Scientific Program
of
SysBio2005

Saturday March 12

Course Registration & Hotel Check-In	**11:00 am - 6:00 pm**
Welcome Reception	**6:00 pm - 6:45 pm**
Official Course Opening	**6:45 pm - 6:55 pm**
Hans Westerhoff and Karl Kuchler	

AstraZeneca Opening Lecture

Douglas Kell **7:00 pm – 8:00 pm**

Metabolomics, machine learning and modelling in systems biology: towards an understanding of the language of cells

Welcome Dinner &	**Musical performance**	**8:30 pm - open end**
Subhendu Ghosh	*Patterns of Passion*	

Sunday March 13

Breakfast *7:00 - 8:30 am*

Principles of Systems Biology **Lectures** **8:30 am - 12:30 pm**

Chair: Hans Westerhoff

Co-chair: Lilia Alberghina

P-L1 **Reinhart Heinrich** 8:30 - 9:15

Dynamics and design of cellular reaction networks

P-L2 **John Doyle** 9:15 - 10:00

Organizational complexity

Coffee & Refreshment Break *10:00 - 10:20*

P-L3 **Albert Goldbeter** 10:20 -11:55

Computational approaches to cellular rhythms

P-L4 **Stefan Schuster** 11:05 - 11:50

Fundamentals and applications of metabolic pathway analysis

Break *11:50 – 12:00*

Guided General Discussion: **Identifying issues; SB Principles** **12:00 - 12:30 pm**

Lunch & Afternoon Break *12:30 - 4:30 pm*

Coffee and Tea Break *4:00 – 4:30 pm*

Chalk/Blackboard teaching **4 in parallel** **4:30 – 5:10 pm**

PT-B1	Uri Alon	Motifs and networks
PT-B2	Reinhart Heinrich/Stefan Schuster	Stability and flux mode analysis
PT-B3	Jacky Snoep/Hans Westerhoff	Control analysis and Silicon cells
PT-B4	Jörg Stelling/Frank Bruggeman	Robustness, network identification and engineering

Principles of Systems Biology **Workshop & Short Talks** **5:15 – 7:00 pm**

Chair: Lilia Alberghina

Co-chair: Hans Westerhoff

P-W1 **Dennis Vitkup** 5:15 - 5:35

Expression dynamics of a cellular metabolic network

P-S1 **Frank Bruggeman** 5:35 - 5:50

Smart regulation of ammonium assimilation by *Escherichia coli*: modularity, robustness, and flux regulation

Coffee & Refreshment Break *5:50 - 6:10*

P-W2 **Sinisa Zampera** 6:10 -6:30

An adaptive system approach for the modelling of genetic regulatory networks

Glucose metabolism study in the yeast

P-S2 **Markus Kollmann** 6:30 - 6:45

Design principles of signal transduction pathways to attenuate noise

P-S3	**Esa Pitkänen** On pathways and distances in metabolic networks	6:45- 7:00
	Resumed General Discussion: **Addressing the issues; SB principles**	7:00 - 7:30
Dinner		*7:30 - 9:00 pm*
	Poster Session 1	**9:00 - 11:00 pm**
	Viewing posters	9:00 - 9:45
	Free poster wandering	9:45 – 10:30
	Round table poster discussion (presenters and teachers only)	10:30 – 11:00

Poster Presentations

P-S01 Smart regulation of ammonium assimilation by *Escherichia coli*: modularity, robustness, and flux regulation. ***Frank J. Bruggeman,*** *Fred C. Boogerd and Hans V. Westerhoff*

P-S02 Design Principles of Signal Transduction Pathways to attenuate Noise ***Markus Kollmann,*** *Kilian Bartholome and Jens Timmer*

P-S03 On pathways and distances in metabolic networks ***Esa Pitkänen****, Ari Rantanen, Juho Rousu and Esko Ukkonen*

P-P01 The use of accurate mass and time tags to measure yeast's glycolytic proteome ***Ronald Aardema,*** *Henk L. Dekker, Jaap Willem Back, Leo J. de Koning, Luitzen de Jong and Chris G. de Koster*

P-P04 Pathways to analysis of microarray data ***R. Keira Curtis*** *and Antonio Vidal-Puig*

P-P07 A dynamic model of cAMP signal transduction in yeast *Dirk Müller****, Helena Diaz-Cuervo,*** *Luciano Aguilera-Vazquez, Klaus Mauch and Matthias Reuss*

P-P10 Modelling of Drosophila segmentation gene expression with and without usage of attractors ***Vitaly V. Gursky,*** *Johannes Jaeger, Konstantin N. Kozlov, John Reinitz and Alexander M. Samsonov*

P-P13 Inferring gene regulatory relationships from time series microarray data based on the trend of expression changes. ***Feng He*** *and An-Ping Zeng*

P-P16 A reductive approach to analyze stochasticity in intracellular networks. ***Tetsuya J. Kobayashi*** *and Kazuyuki Aihara*

P-P19 Modelling and simulation of dynamic signals in cells. ***Thomas Millat*** *and Olaf Wolkenhauer*

P-P22 An *in silico* model for the optimization of threonine production in *Escherichia coli*. ***Juan-Carlos Rodriguez****, Jerome Maury, Christophe Chassagnole, Josep Centelles, Nic Lindley and Marta Cascante*

P-P25 Inferring regulatory networks from experimental data ***Christian Spieth****, Felix Streichert, Nora Speer and Andreas Zell*

T-P01 Genome-scale analysis of *Streptomyces coelicolor* A3(2) metabolism ***Irina Borodina*****,** *Preben Krabben and Jens Nielsen*

T-P04 Reduced order modeling of global regulation - redox regulation in *Escherichia coli* ***Michael Ederer****, Thomas Sauter and Ernst Dieter Gilles*

T-P07 CellDesigner2.0: A process diagram editor for gene-regulatory and biochemical networks. ***Akira Funahashi****, Naoki Tanimura, Yukiko Matsuoka, Naritoshi Yoshinaga and Hiroaki Kitano*

T-P10 Speeding up the central metabolism in *Pichia pastoris* ***Franz Hartner****, Lars Blank, Alexander Kern, Uwe Sauer and Anton Glieder*

T-P13 NMR spectroscopy in systems biology: methods for metabolomics and fluxomics ***Paula Jouhten****, Minna Perälä, Eija Rintala Laura Ruohonen, Perttu Permi, Merja Penttilä and Hannu Maaheimo*

T-P16 An integrative framework for modeling signaling pathways ***Robert Modre-Osprian****, Marc Breit, Visvanathan Mahesh, Gernot Enzenberg and Bernhard Tilg*

T-P19 Application of yeast genomic strategies to link biologically active compounds to their cellular targets ***Ainslie B. Parsons****, David Williams, Satoru Ishihara, Yoshi Ohya, Raymond Andersen, Timothy Hughes and Charles Boone*

T-P22 Glycolytic oscillations in spatially ordered interacting cells ***Jana Schütze*** *& Reinhart Heinrich*

T-P25 Global transcriptional response of *Saccharomyces cerevisiae* to ammonium, alanine, or glutamine limitation ***Renata Usaite****, Birgitte Regenberg and Jens Nielsen*

U-P01 Neisserial DNA uptake sequences: biased distribution and influence on transformation. ***Ole Herman Ambur****, Stephan Frye, Tonje Davidsen, Hanne Tuven and Tone Tønjum*
U-P04 Experimental manipulation and mathematical modeling of arginine biosynthesis in *Escherichia coli*. ***Marina Caldara****, K. Verbrugghe, L. De Vuyst, M. Crabeel, G. Dupont, A. Goldbeter and R. Cunin*
U-P07 Retrograde response to mitochondrial dysfunction is separable from Tor1/2 regulation of retrograde gene expression. ***Sergio Giannattasio****, Zhengchang Liu and Ronald Butow*
U-P10 Extending life by alternative respiration? ***Alexander Kern****, Franz Hartner and Anton Glieder*
U-P13 A dynamic model of cAMP signal transduction in yeast. ***Dirk Mueller,*** *Helena Díaz Cuervo, Luciano Aguilera-Vázquez, Klaus Mauch and Matthias Reuss*
U-P16 Stress induced by weak organic acids in *Saccharomyces cerevisiae*. ***Rick Orij,*** *Jarne Postmus, Gerco van Eikenhorst, Stanley Brul and Gertien Smits*
U-P19 Evolutionary conservation and divergence of fungal promoter sequences ***Riccarda Rischatsch****, Sylvia Voegeli and Peter Philippsen*
U-P22 Unusual group II introns in bacteria of the *Bacillus cereus* group. ***Nicolas Tourasse****, Fredrik Stabell, Lillian Reiter and Anne-Brit Kolstø*
U-P25 LacplantCyc: *in silico* reconstruction of the metabolic pathways of *Lactobacillus plantarum*. ***Frank H.J. van Enckevort****, Bas Teusink, Christof Francke and Roland J. Siezen*

M-P01 Control of the ATP/ADP ratio in pancreatic beta cells ***Charles Affourtit*** *and Martin D. Brand*
M-P04 Sensitivity analysis with respect to initial values of the TNFalpha mediated NF-kappaB signalling pathway. ***Marc Breit,*** *Gernot Enzenberg, Visvanthan Mahesh, Robert Modre-Osprian and Bernhard Tilg*
M-P07 Na,K-ATPase regulation via phospholemman phosphorylation ***Claudia Donnet****, Jia Li Guo, Amy Tucker and Kathleen Sweadner*
M-P10 Generating conceptual models in Zebrafish zinc homeostasis: The first steps towards and holistic view of zinc metabolism. ***Graham Feeney****, Dongling Zheng, Peter Kille and Hogstrand Christer*
M-P13 Impaired gene expression in Sjogren's disease. ***Adi Gilboa-Geffen*** *and Hermona Soreq*
M-P16 Towards a systems biology of signal transduction by insulin and insulin-like growth factors. ***Shaukat Mahmood****, Jane Palsgaard, Soetkin Versteyhe, Maja Jensen and Pierre De Meyts*
M-P19 Molecular dissection of the key LGS residues involved in the control of glycogen biosynthesis. ***Susana Ros*** *and Joan J. Guinovart*
M-P22 Quantitative modeling of EGFR-internalization as a mechanism of signaling specificity ***Hannah Schmidt-Glenewinkel****, Constantin Kappel and Ivayla Vacheva*
M-P25 Modeling emergent networks by dynamic reconstruction *in silico.* ***Hao Zhu*** *and Pawan Dhar*

Power Poster Presentations

P-PoP1 New parameter estimation method with possible application in systems biology ***Ioan Grosu***
P-PoP4 Determination of *in vivo* non-steady-state fluxes and kinetic information using stable isotope labeling and metabolite pool size data: theory and application. ***Junli Liu****, Alisdair R. Fernie and David F. Marshall*
T-PoP1 1/f Noise in Ion Channel: A Theory Based on Self-Organised Criticality Jyotirmoy Banerjee, Mahendra K. Verma and **Subhendu Ghosh**
T-PoP4 Using SRS to develop and populate an information layer for the EMI-CD modeling platform ***Dan Staines****, Daniel Flint and Thure Etzold*
U-PoP1 Modeling and analyses of *Mycobacterium tuberculosis* metabolism ***Asawin Meechai****, Supapon Cheevadhanalak and Sakarindr Bhumiratana*
M-PoP1 ***Niels Aarsaether***
M-PoP4 Module dynamics of the GnRH signal transduction network ***Karen Page*** *and David Krakauer*

Monday March 14

Breakfast *7:00 - 8:30 am*

Tools and methods (part 1) — Lectures — 8:30 am - 12:30 pm

Chair: Karl Kuchler

Co-chair: Igor Goryanin

T-L1	**Rudi Aebersold** Quantitative Proteomics: An essential component of systems biology	8:30 - 9:15
T-L2	**Roland Eils** Modelling and simulation of large-scale signal transduction networks	9:15 - 10:00
Coffee & Refreshment Break		*10:00 - 10:20*
T-L3	**Shoshana Wodak** Analysing networks of biochemical processes: Bioinformatics meets systems biology	10:20 - 11:05
T-L4	**Charlie Boone** Global mapping of synthetic genetic interactions in yeast	11:05 - 11:50
Break		*11:50 – 12:00*

Guided General Discussion: **Identifying issues; Tools, Methods** **12:00 - 12:30**

Lunch & Afternoon Break *12:30 - 4:30 pm*

Coffee and Tea Break *4:00 – 4:30 pm*

Chalk/Blackboard teaching **4 in parallel (repeat)** **4:30 – 5:10 pm**

PT-B1	Uri Alon	Motifs and networks
PT-B2	Reinhart Heinrich/Stefan Schuster	Stability and flux mode analysis
PT-B3	Jacky Snoep/Hans Westerhoff	Control analysis and Silicon cells
PT-B4	Jörg Stelling/Frank Bruggeman	Robustness, network identification and engineering

Tools and methods — Workshop & Short talks — 5:15 - 7:00 pm

Chair: Igor Goryanin

Co-chair: Karl Kuchler

T-W1	**An-Ping Zeng** An integrated interaction network of *Escherichia coli* for studying genotype-phenotype relationship	5:15 - 5:35
T-S1	**Sune Danø** Oscillatory mechanisms derived from phase and amplitude information	5:35 - 5:50
Coffee & Refreshment Break		*5:50 - 6:15*
T-S2	**Adrienne James** Application of modelling and simulation to drug discovery: The ErbB system	6:15 - 6:30
T-S3	**Konstantin Kozlov** Combined optimization technique for biological data fitting	6:30 - 6:45

T-S4	**Balázs Papp** Systematic identification and characterisation of synthetic lethal interactions in the metabolic network of yeast	6:45- 7:00
	Resumed General Discussion: Addressing the issues Tools & Methods	7:00 - 7:30
Dinner		*7:30 - 9:00 pm*
	Poster Session 2	**9:00 - 11:00 pm**
	Viewing posters	9:00 - 9:45
	Free poster wandering	9:45 – 10:30
	Round table poster discussion (presenters and teachers only)	10:30 – 11:00

Poster Presentations

T-S01 Oscillatory mechanisms derived from phase and amplitude information
***Sune Danø**, Mads Madsen and Preben G. Sørensen*

T-S02 Application of modelling and simulation to drug discovery: The ErbB System
*Bart Hendriks, Gareth Griffiths, Jack Beusmans, **Adrienne James**, Julie Cook, Jonathan Swinton and David De Graaf*

T-S03 Combined optimization technique for biological data fitting
***Konstantin N. Kozlov**, Alexander M. Samsonov and John Reinitz*

T-S04 Systematic identification and characterisation of synthetic lethal interactions in the metabolic network of yeast. ***Balázs Papp**, Richard Harrison, Daniela Delneri, Csaba Pál and Stephen Oliver*

P-P02 Metabolic footprinting: its role in systems biology
***Marie Brown**, Rick Dunn, Julia Handl and Douglas Kell*

P-P05 Multiscale modelling of a cell
***Gianni De Fabritiis** and Peter Coveney*

P-P08 Metabolic quorum sensing: experiments with *S. cerevisiae*
***Francesco d'Ovidio**, Silvia De Monte, Sune Danø and Preben Graae Sørensen*

P-P11 Discovering compound mode of action with CutTree
***Kristofer Hallén**, Johan Björkegren and Jesper Tegnér*

P-P14 Secondary metabolites can create coexistence in the chemostat
***Julia Heßeler**, Julia K. Schmidt, Udo Reichl and Dietrich Flockerzi*

P-P17 Linlog Modeling Approach: Theoretical Platform for System Biology
***M.T.A. Penia Kresnowati**, Wouter van Winden and Sef Heijnen*

P-P20 Systems analysis of yeast glucose sensing system
***Hisao Moriya** and Hiroaki Kitano*

P-P23 Kinetic models of phosphorylation cycles: the role of protein-protein interactions
***Carlos Salazar** and Thomas Höfer*

P-P26 First steps towards a multi-dimensional iron regulatory network
***Yevhen Vainshtein**, Martina Muckenthaler, Alvis Brazma and Matthias W. Hentze*

T-P02 Relational learning of biological networks
***Cyril Combe**, Florence d'Alché-Buc, Vincent Schachter and Stan Matwin*

T-P05 Technical variance, quality control and scaling: necessary steps towards meta-analyses on large expression databases. ***Martin Eisenacher**, Harald Funke, Thomas Vogl, Christoph Cichon, Kristina Riehemann, Clemens Sorg and Wolfgang Koepcke*

T-P08 Simulation of epidermal homeostasis including barrier formation
***Niels Grabe** and Karsten Neuber*

T-P11 Software components for analysis of DNA microarray and quantitative proteomics data
***Sergii Ivakhno** and Olexander Kornelyuk*

T-P14 Autonomous oscillations in *Saccharomyces cerevisiae* during batch cultures on trehalose.
***Matthieu Jules**, Jean-Marie Francois and Jean-Luc Parrou*

T-P17 Data visualization for gene selection and modeling in cancer bioinformatics
***Minca Mramor**, Gregor Leban and Blaž Zupan*

T-P20 SCIpath - an integrated environment for systems biology analysis and visualisation.
Manish Patel

T-P23 Database Support for Yeast Metabolomics Data Management
Irena Spasic, Warwick Dunn and Douglas Kell

T-P26 Identification of the C-terminal signal peptides for GPI modification and prediction of the cleavage sites. **Yu Zhang**, Thomas Skoet Jensen, Ulrik de Lichtenberg and Soeren Brunak

U-P02 Gene expression and adaptive responses of *in situ* fermentation
Herwig Bachmann*, Michiel Kleerebezem and Johan E. van Hylckama Vlieg*

U-P05 Comparative metabolomics of Saccharomyces yeasts. ***Robert P. Davey1****, G Lacey1, DA MacKenzie, M Defernez, FA Mellon, K Huber, V Moulton and IN Robert*

U-P08 Unravelling new metabolic metworks in LAB via the thioredoxin system
L. Mariela Hebben-Serrano*, Eddy Smid and Willem M. de Vos*

U-P11 Systematic computational modelling reveals a key operating principle of TOR signalling in yeast
Lars Kuepfer*, Matthias Peter, Jörg Stelling and Uwe Sauer*

U-P14 Natural sweetening of food products: engineering *Lactococcus lactis* for glucose production
Wietske A. Pool, ***Ana R. Neves****, Jan Kok, Helena Santos and Oscar P. Kuipers*

U-P17 Adaptation of yeast glycolysis to temperature changes.
Jarne Postmus*, Jildau Bouwman, Rick Orij, Stanley Brul and Gertien Smits*

U-P20 A Systems Biology approach for the optimization of recombinant protein production in *E. coli*
Eugénio Ferreira and ***Isabel Rocha***

U-P23 The effect of oxygen tension on yeast glycolysis
Isil Tuzun*, Klaas Hellingwerf and M. J. Teixeira de Mattos*

U-P26 High-throughput screening of *Saccharomyces cerevisae* knockout library: method development and stoichiometric profiling. ***Vidya R. Velagapudi****, Christoph Wittmann, Thomas Lengauer, Priti Talwar and Elmar Heinzle*

M-P02 Regulation of the INF-Gamma/JAK/Stat1 signal transduction pathway
Stephan Beirer*, Thomas Meyer, Uwe Vinkemeyer and Thomas Höfer*

M-P05 A domain-oriented approach to the reduction of combinatorial complexity in signal transduction networks ***Holger Conzelmann****, Julio Saez-Rodriguez, Thomas Sauter, Boris Kholodenko and Ernst-Dieter Gilles*

M-P08 System Properties of the Core Reactions of Apoptosis
Thomas Eißing*, Carla Cimatoribus, Frank Allgöwer, Peter Scheurich and Eric Bullinger*

M-P11 Repression of SOX6 transcriptional activity by SUMO modification
Fernandez-Lloris Raquel*, Osses Nelson, Jaffray Ellis, Shen LinNan, Vaughan Owen Anthony, Girdwood David, Bartrons Ramon, Rosa Jose Luis and Ventura Francesc*

M-P14 Modeling the synchronization of circadian oscillators in the suprachiasmatic nucleus
Didier Gonze*, Samuel Bernard, Christian Waltermann, Achim Kramer and Hanspeter Herzel*

M-P17 BOOLEAN analysis of the signaling network triggered by neurotrophic factors and extracellular matrix in sensory neurons. ***Mikhail Paveliev****, Maria Lume and Mart Saarma*

M-P20 Analysis of the signaling network involved in the activation of T-Lymphocytes
Julio Saez-Rodriguez*, Xiaoqian Wang, Birgit Schoeberl, Steffen Klamt, Jonathan Lindquist, Stefanie Kliche, Buckhart Schraven and Ernst Dieter Gilles*

M-P23 Retroelement insertion polymorphism in cell line identification.
Svetlana V. Ustyugova*, Anna L. Amosova, Yuri B. Lebedev and Eugene D. Sverdlov*

Power Poster Presentations

P-PoP2 Effects of noise in metabolic flux analysis. ***Visakan Kadirkamanathan****, Steve Billings, Sarawan Wongsa, Jing Yang and Philip Wright*

P-PoP5 An adaptive system approach for the modelling of genetic regulatory networks. Glucose metabolism study in the yeast. *Sinisa Zampera and* ***Todor Vujasinovic***

T-PoP2 Single cell mechanics and mechano signal transduction using a micro-force loading device.
Hao Zhang, Zhiqing Feng, Ning Fang, Vincent Chan and ***Kin Liao***

T-PoP5 Regulatory Network Reconstruction by Integrative Analysis of Cross-Platform Microarray Data.
Jasmine Zhou*, Ming-Chih Kao, Haiyan Huang, Angela Wong, Juan Nunez-Iglesias, Michael Primig, Oscar Aparicio, Caleb Finch, Todd Morgan and Wing Wong*

U-PoP2 Some changes in the composition of nuclear components during cereal seeds germination.
Liya A. Minasbekyan *and Poghos H. Vardevanyan*

M-PoP2 SYMBIONIC: A European initiative on the Systems Biology of the neuronal cell ***Ivan Arisi***

M-PoP5 Experimental design for model discrimination in cellular signal transduction
Clemens Kreutz, Jörg Stelling, Thomas Maiwald and ***Jens Timmer***

Tuesday March 15

Breakfast ***7:00 - 8:30 am***

Tools & Methods (part 2) Lectures 8:30 am - 10:00 pm

Chair: Karl Kuchler

T-L5 **Jacky Snoep** 8:30 - 9:15

The Silicon Cell approach to building detailed kinetic models of biological systems

T-L6 **Ursula Kummer** 9:15 - 10:00

Mathematical modelling: Choosing the right simulation method

Coffee & Refreshment Break *10:10 - 10:20*

Unicellular Organisms (part 1) Lectures 10:20 am - 12:35 pm

Chair: Stefan Hohmann

U-L1 **Edda Klipp** 10:20 - 11:05

Mathematical modeling of stress response in yeast

U-L2 **Matthias Reuss** 11:05 - 11:50

Hiding behind the population average - cell cycle dynamics of energy metabolism during the lifelines of individual yeast cells

U-L3 **Jörg Stelling** 11:50 - 12:35

Knowledge and data requirements for systems analysis of cellular networks

Lunch & Afternoon Break *12:35 – 13:15*

VISIT to SALZBURG ***13:30 – 23:00 pm***

Buses will leave Hotel at 13:30 pm

Dinner in Salzburg

Return from Salzburg to the venue 22:00 pm

Wednesday March 16

Breakfast		*7:00 - 8:30 am*

Unicellular Organisms (part 2) — Lectures — 8:30 am - 12:30 pm

Chair: Stefan Hohmann

Co-chair:Matthias Reuss

U-L4	**Uwe Sauer** *In vivo* operation of metabolic pathways	8:30 - 9:15
U-L5	**Uri Alon** Simplicity in biology	9:15 - 10:00
Coffee & Refreshment Break		*10:00 - 10:20*
U-L6	**Barry Wanner** Stochastic activation of the response regulator PhoB by noncognate histidine kinases	10:20 - 11:05
U-L7	**Masaru Tomita** Metabolome analysis and systems biology	11:05 - 11:50
Break		*11:50 – 12:00*
	Guided General Discussion: Identifying issues; unicellular organisms	12:00 - 12:30
Lunch & Afternoon Break		*12:30 - 4:30 pm*
Coffee and Tea Break		*4:00 – 4:30 pm*

Unicellular Organisms — Workshop & Short Talks — 4:30 - 6:50 pm

Chair: Matthias Reuss

Co-chair: Stefan Hohmann

U-W1	**Guillaume Beslon** Modelling evolution of prokaryotic genomes: an integrative approach	4:30 - 4:50
U-W2	**Victor Sourjik** Signal processing in bacterial chemotaxis	4:50 - 5:10
U-W3	**Bas Teusink** Combining experimental data and *in silico* analysis to model the metabolic and regulatory network of *Lactobacillus plantarum*	5:10 - 5:30
Coffee & Refreshment Break		*5:30 - 5:50*
U-S1	**Attila Csikasz-Nagy** Modelling fission yeast morphogenesis	5:50 - 6:05
U-S2	**Silvia De Monte** Metabolic quorum sensing: onset of density-dependent oscillations	6:05 - 6:20
U-S3	**Ana Sofia Figueiredo** Integration of software tools for the *in silico* design of metabolic pathways using flux balance analysis	6:20- 6:35

U-S4	**Douglas Murray** Uncovering the control of the respiratory clock in yeast	6:35- 6:50
	Resumed General Discussion: Addressing the issues; unicellular organisms	6:50- 7:30
Dinner		*7:30 - 9:00 pm*
	Poster Session 3	**9:00 - 11:00 pm**
	Viewing posters	9:00 - 9:45
	Free poster wandering	9:45 – 10:30
	Round table poster discussion (presenters and teachers only)	10:30 – 11:00

Poster Presentations

U-S01 Modelling fission yeast morphogenesis.***Attila Csikasz-Nagy***, *Bela Gyorffy, Wolfgang Alt, John J. Tyson and Bela Novak*
U-S02 Metabolic quorum sensing: onset of density-dependent oscillations ***Silvia De Monte***, *Francesco d'Ovidio, Sune Danø and Preben Grae Sørensen*
U-S03 Integration of software tools for the *in silico* design of metabolic pathways using flux balance analysis. ***Ana Sofia Figueiredo***, *Pedro Fernandes, Pedro Pissarra and António Ferreira*
U-S04 Uncovering the control of the respiratory clock in yeast ***Douglas B. Murray*** *and Hiroaki Kitano*
M-S01 Inferring feedback mechanisms in cellular transformation due to oncogenic RAS ***Nils Bluethgen***, *Christine Sers, Jana Keil, Szymon M. Kielbasa, Reinhold Schaefer and Hanspeter Herzel*
M-S02 Regulation of MAPK signalling determining cell fate in PC-12 cells - a step beyond biochemistry ***Silvia D. Santos***, *Eli Zamir, Peter Verveer and Philippe Bastiaens*
M-S03 Mathematical modeling of neuronal response to neuropeptides: Angiotensin II signaling via G-protein coupled receptor. ***Thomas Sauter***, *Rajanikanth Vadigepalli and James Schwabe*

P-P03 Genetic network model for the AP-1 system. ***David Camacho*** *and Roland Eils*
P-P06 A genetical genomics approach to gene network inference. ***Alberto de la Fuente***, *Bing Liu and Ina Hoeschele*
P-P09 Phylogenetic analysis based on structural information of metabolic networks ***Oliver Ebenhöh***, *Thomas Handorf and Reinhart Heinrich*
P-P12 Scopes: A new concept for the structural analysis of metabolic networks ***Thomas Handorf***, *Oliver Ebenhöh and Reinhart Heinrich*
P-P15 Two Numerical Model Analyses for the Movement of a Restriction Enzyme. ***Noriko Hiroi***, *Akira Funahashi and Hiroaki Kitano*
P-P18 Knowledge discovery by integrated analysis of metabolic and regulatory networks ***Hong-Wu Ma*** *and An-Ping Zeng*
P-P21 Investigating the structure of integrated biological networks ***Venkata Gopalacharyulu Peddinti***, *Erno Lindfors and Matej Oresic*
P-P24 Modelling transient dynamics of osmo-stress response in Yeast.***Jörg Schaber,*** *Bodil Nordlander and Edda Klipp*
P-P27 Nutrient starvation in baker's yeast, and the implication of protein degradation for Vertical Genomics. ***Karen van Eunen***, *Jildau Bouwman, Sergio Rossell, Rob J.M. Spanning, Barbara M. Bakker and Hans V. Westerhoff*

T-P03 A new Information System to manage and analyse information on biochemical interactions ***Holger Dach***, *Juliane Fluck, Kai Kumpf and Rainer Manthey*
T-P06 Genomic rearrangements : influence of the genetic context on chromosomal dynamics ***Emilie Fritsch***, *Jean-luc Souciet, Serge Potier and Jacky de Montigny*
T-P09 Modelling protein motions for systems biology.***Benjamin A Hall*** *and Mark Sansom*
T-P12 Systemic models for metabolic dynamics and regulation of gene expression – easy access, retrieval and search for publicly available gene expression data.***Per Harald Jonson*** *and M. Minna Laine*
T-P15 Automated construction of genetic networks from mutant data ***Peter Juvan***, *Gad Shaulsky and Blaz Zupan*
T-P18 Accelerating the construction of genome-scale metabolic models: a test case for *Lactococcus lactis.* ***Richard A. Notebaart***, *Frank H.J. van Enckevort, Bas Teusink and Roland J. Siezen*
T-P24 Fokker-Planck equations for IP_3 mediated Calcium dynamics.***Rüdiger Thul*** *and Martin Falcke*

T-P27 The *Genevestigator* gene function discovery engine.***Philip Zimmermann**, Matthias Hirsch-Hoffmann, Lars Hennig and Wilhelm Gruissem*

U-P03 Metabolic functions of duplicate genes in *Saccharomyces cerevisiae*
***Lars M. Blank**, Lars Küpfer and Uwe Sauer*

U-P06 Metabolic network analysis in six microbial species. ***Tobias Fuhrer**, Eliane Fischer and Uwe Sauer*

U-P09 The regulatory circuitry of arabinases in *Bacillus subtilis* .***José M. Inácio** and Isabel de Sá-Nogueira*

U-P12 Dynamic on-line investigation of lactic acid bacteria.
***Ann Zahle Larsen**, Lars Folke Olsen and Frants Roager Lauritsen*

U-P15 Adaptative response of the central metabolism in *Escherichia coli* to quantitative modulations of a single enzyme: glucose-6-phosphate dehydrogenase.***Cécile Nicolas**, Fabien Létisse and Jean-Charles Portais*

U-P18 Progressive adaptation of *Lactococcus lactis* to stress.
***Emma Redon**, Pascal Loubière and Muriel Cocaign-Bousquet*

U-P21 Some properties and partial purification of *Candida Guilliermondii* NP-4 and Paramcium Multimcronucleatum glutaminase. ***Ara H. Tamrazyan**, Misak A. Davtyan and Susanna A. Karapetyan*

U-P24 Vertical genomics in baker's yeast: adaptation of respiring cells to anaerobic sugar-excess conditions. **Joost van den Brink**, Pascale Daran-Lapujade, Han de Winde and Jack Pronk

U-P27 A Sysytems Biology Strategy For Understanding The Genome-wide Control Of Growth Rate And Metabolic Flux In Yeast. *Jian Wu, Nianshu Zhang, Andy Hayes, Douglas Kell, Stephen Oliver and **Jian Wu***

M-P03 Comprehensive analysis of the cancer Tyrosine Kinome & Phosphatome
***Martin Bezler**, Christian Mann, Detlev T. Bartmus, Pjotr Knyazev, Tatjana Knyazeva, Sylvia Streit and Axel Ullrich*

M-P06 Model building in a systems biology company: the cell cycle and apoptosis
***Cathy Derow**, Chris Snell, Christophe Chassagnole, John Savin and David Fell*

M-P09 Meshfree modelling of biological transport processes in complex domains
***Martin Eigel** and Markus Kirkilionis*

M-P12 Network synchronization from population to cell level
***Laurent Gaubert** and Magali Roux-Rouquié*

M-P15 Modelling, Enzyme kinetics & Fluorescence Imaging of the NF-kappaB Signalling Pathway ***Adaoha EC. Ihekwaba**, Rachel Grimley, Neil Benson, David Broomhead and Douglas B. Kell*

M-P18 A topological analysis of the human transcription factor interacting network
***Carlos Rodríguez-Caso**, Miguel Ángel Medina and Ricard V Solé*

M-P21 Flavo-di-iron proteins: role in microbial detoxification by NO
***Francesca Maria Scandurra**, Paolo Sarti, PierLuigi Fiori, Elena Forte, Alessandro Giuffrè, P. Rappelli, G. Sanciu, Daniela Mastronicola, Miguel Teixeira and Maurizio Brunori*

M-P24 RNAi screening for novel components of mammalian Hedgehog and Wnt pathways
***Markku Varjosalo**, Antti Oinas and Jussi Taipale*

Power Poster Presentations

P-PoP3 A new dynamic complexity reduction method for biochemical reaction networks
***Dirk Lebiedz**, Jürgen Zobeley, Julia Kammerer and Ursula Kummer*

T-PoP3 Connectivity matrix for describing all the atom-level connectivities in a given metabolic network and its use for analysis of the network structure.***Jun Ohta***

T-PoP6 Oxygen consumption and glycolytic redox state in skeletal muscle
***Bjørn Quistorff**, Sune Danø, Mads Madsen, Brian Lindegaard Petersen and Peter Fæster Nielsen*

U-PoP3 Differentiation in a genetic network with duplicate repressors: simulating evolutionary pathways based on Lac mutational data. *Frank Poelwijk, Daniel Kiviet and **Sander Tans***

M-PoP3 *In vitro* systems for modelling of signal transduction in hepatocytes
***Patricio Godoy**, Katja Breitkopf, Loredana Ciuclan, Eliza Wiercinska and Steven Dooley*

M-PoP6 Integration of genomics and proteomics with metabolic/signaling pathways for generating/improving novel anti-cancer drug targets. ***He Yang***

Thursday March 17

Breakfast *7:00 - 8:30 am*

Multicellular Organisms **Lectures** **8:30 am - 12:30 pm**

Chair: Hiraoki Kitano

Co-chair: Marta Cascante

M-L1 **Michel Eichelbaum** 8:30 - 9:15

Pharmacogenomics: a holistic approach to drug organism interaction

M-L2 **Boris Kholodenko** 9:15 - 10:00

Systems biology of receptor tyrosine kinase signaling

Coffee & Refreshment Break *10:00 - 10:20*

M-L3 **Nicolas Le Novere** 10:20 - 11:05

Computational systems biology of neuronal signalling

M-L4 **Ursula Klingmüller** 11:05 - 11:50

Signal transduction and cancer – generation of high quality quantitative data

Break *11:50 – 12:00*

Guided General Discussion: Identifying issues; multicellular organisms 12:00 - 12:30

Lunch & Afternoon Break *12:30 - 4:30 pm*

Coffee and Tea Break *4:00 – 4:30 pm*

Multicellular Organisms **Workshop & Short Talks** **4:30 -5:55 pm**

Chair: Marta Cascante

Co-chair: Hiraoki Kitano

M-W1 **Mariko Hatakeyama** 4:30 - 4:50

Computer simulation analysis of ErbB signaling for understanding of cellular transformation mechanism

M-W2 **Thomas Höfer** 4:50 - 5:10

Integration of signal transduction and cytokine expression in T lymphocytes

M-S1 **Nils Bluethgen** 5:10 - 5:25

Inferring feedback mechanisms in cellular transformation due to oncogenic RAS

M-S2 **Silvia Santos** 5:25 - 5:40

Regulation of MAPK signalling determining cell fate in PC-12 cells - a step beyond biochemistry

M-S3 **Thomas Sauter** 5:40- 5:55

Mathematical modeling of neuronal response to neuropeptides: Angiotensin II signaling via G-protein coupled receptor

Coffee & Refreshment Break *5:55 - 6:15*

Resumed General Discussion:Addressing the issues; multicellular organisms 6:15 - 6:45

NovoNordisk Closing Lecture

Denis Noble **7:00 pm – 8:00 pm**

Highlights of SysBio2005: From genes to whole organs

Vertical integration using mathematical simulation

Banquet and Farewell Party **8:00 pm - open end**

Presentation of "Gosau YOUNG SysBio INVESTIGATOR AWARDS" 8:30 - 8:45

Marta Cascante, Lilia Alberghina, Roel van Driel, Stefan Hohmann

Official Course Closure 8:45 - 9:00

Hans Westerhoff and Karl Kuchler

Friday March 18

Breakfast	*7:00 - 8:30 am*
Hotel Check-Out & Departure	**7:00 - 11:00 am**
End of SysBio 2005	11:00 am
Shuttle Buses to Salzburg (detailed schedule to be announced)	