-objective optimisation of metabolic systems
1.15	L.M. Blank, L. Kuepfer, U. Sauer, ETH Zurich/CH	Deciphering metabolic network robustness
1.16	T. Plusnina, Moscow State University/RUS; O. Demin, A.N. Belozersky Institute of Physico-Chemical Biology, Moscow/RUS	Kinetic modelling of biosynthesis of the branched chain amino acids in E.coli
1.17	L. Salusjärvi, M. Oresic, H. Maaheimo, E. Rintala, H. Simolin, L. Ruohonen, M. Penttilä, VTT Biotechnology, Espoo/FIN	Integrative approaches for studying pentose metabolism in Saccharomyces cerevisiae
1.18	R. Gabdoulline, U. Kummer, EML Research, Heidelberg/D; L. Olsen, University of Southern Denmark, Odense/DK; R. Wade, EML Research, Heidelberg/D	Concerted structure-based and biochemical simulations applied to peroxidase-oxidase oscillator
1.19	D. Degenring, J. Lemcke, A. M. Uhrmacher, University of Rostock/D	Towards re-using model components in systems biology
1.20	S. Biermann, H. Schumann, A.M. Uhrmacher, M. Röhl, D. Degenring, University of Rostock/D	Supporting multi-level models by visual methods
1.21	R. Tanaka, J. Doyle, California Institute of Technology, Pasadena, CA/USA	Simple model of bow-tie structures in metabolic networks

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1.22	Y.G. Assaraf, I. Ifergan, W.N. Kadry, R.Y. Pinter, Technion, Haifa/IL	HFPN-based simulation of the reduced folates metabolic pathway with applications to cancer chemotherapy
1.23	V. R. Velagapudi, C. Wittmann, University of Saarland, Saarbrücken/D; P. Talwar, T. Lengauer, MPI for Informatics, Saarbrücken/D; E. Heinzle, University of Saarland, Saarbrücken/D	Functional genomics of yeast by metabolic flux profiling stoichiometry and kinetics of growth and product formation of mutants with deletion of genes in central metabolism
1.24	cancelled	
1.25	A.N. Goltsov, Moscow Institute of Radioelectronics and Automatics/RUS; G.V. Lebedeva, Moscow State University/RUS; A.I. Lavrova, Moscow Lomonosov State University/RUS; O.V. Demin, Moscow State University/RUS	Modeling of purine nucleotides biosynthesis in E.coli
1.26	cancelled	
1.27	E. Klipp, W. Liebermeister, MPI for Molecular Genetics, Berlin/D	Dynamics of biochemical networks with known topology and uncertain parameters
1.28	P. Talwar, T. Lengauer, J. Rahnenführer, MPI für Informatik, Saarbrücken/D; V. Velagapudi, C. Wittmann, E. Heinzle, Saarland University, Saarbrücken/D	Computational methods for metabolite screening
1.29	R. Guthke, W. Schmidt-Heck, Hans Knoell Institute for Natural Products Research, Jena/D; M. Pfaff, S. Töpfer, D. Wötzel, BioControl Jena GmbH, Jena/D; K. Iding, H. Büntemeyer, H. Lehmann, University Bielefeld/D; K. Zeilinger, G. Pless, J.C. Gerlach, Charite, Berlin/D	Kinetic characterization of amino acid metabolism in a 3D liver cell bioreactor by fuzzy clustering and rule based analysis
1.30	S. Schmeier, A. Kowald, MPI for Molecular Genetics, Berlin/D; J. Hakenberg, U. Leser, Humboldt-Universität Berlin/D; E. Klipp, MPI for Molecular Genetics, Berlin/D	Fighting the data acquisition bottleneck
1.31	H.E. Assmus, M.G. Poolman, Oxford Brookes University/UK; S.A. Coates, Advanced Technologies Cambridge Ltd., Cambridge/UK; M.M. Burrell, University of Sheffield/UK; D.A. Fell, Oxford Brookes University/UK	A mathematical model of potato tuber carbohydrate metabolism
1.32	E.W.J. van Niel, H. Grage, Lund University/S	Towards a descriptive kinetic model of the maltose metabolism in <i>Lactococcus lactis</i>
1.33	O. Ebenhöf, T. Handorf, R. Heinrich, Humboldt University Berlin/D	Expanding networks: Alternative approaches to investigate the structural design of metabolic pathways
1.34	A.González González, C. Chaouiya, LGPD-IBDM, Marseille/F; Y. Vaxes, LIF, Marseille/F; L. Sánchez, CIB-CSIC, Madrid/E; D. Thieffry, LGPD-IBDM, Marseille/F	Extension of a multi-level discrete formalism to simulate regulatory networks within a large number of cells
1.35	K. Mauch, INSILICO biotechnology, Stuttgart/D; J.W. Schmid, M. Reuss, University of Stuttgart/D; H. Ulmer, University of Tübingen/D	In silico identification of whole cell metabolite dynamics through evolutionary algorithms and parallel computing
1.36	I. Koch, Technical University of Applied Sciences, Berlin/D; B. Junker, MPI for Molecular Plant Physiology, Golm/D; M. Heiner, Brandenburg University of Technology, Cottbus/D	A model validation technique of the central carbon metabolism of <i>Solanum tuberosum</i>
1.37	T. Aho, O.-P. Smolander, A. Pettinen, O. Yli-Harja, Tampere University of Technology/FIN	Metabolic simulation in matlab environment
1.38	N. Kelley-Loughnane, Geo-Centers, Inc. Wright-Patterson Air Force Base, OH/USA; M.E. Thrash, A. Soto, ManTech Environmental Technology, Dayton, OH/USA; M.H. Linger, Geo-Centers, Inc. Wright-Patterson Air Force Base, OH/USA; D.L. Pollard, ManTech Environmental Technology, Dayton, OH/USA; J.M. Frazier, Applied Biotechnology Branch, Wright Patterson Air Force Base, OH/USA	Modeling the metabolic network of glutathione synthesis in <i>Escherichia coli</i>
1.39	H. Schmidt, E.W. Jacobsen, KTH, Stockholm/S	On the decomposition of dynamic metabolic networks
1.40	F. Centler, P. Speroni di Fenizio, N. Matsumaru, P. Dittrich, Friedrich-Schiller-University Jena/D	Hierarchical organization of microbial metabolism
1.41	K. Maier, University of Stuttgart/D; M. Schwehm, University of Tübingen/D	Parameter estimation for metabolic systems by evolution strategies

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1.42	B. Foy, Wright State University, Dayton, OH/USA	Implementation of biochemical complexes in stochastic simulations
1.43	A. Provost, G. Bastin, Université catholique de Louvain, Louvain-la-neuve/B	Metabolic model for CHO cells
1.44	J. Schütze, R. Heinrich, Humboldt-Universität Berlin/D	Glycolytic oscillations in spatially ordered interacting cells
1.45	A. Prelic, S. Bleuler, P. Zimmermann, P. v. Rohr, A. Wille, P. Buehlmann, W. Grisssem, L. Thiele, E. Zitzler, ETH Zuerich/CH	Studying the usefulness of biclustering on a global scale
1.46	J. Rahnenführer, F.S. Domingues, J. Maydt, T. Lengauer, MPI for Informatics, Saarbrücken/D	Calculating the statistical significance of changes in pathway activity from gene expression data
1.47	F. He, H.-W. Ma, German Research Center for Biotechnology, Braunschweig/D; Y. Yuan, Tianjin University/VRC; W.-D. Deckwer, A.-P. Zeng, German Research Center for Biotechnology, Braunschweig/D	A method for calculation of elementary flux modes in genome-based metabolic network
1.48	K.Y. Arga, F.B. Kavun, K.Ö. Ülgen, Bogazici University, Istanbul/TR	In silico metabolic analysis of human disease: Ischemia and cardiac muscle cell energy metabolism
1.49	K. Arakawa, Y. Yamada, K. Shinoda, Y. Nakayama, M. Tomita, Keio University, Fujisawa/J	GEM System: Automatic generation of dynamic cell-wide metabolic pathway model from the genome
1.50	M. Anguelova, M. Johansson, C.J. Franzén, B. Wennberg, Chalmers University of Technology, Gothenburg/S	Identifiability of kinetic models of metabolism
1.51	J. Sun, A.-P. Zeng, German Research Center for Biotechnology, Braunschweig/D	IdentiCS - A program for reconstruction of metabolic network from unfinished genomic sequences
1.52	D. Bannasch, A. Mehrle, K.-H. Glatting, German Cancer Research Center, Heidelberg/D; R. Pepperkok, EMBL, Heidelberg/D; A. Poustka, S. Wiemann, German Cancer Research Center, Heidelberg/D	LIFEdb: A database for localization, interaction, functional assays and expression of proteins
1.53	H. Ma, J. Buer, A.-P. Zeng, German Research Center for Biotechnology, Braunschweig/D	The hierarchical modular structure of E. coli transcriptional regulatory network and its functional relation to metabolic network
1.54	A. Wille, P. Zimmermann, S. Bleuler, L. Hennig, A. Prelic, P. v. Rohr, L. Thiele, E. Zitzler, W. Grisssem, P. Buehlmann, ETH Zuerich/CH	Adjusting graphical models for reverse engineering of genetic regulatory networks
1.55	R. Steuer, University Potsdam/D	Optimal response to fluctuations in metabolic and signaling pathways
1.56	M. Ederer, T. Sauter, E. Bullinger, F. Allgöwer, University of Stuttgart/D; E.D. Gilles, University of Stuttgart/D and MPI for Dynamics of Complex Technical Systems, Magdeburg/D	Identifying modules in metabolic reaction networks and their reduced-order modeling
1.57	P.O. Westermark, J. Hellgren-Kotaleski, A. Lansner, Royal Institute of Technology, Stockholm/S	NADH shuttles, TCA cycle and anaplerosis in the pancreatic beta-cell - insights from modeling
1.58	S. Aytuna, C. Ulubas, A. GURSOY, O. Keskin, Koc University, Istanbul/TR	Biological classification of potential protein-protein Interactions
1.59	cancelled	
1.60	A. Jouraku, Keio University, Yokohama/J; A. Funahashi, H. Kitano, ERATO-SORST Kitano Symbiotic Systems Project, Tokyo/J	Converting the KEGG pathway database to SBML
1.61	M. Sugimoto, T. Soga, S. Kikuchi, M. Tomita, Keio University, Tsuruoka, Yamagata/J	Prediction of migration behaviour of cations in capillary electrophoresis – mass spectrometry using artificial neural networks
1.62	H.V. Westerhoff, J.J. Hornberg, F.J. Bruggeman, Vrije Universiteit Amsterdam/NL; M.A. Peletier, Centrum for Wiskunde en Informatica, Amsterdam/NL; J.L. Snoep, Vrije Universiteit Amsterdam/NL and Stellenbosch University/ZA; B.N. Kholodenko, Thomas Jefferson University, Philadelphia, PA/USA	Biology outlawed? Systems biology discovering new laws of biology

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Nr.	Authors	Poster Title
1.63	H. Roubos, M. Hillebrand, J. van Santen, S. Hartmans, H. Pel, DSM Food Specialties, Delft/NL	Functional genomics for <i>Propionibacterium freudenreichii</i> : Learning from biochemical network reconstruction and transcriptomics
1.64	J. Ciapaite, G. Van Eikenhorst, Vrije Universiteit Amsterdam/NL; S.J.L. Bakker, University Hospital, Groningen/NL; M. Diamant, R.J. Heine, C. Schalwijk, T. Teerlink, University Medical Center, Amsterdam/NL; M.J. Wagner, H.V. Westerhoff, K. Krab, Vrije Universiteit Amsterdam/NL	Application of modular kinetic analysis to determine the effect of palmitoyl-CoA on the mitochondrial oxidative phosphorylation

Signal Transduction		
Nr.	Authors	Poster Title
2.1	cancelled	
2.2	R. Gebhardt, University of Leipzig/D	Patterning role of Wnt/ β -catenin signaling in liver heterogeneity: Implications for systems biology
2.3	M. Ullah, O. Wolkenhauer, University of Rostock/D; W. Kolch, Cancer Research UK, Glasgow/UK; K.-H. Cho, University of Ulsan/ROK	Choosing an appropriate modelling framework: How deterministic are random processes?
2.4	M. Hatakeyama, A. Suenaga, S. Kimura, RIKEN Genomic Sciences Center, Yokohama/J; T. Naka, Kyushu Sangyo University, Fukuoka/J; M. Taiji, RIKEN Genomic Sciences Center, Yokohama/J; B.N. Kholodenko, Thomas Jefferson University, Philadelphia, PA/USA; A. Konagaya, RIKEN Genomic Sciences Center, Yokohama/J	Molecular simulation for system modeling
2.5	M. Mizuno, S. Kawakami, Kobe University/J	Immunomodulating polysaccharide from <i>Agaricus blazei</i> Murrill activates macrophages through Toll-like receptor 4
2.6	J.R. Weimar, Technical University Braunschweig/D	Hybrid numerical and Monte-Carlo approach for more efficient stochastic simulation of regulatory processes
2.7	C. Borner, University of Freiburg/D; T. Dandekar, University of Würzburg/D; L. Egger, C. Kreuz, University of Freiburg/D; J. Thakar, University of Würzburg/D; J. Timmer, University of Freiburg/D	A system and its components: Modelling Fas ligand-induced apoptotic and mitogenic signaling in hepatocytes
2.8	K.-H. Cho, S.-Y. Shin, University of Ulsan/ROK; W. Kolch, University of Glasgow/UK; O. Wolkenhauer, University of Rostock/D	Modeling and analysis of two feedback loop dynamics in Ras/Raf-1/MEK/ERK signaling pathway
2.9	K.-H. Cho, University of Ulsan/ROK; K.H. Johansson, Royal Institute of Technology, Stockholm/S; O. Wolkenhauer, University of Rostock/D	A system-theoretic modeling framework for cellular processes
2.10	H. Conzelmann, University of Stuttgart/D; J. Saez-Rodriguez, MPI for Dynamics of Complex Technical Systems, Magdeburg/D; T. Sauter, E. Bullinger, F. Allgöwer, University of Stuttgart/D; E.D. Gilles, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	Domain oriented reduction of signal transduction models
2.11	M. Pogson, M. Holcombe, E. Qwarnstrom, University of Sheffield/UK	An agent-based model of the NF- κ B signalling pathway
2.12	F.R. Pinto, ITQB-UNL, Oeiras/P; J. Almeida, MUSC, Charleston, SC/USA	Comparative study of network distance metrics to explore gene transcription network local composition
2.13	L. Kuepfer, ETH Zurich/CH; J. Stelling, MPI for Dynamics of Complex Technical Systems, Magdeburg/D; U. Sauer, ETH Zurich/CH	Comparative computational modeling reveals operating principles of TOR signaling in <i>Saccharomyces cerevisiae</i>
2.14	T. Manninen, M.-L. Linne, Tampere University of Technology/FIN	Simulating the behavior of the PKC signaling pathway in a neuron
2.15	B. Kofahl, E. Klipp, MPI for Molecular Genetics, Berlin/D	A mathematical model of the yeast pheromone pathway
2.16	T. Manke, C. Dieterich, MPI for Molecular Genetics, Berlin/D; J. Laub, Fraunhofer FIRST, Berlin/D; M. Vingron, MPI for Molecular Genetics, Berlin/D	Transcription factor modules in the human genome

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Signal Transduction		
Nr.	Authors	Poster Title
2.17	J. Saez-Rodriguez, X. Wang, MPI for Dynamics of Complex Technical Systems, Magdeburg/D; B. Schoeberl, Merrimack Pharmaceuticals, Cambridge, MA/USA; B. Schraven, Otto-von-Guericke University, Magdeburg/D; E.D. Gilles, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	Analysis of the regulation of the MAP kinase cascade in T-lymphocytes
2.18	S. Ziagos, P. Dittrich, S. Knoth, University Jena/D; S. Wöfl, University Heidelberg/D	Investigation of cell differentiation processes by stability analysis of signal transduction networks
2.19	V. Bhargava, K.-H. Chiam, S.S. Lim, G. Rajagopal, Bionformatics Institute, Singapore/SGP	Stochastic simulations of a model of protein kinase signal transduction
2.20	K.-H. Chiam, G. Rajagopal, Bionformatics Institute, Singapore/SGP	Modeling the sensitivity of the mitogen-activated protein kinase cascade to parametric and initial-condition perturbations
2.21	S. Smidtas, Genoscope CNS CNRS UMR 8030, Evry/F; P. Bourguin, CREA, Ecole Polytechnique, Paris/F; F. Képès, ATelier Génomique Cognitive, CNRS UMR 8071, Genopole, Evry/F; V. Schachter, Genoscope CNS CNRS UMR 8030, Evry/F	Completion of the yeast transcriptional regulation network by protein-protein interactions
2.22	R. Tzafiriri, D. Wu, R.E. Edelman, Biomedical Engineering Center, Cambridge, MA/USA	Analysis of compartmental models of ligand-induced endocytosis
2.23	K. Amonlirdviman, N.A. Khare, D.R.P. Tree, J.D. Axelrod, C.J. Tomlin, Stanford University, CA/USA	Mathematical modeling of planar cell polarity to understand domineering non-autonomy
2.24	K.Y. Tsai, F.S. Wang, National Chemg Chung University, Chia-Yi/RC	Parameter estimation of a genetic network by A global/local optimization algorithm
2.25	L. Nedbal, Institute of Physical Biology, Nove Hradý/CZ; M. Sicner, M. Trtílek, PSI, Ltd., Brno/CZ	Double feedback regulation is responsible for the rapid and robust response of Synechocystis sp. to harmonic forcing
2.26	J. Fisher, N. Piterman, Weizmann Institute of Science, Rehovot/IL; E.J.A. Hubbard, New York University, New York, NYC/USA; M.J. Stern, Yale School of Medicine, New Haven, CT/USA; D. Harel, Weizmann Institute of Science, Rehovot/IL	On the advantages of formalizing and executing biological mechanistic models: Gaining insights into C. elegans vulval development
2.27	N. Blüthgen, Humboldt University, Berlin/D; C. Sers, A. Schramme, C. Ha-Thi, R. Schäfer, Charite, Berlin/D; H. Herzog, Humboldt University, Berlin/D	Dissecting the role of feedback mechanisms in MEK-ERK-mediated signal transduction
2.28	V. Singh, P. Dixit, R. Gupta, Indian Institute of Information Technology, Allahabad/IND	Wavelet-analysis of genomic sequence to explore evolutionary self-organisation
2.29	O. Eriksson, Stockholm University/S; J. Tegnér, Linköping University/S	Module identification by pairwise parameter perturbations
2.30	P. Lorenz, D. Runge, D. Koczan, D. Haase, H.-J. Thiesen, University of Rostock/D	Studying transcriptional networks in primary human hepatocytes
2.31	K.G. Gadkar, R. Gunawan, F.J. Doyle III, University of California, Santa Barbara, CA/USA	Measurement selection for identifiability of biological networks
2.32	R. Gunawan, Y. Cao, S. Lampoudi, L. Petzold, F.J. Doyle III, University of California, Santa Barbara, CA/USA	Stochastic sensitivity analysis of a circadian gene network
2.33	cancelled	
2.34	N. Cuong, C.N. Yoon, S.K. Han, Chungbuk National University Cheongju/ROK	Bifurcation analysis of cell cycle regulation in the budding yeast
2.35	T. Yamamoto, Y. Kaji, Japan Advanced Institute of Science and Technology, Tatsunokuchi, Ishikawa/J	Crosstalks as a "wet circuit" for informatic processing: Noise reduction via hierarchical network
2.36	L. Mendoza, Sero Pharmaceutical Research Institute, Geneva/CH	A regulatory network for the differentiation of T helper cells
2.37	W. Huber, D. Arlt, German Cancer Research Centre, Heidelberg/D; U. Liebel, EMBL, Heidelberg/D; S. Bechtel, D. Bannasch, A. Mehrle, H. Rosenfelder, C. Schmidt, I. Schupp, M. Seiler, German Cancer Research Centre, Heidelberg/D	Sixteen cancer relevant cell cycle modulators identified in an automated cell-based assay

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Signal Transduction		
Nr.	Authors	Poster Title
2.38	I. Vacheva, M. Bentele, R. Eils, German Cancer Research Center, Heidelberg/D	Optimal experimental design for discrimination of competing signal transduction models
2.39	F. Kolpakov, Design Technological Institute of Digital Techniques, Novosibirsk/RUS	BioUML – open source extensible workbench for systems biology
2.40	F. Kolpakov, Design Technological Institute of Digital Techniques, Novosibirsk/RUS; I. Deineko, Institute of Cytology and Genetics, Novosibirsk/RUS; A. Kel, BIOBASE GmbH, Wolfenbuettel/D	Cyclonet a database on cell cycle regulation
2.41	D. Camacho Trujillo, German Cancer Research Center, Heidelberg/D; J. Lagunez Otero, Universidad Nacional Autónoma de México, Mexico-City/MEX; R. Eils, German Cancer Research Center, Heidelberg/D	Modelling of the AP-1 related genetic network
2.42	B. Nordlander, Göteborg University/S; P. Gennemark, D. Wedelin, Chalmers University of Technology, Göteborg/S; S. Hohmann, Göteborg University/S	Termination of activation is the decisive event in HOG pathway feedback control during osmotic adaptation
2.43	C. Röder, M. Kühl, Universitätsklinikum Schleswig-Holstein, Kiel/D; M. Bentele, German Cancer Research Center, Heidelberg/D; A. Trauzold, S. Westphal, Universitätsklinikum Schleswig-Holstein, Kiel/D; A. Bulashevskaya, R. Eils, German Cancer Research Center, Heidelberg/D; H. Kalthoff, Universitätsklinikum Schleswig-Holstein, Kiel/D	Comparison of experimental semi-quantitative measurements of protein expression with simulation predictions in a complex computational apoptosis model
2.44	M. Swat, Humboldt Universität Berlin/D; W. Swat, Washington University, St.Louis/USA; A. Kel, BIOBASE GmbH, Wolfenbüttel/D; H. Herzel, Humboldt Universität Berlin/D	Bifurcation analysis of cell regulatory modules
2.45	K. Behrendt, INSILICO biotechnology, Stuttgart/D; M. Reuss, University of Stuttgart/D; K. Mauch, INSILICO biotechnology, Stuttgart/D	Mathematical definition and algorithm for detecting elementary signal transduction pathways
2.46	T. Crass, M. Haubrock, H. Michael, I. Liebich, E. Wingender, Georg August University, Göttingen/D	A general model for biomolecular interaction networks and their spatio-temporal constraints
2.47	T. Eißing, H. Conzelmann, E.D. Gilles, F. Allgöwer, E. Bullinger, P. Scheurich, University of Stuttgart/D	Mathematical modelling applied to caspase activation reveals a requirement for additional control
2.48	A. Kel, N. Voss, V. Matys, BIOBASE GmbH, Wolfenbuettel/D; E. Wingender, University of Goettingen/D	Modeling of signal transduction network of response of hepatocytes to toxins using TRANSPATH and TRANSFAC
2.49	F. Ortega, Universitat de Barcelona/E; L. Acerenza, Universidad de la República, Montevideo/ROU; H.V. Westerhoff, Vrije Universiteit, Amsterdam/NL; F. Mas, M. Cascante, Universitat de Barcelona/E	Limits in the sensitivity of metabolic cascades
2.50	C. Salazar, A. Politi, T. Höfer, Humboldt University, Berlin/D	Effect of cooperativity on the decoding of calcium oscillations
2.51	S. Wils, University of Antwerp, Wilrijk/B	Stochastic simulation of biological reaction-diffusion processes in 3 dimensions
2.52	M. Kschischo, University of Applied Sciences Koblenz, Remagen/D; L. Rychlewsky, BioInfoBank Institute, Poznan/PL; L. Dong, M. Schutkowski, U. Reimer, Jerini AG, Berlin/D	Computational prediction of kinase substrates from peptide microarray data
2.53	J. Hollunder, A. Beyer, T. Wilhelm, Institute of Molecular Biotechnology, Jena/D	Identification and characterization of protein subcomplexes in yeast
2.54	M. Schilling, U. Klingmüller, German Cancer Research Center, Heidelberg/D; T. Maiwald, K. Bartholomé, G. Fritz, M. Kollmann, J. Timmer, University of Freiburg/D	Identification of damped oscillation as a crucial property of the MAP-kinase pathway revealed by data-based modeling
2.55	X. Fang, J. Wilpert, H. Barth, B. Gissler, C. Kreutz, J. Timmer, J. Donauer, F. v. Weizsäcker, H.E. Blum, T.F. Baumert, University of Freiburg/D	Binding of hepatitis C virus envelope to human hepatoma cells induces a cascade of cell signals important for antiviral immune responses and lipid metabolism
2.56	B.E. Shapiro, M. Hucka, California Institute of Technology, Pasadena, CA/USA; A. Finney, University of Hertfordshire, Hatfield/UK	MathSBML: A mathematica package for systems biology
2.57	cancelled	

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Signal Transduction		
Nr.	Authors	Poster Title
2.58	R. Milo, S. Itzkovitz, N. Kashtan, R. Levitt, I. Ayzenshtat, M. Sheffer, U. Alon, Weizmann Institute of Science, Rehovot/IL	Super-families of evolved and designed networks
2.59	S. Reymann, J. Borlak, Fraunhofer Institute of Toxicology and Experimental Medicine, Hannover/D	Delineating an Aroclor 1254-induced regulatory gene network
2.60	A. Finney, University of Hertfordshire, Hatfield/UK; M. Hucka, California Institute of Technology, Pasadena, CA/USA	Proposals for extensions to SBML: Creating level 3
2.61	S. Maere, M. Kuiper, RUG/VIB, Gent/B	Modularity and crosstalk in the transcriptional behavior of <i>S. cerevisiae</i>
2.62	K. Seidl, German Research Center for Biotechnology, Braunschweig/D	Towards the generation of virtual experiments on cellular and systemic levels by the PheGe-platform
2.63	O. Babur, E. Demir, A. Ayaz, U. Dogrusoz, O. Sakarya, Bilkent University, Ankara/TR	Microarray data analysis and pathway activity inference in PATIKA
2.64	J.M. Kowalewski, Royal Institute of Technology, Stockholm/S; P. Uhlén, Yale University, New Haven, CT/USA; H. Kitano, Sony Computer Science Labs, Inc., Tokyo/J; H. Brismar, Royal Institute of Technology, Stockholm/S	Generation of slow calcium oscillations in spatial cell models driven by store operated calcium entry
2.65	M. Jirstrand, Fraunhofer-Chalmers Centre, Göteborg/S; J. Gunnarsson, H. Johansson, InNetics AB, Linköping/S	PathwayLab – A customizable modeling and simulation tool
2.66	S. Kikuchi, K. Fujimoto, N. Kitagawa, T. Fuchikawa, M. Abe, Keio University, Fujisawa/J; K. Oka, Keio University, Yokohama/J; K. Takei, Yokohama City University/J; M. Tomita, Keio University, Fujisawa/J	Kinetic simulation of signal transduction in hippocampal long-term potentiation with dynamic modeling of PP2A
2.67	R. Lund, I. Saarikko, R. Laheesmaa, University of Turku und Abo Akademi University/FIN; O. Nevalainen, T. Aittokallio, University of Turku/FIN	Gene regulatory networks leading to generation of a Th2 lymphocyte phenotype

Microbial Systems Biology		
Nr.	Authors	Poster Title
3.1	S.J. Lynden, O.C Idowu, P. Periorellis, M.P. Young, P. Andras, Newcastle UniversityUK	Integrating protein interaction data for network topology analysis
3.2	M. Caldara, K. Verbrugge, L. De Vuyst, M. Crabeel, G. Dupont, A. Goldbeter, R. Cunin, Université Libre de Bruxelles/B	Experimental manipulation for the mathematical modeling of arginine biosynthesis in <i>Escherichia coli</i> .
3.3	A. Kremling, MPI for Dynamics of Complex Technical Systems, Magdeburg/D; R. Heermann, K. Jung, Technical University Darmstadt/D; E.D. Gilles, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	Dynamics of two-component signal transduction of the KdpD/KdpE system in <i>Escherichia coli</i>
3.4	A. Kremling, U. Liebal, S. Fischer, K. Bettenbrock, E.D. Gilles, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	Dynamics of <i>Escherichia coli</i> lac operon mRNA and protein synthesis: Influence of different inducers and growth conditions
3.5	B. Teusink, Wageningen Centre for Food Sciences//NL and NIZO Food Research, Ede/NL and Centre for Molecular and Biomolecular Informatics, Nijmegen/NL; F.H.J. van Enckevort, NIZO Food Research, Ede/NL and Centre for Molecular and Biomolecular Informatics, Nijmegen/NL; A. Wegkamp, D. Molenaar, J.	Combining experimental data and in silico analysis to model the metabolic and regulatory network of <i>Lactobacillus plantarum</i>
3.6	W. Schmidt-Heck, R. Guthke, Hans-Knoell Institute for Natural Products Research, Jena/D; S. Töpfer, BioControl Jena GmbH, Jena/D; H. Reischer, K. Dürrschmid, K. Bayer, University of Agricultural Sciences, Vienna/A	Stress by recombinant protein synthesis in <i>Escherichia coli</i> : Model construction, model validation and model aided experimental design
3.7	D. Ropers, H. de Jong, M. Page, INRIA Rhone-Alpes, Saint Ismier/F; D. Schneider, J. Geiselmann, Université Joseph Fourier, Grenoble/F	Qualitative simulation of the nutritional stress response in <i>E. coli</i>
3.8	D. Mueller, L. Aguilera-Vázquez, E. Guerrero-Martín, M. Reuss, University of Stuttgart/D	Hiding behind the population average – cell cycle dynamics of energy metabolism during the lifelines of individual yeast cells

Poster Programme

Microbial Systems Biology		
Nr.	Authors	Poster Title
3.9	S.P. Hildebrandt, University of California, Santa Barbara, CA/USA; D. Raden, A.S. Robinson, University of Delaware, Newark, DE/USA; F.J. Doyle, University of California, Santa Barbara, CA/USA	Modeling the unfolded protein response in <i>S. Cerevisiae</i>
3.10	M. Schümperli, M. Heinemann, S. Panke, ETH Zürich/CH	EFM-supported design of systems of biotransformations
3.11	E. Dassau, D.R. Lewin, Technion, Haifa/IL	Integrated design and control and six-sigma for bioprocessing applications
3.12	K. Abd-El Rahman, M.G. Surette, University of Calgary, Alberta/CDN	Reverse engineering ecology of microbial systems
3.13	S. Ogishima, Y. Suzuki, T. Hase, S. Nakagawa, H. Tanaka, Tokyo Medical and Dental University/J	Modular evolution of protein-protein interaction network
3.14	H. El-Samad, C. Homescu, M. Khammash, L. Petzold, University of California, Santa Barbara, CA/USA	The heat shock response: Optimization solved by evolution?
3.15	T. Baba, Keio University, Tsuruoka/J; N. Yamamoto, Nara Institute of Science & Technology, Ikoma/J; M. Tomita, Keio University, Tsuruoka/J; H. Mori, Keio University & Nara Institute of Science & Technology, Ikoma/J	Essential gene and minimization of <i>E. coli</i> genome
3.16	H. Mori, N. Yamamoto, Nara Institute of Science and Technology, Ikoma/J; T. Baba, Keio University, Tsuruoka/J; K.A. Datsenko, L. Zhou, B.L. Wanner, Purdue University, West Lafayette, IN/USA	Systematic approaches for the modeling of <i>E. coli</i>
3.17	R. Manzonì, R.L. Rossi, M. Vanoni, L. Alberghina, Università di Milano-Bicocca/I; E. Klipp, MPI for Molecular Genetics, Berlin/D	Modelling signal transduction pathways and the G1 to S transition in budding yeast
3.18	K. Engelen, K. Marchal, J. De Brabanter, B. De Moor, K.U.Leuven/B	Comparison of different methodologies to identify differentially expressed genes in two-sample cDNA microarrays
3.19	K. Marchal, K.U.Leuven/B; B. Naudts, K. Van Leemput, University of Antwerp/B; K. Engelen, K.U.Leuven/B; A. Verschoren, University of Antwerp/B; B. De Moor, K.U.Leuven/B	Is it realistic to infer a gene network from a small set of microarray experiments?
3.20	A. Dubey, M.J. Reaff, J.H. Lee, A.S. Bommarius, Georgia Institute of Technology, Atlanta, GA/USA	Support vector machines for predicting the critical positions of a protein
3.21	V.F. Wendisch, Research Center Juelich/D	Towards <i>Corynebacterium glutamicum</i> systems biology: Definition of regulons and stimulons in an amino acid producing bacterium
3.22	F.J. Bruggeman, F.C. Boogerd, H.V. Westerhoff, Vrije Universiteit, Amsterdam/NL	Hierarchical regulation of ammonium assimilation by <i>Escherichia coli</i> , investigations with a silicon cell

Poster Programme

Microbial Systems Biology		
Nr.	Authors	Poster Title
3.23	A. <u>Beyer</u> , J. Hollunder, T. Wilhelm, IMB-Jena/D	Distinguishing transcriptional and post-transcriptional expression regulation on a genomic scale
3.24	A. <u>Beyer</u> , T. Wilhelm, IMB-Jena/D	Dynamic simulation of protein complex formation on a genomic scale
3.25	H.-W. Ma, J. Buer, A.-P. Zeng, German Research Center for Biotechnology, Braunschweig/D	The hierarchical modular structure of E. coli transcriptional regulatory network and its functional relation to metabolic network
3.26	H. Kobayashi, M. Kaern, M. Araki, K. Chung, C.R. Cantor, J.J. Collins, Boston University, MA/USA	Programmable Cells: Interfacing Natural and Engineered Gene Networks
3.27	B. <u>Hu</u> , K. Takahashi, M. Tomita, Keio University, Tsuruoka/J	Multi-algorithm simulation of E.coli heat shock response using E-CELL version 3
3.28	Y.T. <u>Maeda</u> , M. Sano, University of Tokyo/J	Quantitative experimental analysis of a genetic network: Response delay in an auto-positive feedback system
3.29	F. <u>Miyoshi</u> , Y. Nakayama, K. Kaizu, M. Tomita, Keio University, Fujisawa/J	Systems analysis of the cyanobacteria circadian rhythm using E-cell dynamic simulator
3.30	K. Nilsson, Swedish University of Agricultural Sciences, Uppsala/S; A. Ringheim, J. Elf, S. Dasgupta, K. Nordström, M. Ehrenberg, Uppsala University/S	A model of the initiation of replication in Escherichia coli
3.31	M. <u>Lovmar</u> , A. Antoun, M. Ehrenberg, Uppsala University/S	Initiation of translation in Eubacteria revisited
3.32	R. <u>Saito</u> , Keio University, Tsuruoka/J; S. Nakamura, H. Kimura, Keio University, Fujisawa Kanagawa/J; T. Ara, A. Itoh, Keio University, Tsuruoka/J; M. Arifuzzaman, M. Maeda, T. Oshima, Nara Institute of Science and Technology, Ikoma Nara/J; C. Wada, Kyoto University/J; H. Mori, Nara Institute of Science and Technology, Ikoma Nara/J; M. Tomita, Keio University, Fujisawa Kanagawa/J	Construction and mining of reliable protein-protein interaction network in Escherichia coli
3.33	T. <u>Backfisch</u> , E.D. Gilles, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	Mathematical modeling of the regulation of the stress sigma factor sigma(s) in E. coli
3.34	J. Elf, M. Ehrenberg, Uppsala University/S	Bacterial growth during amino acid limitation
3.35	I. <u>Nobuyoshi</u> , T. Yoshihiro, O. Masahito, N. Yoichi, M. Tomita, Keio University, Tsuruoka/J	Dynamic simulation of Escherichia coli with hybrid dynamic/static simulation algorithm based on a static model generated by GEM system
3.36	K. Takahashi, T. Sakurada, K. Kaizu, S. Arjunan, Keio University, Fujisawa/J; M. Sugimoto, Keio University, Tsuruoka/J; T. Ishida, T. Kitayama, K. Maruoka, D. Ito, M. Tomita, Keio University, Fujisawa/J	E-Cell3: A multi-algorithm, parallel software platform for systems biology
3.37	M.V. Jose, T. Govezensky, J.R. Bobadilla, Universidad Nacional Autónoma de México/MEX	A renormalization group analysis of DNA coding sequences of bacterial chromosomes
3.38	F. Poelwijk, S. <u>Tans</u> , Institute for Atomic and Molecular Physics, Amsterdam/NL	Modularity as key to repressor evolvability
3.39	E. <u>Taberman</u> , M. Ehrenberg, Uppsala University/S	Modelling the control of the tryptophan biosynthesis in Bacillus subtilis
3.40	M. <u>Djordjevic</u> , Columbia University, New York, NYC/USA; A.M. Sengupta, B.I. Shraiman, Rutgers University, Piscataway, NJ/USA	Quantitative Modeling and Analysis of Data for SELEX experiments
3.41	K. Lemuth, R.D. Schmid, S. <u>Lange</u> , University of Stuttgart/D	A systems biology approach to analyse the stringent response in E. coli by expression profiling
3.42	A.M. Martins, D. Camacho, J. Shuman, P. Mendes, V. Shulaev, Virginia Bioinformatics Institute, Blacksburg, VA/USA	Characterizing distinct yeast physiological states through the metabolome and transcriptome
3.43	E. Werner, Cellnomica, Inc., Fort Myers, FL/USA	Minimal genomes for minimal multicellular systems
3.44	D.P. Wall, Computational Biology Initiative, Boston, MA/USA	Simultaneous detection of orthologous sequences among many bacterial genomes
3.45	cancelled	
3.46	J. Alex, M. Schütze, Institut für Automation und Kommunikation e.V. Magdeburg, Barleben/D	Application of SBML to wastewater systems
3.47	M. <u>Amdaoud</u> , I. Mihalcescu, Université Joseph Fourier-Grenoble, Saint Martin d'Hères/F	Estimation of the coupling strength among a population of cyanobacterial circadian oscillators

Poster Programme

Methods and Software for Systems Biology		
Nr.	Authors	Poster Title
4.1	D. Runge, D. Koczan, D. Haase, H. Christoph, P. Lorenz, P. Kohlschein, P. Schuff-Werner, M.O. Glocker, H.J. Thiesen, University of Rostock/D	Primary human hepatocytes – A fascinating tool in systems biology
4.2	K. Zeilinger, G. Pless, I.M. Sauer, E. Efimova, P. Neuhaus, J.C. Gerlach, Charité, Berlin/D	Multicompartment bioreactor for three-dimensional high-density culture of primary human hepatocytes
4.3	P.K. Murugan, University of Stuttgart/D; K. Mauch, INSILICO biotechnology, Stuttgart/D; M. Reuss, University of Stuttgart/D	Mathematical modeling and simulation of CYP gene expression in hepatocytes
4.4	J. Bucher, University of Stuttgart/D; K. Mauch, INSILICO biotechnology, Stuttgart/D; M. Reuss, University of Stuttgart/D	In silico reconstruction and topological analysis of the detoxification network in hepatocytes
4.5	A. Politi, Humboldt University, Berlin/D; L.D. Gaspers, A.P. Thomas, New Jersey Medical School, Newark, NJ/USA; T. Höfer, Humboldt University, Berlin/D	The role of the inositol-1,4,5-trisphosphate dynamics in shaping calcium signals
4.6	Please find this poster at the German Federal Funding Initiative "Systems of Life - Systems Biology"	
4.7	U.M. Zanger, K. Klein, T. Richter, J. Bliedernicht, M. Schwab, M. Eichelbaum, Dr. Margarete Fischer-Bosch Institute of Clinical Pharmacology, Stuttgart/D	Use of a large liver tissue bank to dissect factors that determine functional properties of the drug biotransformation system in man
4.8	Please find this poster at the German Federal Funding Initiative "Systems of Life - Systems Biology"	
4.9	Please find this poster at the German Federal Funding Initiative "Systems of Life - Systems Biology"	

Spatial Models		
Nr.	Authors	Poster Title
5.1	D. Lebedez, U. Brandt-Pollmann, University of Heidelberg/D	Control of spatio-temporal dynamics in complex biological systems
5.2	A.V. Koptioug, Mid Sweden University, Östersund/S; E. Mamontov, Chalmers University of Technology, Gothenburg/S; Z. Taib, AstraZeneca R&D, Mölndal/S; M. Willander, Gothenburg University/S	The phase-transition morphogenic model for oncogeny as a genotoxic homeostatic dysfunction: Interdependence of modeling, advanced measurements, and numerical simulation
5.3	H. Tiedemann, E. Schneltzer, M. Hrabé de Angelis, GSF, Neuherberg/D	E-cells: Describing collective cell behaviour with java objects

Poster Programme

Spatial Models		
Nr.	Authors	Poster Title
5.4	<u>S.T. Coakley</u> , R. Smallwood, University of Sheffield/UK	Parallelisation of cell agent-based modelling
5.5	<u>D.C. Walker</u> , R.H. Smallwood, M. Holcombe, University of Sheffield/UK; G. Hill, J. Southgate, University of York/UK	Agent based computational model of wound healing in epithelial cell cultures
5.6	A.A. Alonso, C.V. Fernández, <u>J.R. Banga</u> , IIM-CSIC, Vigo/E	On the robust control of biological waves
5.7	<u>S.R. Veflingstad</u> , E. Plahte, Agricultural University of Norway, Ås/N; N.A.M. Monk, University of Sheffield/UK	Effect of time delay on pattern formation: Competition between homogenisation and patterning
5.8	Y. Suzuki, S. Ogishima, T. Hase, S. Nakagawa, <u>H. Tanaka</u> , Tokyo Medical and Dental University/J	Hierarchical modularity in the protein protein interaction network in yeast
5.9	Y. Cao, H. Li, <u>L. Petzold</u> , University of California, Santa Barbara, CA/USA	Efficient formulation of the stochastic simulation algorithm for chemically reacting systems
5.10	<u>T. Plusnina</u> , A. Lavrova, G Riznichenko, Moscow State University, Moscow/RUS	The contribution of voltage-dependent membrane transport to the pattern formation of pH and electric potential along the cell membrane of algae Chara corallina
5.11	<u>G. Jentsch</u> , R. Kree, Universität Göttingen/D	A Monte Carlo simulation of intracellular signalling by chemical wave fronts - The role of membrane inhomogeneities
5.12	<u>M. Oresic</u> , H. Maaheimo, I. Mattila, E. Rintala, L. Salusjärvi, H. Simolin, L. Ruohonen, M. Penttilä, VTT Biotechnology, Espoo/FIN	Towards mitochondrial metabolomics
5.13	<u>M. Ulrich</u> , M. Bentele, I. Lavrik, P.H. Krammer, R. Eils, German Cancer Research Center, Heidelberg/D	Reaction-diffusion model of the apoptotic signalling pathway
5.14	<u>C. Kappel</u> , German Cancer Research Center, Heidelberg/D; T. Misteli, National Cancer Institute, Bethesda, MD/USA; R. Eils, German Cancer Research Center, Heidelberg/D	From models to experiments and back: Protein dynamics in the mammalian cell nucleus
5.15	H. Jönsson, Lund University/S; B.E. Shapiro, V. Gor, M. Heisler, G.V. Reddy, E.M. Meyerowitz, California Institute of Technology, Pasadena, CA/USA; E. Mjolsness, University of California, Irvine, CA/USA	A multicellular model of a feedback network regulating spatial gene expression domains in the shoot apical meristem
5.16	<u>J. Elf</u> , M. Ehrenberg, Uppsala University/S	Stochastic reaction diffusion kinetics of bi-stable systems
5.17	<u>J.C. Schaff</u> , B.M. Slepchenko, I.I. Moraru, L.M. Loew, University of Connecticut Health Center, Farmington, CT/USA	New modeling capabilities of the virtual cell environment
5.18	<u>R.A. El-Badrawi</u> , J.C. Schaff, I.I. Moraru, L.M. Loew, University of Connecticut Health Center, Farmington, CT/USA	Virtual cell interoperability
5.19	<u>M. Isalan</u> , C. Lemerle, L. Serrano, EMBL, Heidelberg/D	Engineering and modelling of artificial spatial gene networks
5.20	M. Ander, P. Beltrao, B. Diventura, M. Foglierini, C. Lemerle, I. Oliveira, A. Kaplan, <u>L. Serrano</u> , EMBL, Heidelberg/D	SMARTCELL spatially-resolved stochastic simulation framework for biologists
5.21	J.W. Jenkins, <u>S. Sundaram</u> , CFD Research Corporation, Huntsville, AL/USA	Spatial and transport-resolved mechanism/pathway inference from fluidic biosensors
5.22	<u>N. Brady</u> , University of California, San Diego, CA/USA; M. Bentele, R. Eils, German Cancer Research Center, Heidelberg/D; H.V. Westerhoff, Vrije Universiteit Amsterdam/NL	An ageing wave? Reactive Oxygen Species (ROS)-Induced ROS release in cardiomyocytes

Poster Programme

Systems Biology for Medicine		
Nr.	Authors	Poster Title
6.1	<u>S. Wiemann</u> , A. Poustka, German Cancer Research Center, Heidelberg/D; The German cDNA Network/D	From high-throughput molecular and cellular functional gene analysis towards systems biology
6.2	<u>J.A. García</u> , La Salle University, Mexico City/MEX; T. Govezensky, M.V. José, UNAM, Mexico City/MEX	HIV-1 antiretroviral therapy prognosis based upon time dependent parameters
6.3	<u>S. Nagl</u> , M. Patel, A. Folarin, University College London/UK	A systems biology framework for signal transduction and target discovery in cancer
6.4	<u>A. Lara</u> , T. Govezensky, M.V. José, Universidad Nacional Autonoma de Mexico, Mexico City/MEX	A power law governs the dynamics of rotavirus epidemics
6.5	<u>W. Schmidt-Heck</u> , U. Möller, R. Guthke, Hans-Knöll-Institut für Naturstoff-Forschung (HKI), Jena/D; S. Töpfer, D. Driesch, D. Pfaff, BioControl Jena GmbH, Jena/D; E. Möller, SIRS-Lab GmbH, Jena/D; K Reinhart, Friedrich-Schiller-University, Jena/D; H.P. Deigner, S. Russwurm, SIRS-Lab GmbH, Jena/D	Mining in gene expression data to reconstruct networks of molecular interaction during sepsis
6.6	<u>M. Oresic</u> , T. Seppänen-Laakso, VTT Biotechnology, Espoo/FIN; S. Aparicio, Paradigm Therapeutics, Cambridge/UK; G. Medina, A. Vidal-Puig, University of Cambridge/UK	Characterization of animal models in studies of metabolic diseases
6.7	<u>K. Hallén</u> , J. Tegnér, Linköping University/S	Identifying compound mode of action
6.8	<u>T.-W. Huang</u> , H.-S. Chiu, C.-Y. Kao, NTU, Taipei/RC; C.-Y. Huang, National Health Research Institutes, Taipei/RC	Revealing the HCC transcriptional network from gene expression data and promoter sequence
6.9	<u>N. Sarai</u> , A. Noma, Kyoto University/J	simBio: A Java package for biological simulation
6.10	<u>G. Lei</u> , J. He, J. Tegner, Linköping University/S	Local structure repair for hill climbing search for the best bayesian networks
6.11	D. Runge, University of Rostock/D; M. Ruhnke, University SH, Kiel/D; D. Koczan, D. Haase, University of Rostock/D; R. Guthke, HKI, Jena/D; F. Faendrich, University SH, Kiel/D; <u>H.-J. Thiesen</u> , University of Rostock/D	Programming of monocytes into neo-hepatocytes: Comparison of transcriptome expression profiles with transcriptomes of standardized human hepatocytes
6.12	<u>K. Xiang</u> , E. Plahte, <u>S.W. Omholt</u> , Agricultural University of Norway, Ås/N	Systemic silencing of genetic polymorphism in regulatory networks
6.13	<u>F.E. Hauser</u> , Project SEGMENTA, Bad Lippspringe/D	Clinical pattern formations in complex disease systems
6.14	<u>R. König</u> , F. Westermann, A. Bulashevka, B. Brors, R. Eils, German Cancer Research Center, Heidelberg/D	Reconciling signal transduction networks with gene expression data by a Potts spin model based approach
6.15	<u>A. Gjuvslund</u> , B. Hayes, T. Meuwissen, E. Plahte, S.W. Omholt, Agricultural University of Norway, Ås/N	QTL mapping in epistatic structures
6.16	<u>E. Plahte</u> , Agricultural University of Norway, Ås/N; S. Kjøglum, Norwegian School of Veterinary Science, Oslo/N	Modelling approaches to gene regulatory networks
6.17	<u>S. Hido</u> , N. Sarai, H. Kawano, K. Koyamada, A. Noma, Kyoto University/J	Extrapolation method of the drug effects on cardiac action potential by the combination of models and experiments
6.18	<u>Y. Sidorenko</u> , U. Reichl, MPI for Dynamics of Complex Technical Systems, Magdeburg/D	A model for the influenza virus life-cycle in a single cell
6.19	<u>J. Stelling</u> , MPI for Dynamics of Complex Technical Systems, Magdeburg/D; F.J. Doyle III, University of California, Santa Barbara, CA/USA	Approaching the design of intervention strategies by systematic analysis of network sensitivities
6.20	<u>J. van Beek</u> , Centre for Medical Systems Biology, Amsterdam/NL; A.B.J. Groeneveld, D.J.C. Alders, VU University Medical Centre, Amsterdam/NL	Quantifying metabolic fluxes in vivo in mammalian myocardial tissue samples from pre-steady-state Carbon-13 NMR multiplets
6.21	<u>I.V. Deineko</u> , GBF, Braunschweig/D; O.V. Kel-Margoulis, A. Kel, BIOBASE GmbH, Wolfenbüttel/D	Mathematical model of the mitogen-dependent G1/S transition in mammalian cell cycle
6.22	cancelled	
6.23	<u>M. Cascante</u> , A. Ramos, P. Vizán, P. de Atauri, J.J. Centelles, Universitat de Barcelona/E; L.G. Boros, S. Mazurek, University of California Los Angeles, CA/USA; W.M. Frederiks, University of Amsterdam/NL; P. Lee, University of California Los Angeles, CA/USA; J. Boren, Universitat de Barcelona/E	Looking for new targets in cancer therapy from a systems biology approach

Poster Programme

Systems Biology for Medicine		
Nr.	Authors	Poster Title
6.24	M. Or-Guil, Humboldt-University Berlin/D; J. Carneiro, Gulbenkian Institute of Science, Oeiras/P; R. Volkmer-Engert, Charité, Berlin/D; C. Berek, German Rheumatism Research Center, Berlin/D	Towards understanding the evolution of antibodies during an immune response, and representing their binding properties
6.25	N. Matsumaru, F. Centler, Friedrich-Schiller-University Jena/D; K.-P. Zauner, University of Southampton/UK; P. Dittrich, Friedrich-Schiller-University Jena/D	Towards applied systems biology: Application centered models from autonomous experimentation
6.26	cancelled	
6.27	D. Busse, Humboldt University, Berlin/D; A. Scheffold, German Arthritis Research Center, Berlin/D; T. Höfer, Humboldt University, Berlin/D	Mathematical modelling of intercellular communication of T-lymphocytes mediated by Interleukin 2
6.28	M. Katajamaa, University of Turku/FIN; M. Oresic, VTT Biotechnology, Espoo/FIN	Integrated solutions for LC/MS data processing, with applications in biomarker discovery
6.29	D. Zhou, S. Luo, E. Vermaas, R. Walker, Lynx Therapeutics Inc., Hayward, CA/USA; I.R. Kirsch, National Cancer Institute, Bethesda, MD/USA; G.E. Crawford, F.S. Collins, National Human Genome Research Institute, NIH, Bethesda, MD/USA; J. Mao, T.J. Vasicek, Lynx Therapeutics Inc., Hayward, CA/USA	Comprehensive analysis of genome structure, epigenomics, and gene expression with high volume, short sequence reads
6.30	W. Huisinga, Free University Berlin and DFG Research Center, Berlin/D	Systems biology integrated into physiologically based pharmacokinetics
6.31	D. Stahl, W. Sibrowski, University of Muenster/D	Investigation of immunoglobulin-mediated immunoregulation in humans at the level of complex biological systems
6.32	B.J. Bornstein, NASA Jet Propulsion Laboratory, Pasadena, CA/USA; B. Kovitz, California Institute of Technology, Pasadena, CA/USA; S. Keating, University of Hertfordshire, Hatfield/UK; M. Hucka, California Institute of Technology, Pasadena, CA/USA; A. Finney, University of Hertfordshire, Hatfield/UK	libSBML: A software library for the Systems Biology Markup Language (SBML)
6.33	A. Svantesson, P.O. Westermark, J. Hellgren Kotaleski, A. Lansner, Royal Institute of Technology (KTH), Stockholm/S; B. Gharizadeh, Stanford University, Palo Alto, CA/USA; P. Nyrén, Royal Institute of Technology (KTH), Stockholm/S	Pyrosequencing TM reaction system explored through mathematical modelling
6.34	cancelled	
6.35	S.M. Keating, University of Hertfordshire, Hatfield/UK; B.J. Bornstein, NASA Jet Propulsion Laboratory, Pasadena, CA/USA; M. Hucka, California Institute of Technology, Pasadena, CA/USA; A. Finney, University of Hertfordshire, Hatfield/UK	SBMLToolbox: A MATLAB toolbox for SBML users
6.36	C.K. Wierling, E. Maschke-Dutz, E. Klipp, R. Herwig, H. Lehrach, MPI for Molecular Genetics, Berlin/D	PyBioS - An object-oriented tool for modelling and simulation of cellular processes
6.37	cancelled	
6.38	A. Kinoshita, Keio University, Fujisawa/J; Y. Nakayama, Keio University, Tsuruoka/J; M. Suematsu, Keio University, Shinjuku/J; M. Tomita, Keio University, Tsuruoka/J	In silico analysis of human erythrocyte using hybrid dynamic/static simulation method for large scale pathway simulation
6.39	E. Pokojška, Masaryk University, Brno/CZ & Institut J. Monod, CNRS-Université Paris/F; R. Ouifki, IRD, Bondy/F; K. Pakdaman, Université Paris/F	Transcriptional repressor autoregulation: Bifurcation, transient behavior, and periodic solutions in a negative regulatory loop with delay
6.40	E. Pokojška, Masaryk University, Brno/CZ & Institut J. Monod, CNRS/Université Paris/F	Computational model for steroid regulation of hypothalamo-pituitary axis dynamics
6.41	V. Hopp, University Rostock/D	Biological systems and biological principles – how can these be formulated?
6.42	V. Hopp, University of Rostock/D	Systems of nature

'German Federal Funding Initiative "Systems of Life - Systems Biology"'

Authors	Poster Title
BMBF Competence Network	BMBF Competence Network 'Systems of Life - Systems Biology'
J. Heinrich, R. Gebhardt, A. Bader, M. Brulport, M. Hermes, S. Diekmann, A. Steffen, R. Santos, C. Elstner, J.G. Hengstler, University of Leipzig/D	Hepatocyte in vitro systems for studies in systems biology
M. Reuss, University of Stuttgart/D; M. Dauner, INSILICO biotechnology GmbH, Stuttgart/D; M. Eichelbaum, Robert Bosch society for medical research mbH, Stuttgart/D; J. Gasteiger, Friedrich-Alexander University Erlangen-Nuremberg, Erlangen/D; K. Mauch, INSILICO biotechnology GmbH, Stuttgart/D; R.D. Schmid, University of Stuttgart/D; U. Zanger, Institute for Clinical Pharmacology, Stuttgart/D	A systems biology approach to detoxification and dedifferentiation in hepatocytes: Cooperative project within the BMBF-Research and Funding Program: Systems of Life - Systemsbiology
The "Systems Biology of Regenerative Hepatocyte" Consortium, Universitätsklinikum Freiburg/D; Universität Freiburg/D; DKFZ Heidelberg/D; Universität Würzburg/D; Universität Tübingen/D	Systems biology of regenerative hepatocytes
E.D. Gilles, MPI Magdeburg; H.-G. Holzhütter, Humboldt University Berlin; Ursula Kummer, EML Research gGmbH, Heidelberg/D; (and others)	Modelling Platform Systems Biology of Hepatocytes: A challenge for mathematical modelling