

**2nd FEBS Advanced Lecture Course on
Systems Biology:
From Molecules to Life
Gosau, Austria, EU, March 10-16, 2007**



Scientific Program

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Saturday March 10: Opening (co-organized with AstraZeneca)

**Saturday March 10: 18h00-24h00
Main lecture hall (also the music and the dinner)**

Course Registration & Hotel Check-in 11:00 am - 6:00 pm
Welcome Reception 5:30 pm - 6:15 pm
Official Course Opening 6:15 pm - 6:25 pm
 Hans Westerhoff and Karl Kuchler

Opening session **Chair: Hans V. Westerhoff** 6:25 pm - 10:30 pm

AstraZeneca Opening Lecture

OL-01 Leroy Hood 6:30 pm - 7:30 pm
 Systems Biology and Systems Medicine

Welcome Dinner 7:30 pm - 8:30 pm

Musical intermezzo

Frits Kamp and Jelena Petronovic 8:15 pm - 8:45 pm
 Hommage to Reinhart Heinrich

Reinhart Heinrich Memorial Lecture

OL-02 Hans Meinhardt 8:45pm-9:45pm
 Making Systems Biology work -Models of biological pattern formation: from elementary steps to the organization of embryonic axes

Opening discussion and drinks 9:45 - 10:30 pm

Bar 10:30- 00 am

Sunday March 11: Symposium on Principles

Sunday March 11: 8h30-23h00
 8h30 - 12h30: Main lecture hall in 1
 10h20-11h05: Main lecture hall in 1, plus Yellow room, plus Gosau room
 16h30-18h05: Main lecture hall split in 3, plus Yellow room, plus Gosau room
 18h20 - 19h25: Main lecture hall in 1
 21h00- 23h00: Poster hall

Breakfast 7:00 - 8:30 am

Principles of Systems Biology Lectures 8:30 am - 12:30 pm
Chair: Edda Klipp

Chairs introduction 8:30 am - 8:35 am

P-L01 Jan-Hendrik S. Hofmeyr [Main lecture hall] (plenary) 8:35 am - 9:20 am
 The Regulatory Design of Cellular Processes:
 Principles of Supply and Demand (didactic lecture)

P-L02 Adriano Henney [Main lecture hall] (plenary) 9:20 am - 9:40 am
 How does systems biology work in and for industry? (methodology)

P-L03 Johan Paulsson [Main lecture hall] (plenary) 9:40 am - 10:00 am
 Towards a coherent stochastic theory for cellular kinetics (methodology)

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

Tutorials corresponding to lectures (3 in parallel) 10:20 am - 11:05 am

Jan-Hendrik S. Hofmeyr [Main lecture hall]
Adriano Henney [Yellow room]
Johan Paulsson [Gosau room]

Coffee & Refreshment Break 11:05 am-11:20 am

Program 3

Differential Equation Models: Parameter Estimation and Optimum Experimental Design (Black Board Teaching)

CP-02 Jacky L. Snoep [Yellow room] 5:20 pm - 6:05 pm
 Tools for Systems Biologists: using JWS Online for integration and storage of data and models (Computer Practicals)

CP-03 Igor Goryanin and Anatoly Sorokin [Gosau room] 5:20 pm - 6:05 pm
 Edinburgh Pathway Editor (Computer Practicals)

Coffee & Refreshment Break 6:05 pm - 6:20 pm

Sunday: Principles of Systems Biology Short Talks and discussion (plenary) 6:20 pm - 7:05 pm

P-S01 Naomi Siew [Main lecture hall] (plenary) 6:20 pm - 6:35 pm
 Shedding Light on the ORFan Puzzle (short talk)

P-S02 Tetsuya Yomo [Main lecture hall] (plenary) 6:35 pm - 6:50 pm
 Adaptive response of a gene network to environmental changes by fitness-induced attractor selection (short talk)

P-S03 Frank J Bruggeman [Main lecture hall] (plenary) 6:50pm-7:05 pm
 Analysis of noise in a detailed kinetic model of an operon (ghALG) activated by two-component signal transduction (NRI/NRII) (short talk)

Speaker's Panel addressing issues raised in the morning 7:05 pm - 7:25 pm

Dinner 7:30 - 9:00 pm

Poster Session 1 [Poster hall] 9:00 - 11:00 pm

Viewing posters 9:00 - 9:45 pm
 Free poster wandering 9:45 - 10:30 pm
 Round table poster discussion (presenters and teachers only) 10:30 - 11:00 pm

Today's (Sunday's) Poster Presentations:

Principles of Systems Biology (Sunday posters)
 P-P01 A kinetic model for peptide-induced leakage from cells
August Andersson, Jens Danielsson, Lena Måler & Astrid Gråslund
 P-P04 Autoregulation of cortisol action and differentiation in human bone cells
Marcus Eijken, Kerstin Drabek, Katja Rybakova, Alexey Kolodkin, Frank Bruggeman, Hans V. Westerhoff, Hub Pois & Hans van Leeuwen
 P-P07 Pattern formation in plant development
Bettina Griesse, Jens Timmer, Martin Hüskamp & Christian Fleck

M-P07 Human osteoblasts as a model to study Peroxisome Proliferator-Activated Receptor Gamma (PPARG) signaling during differentiation and proliferation using integrative systems-biology approaches

Claudia Brudedgam, Marco Eijken, Alexey Kolodkin, Katja Rybakova, Marijke Koedam, Frank Bruggeman, Hans Westerhoff, Hub Pois & Hans van Leeuwen
M-P10 Setting the framework for large scale system biology: The integration of human protein interactome

Mathias E. Futschik, Gautam Chaurasia, Erich Wanker & Hanspeter Herzel
M-P13 Gene expression profiling in Vitamin D₃ treated MCF3T3-E1 mouse osteoblasts
Carsten Kribbenitzsch, Lars Verbruggen, Guy Eiken, Roger Boulton & Miele Verschuyl
M-P16 Dynamic modeling of dual negative feedback regulation of TGFbeta-SMAD signaling in primary hepatocytes

Peter J. Nickel, Thomas Malwald, Stefan Legewie, Patricia Godoy, Sebastian Bohl, Thomas Frahm, Steven Dooley, Hanspeter Herzel, Jens Timmer & Ursula Klingmüller
M-P19 Analysis of murine models with tissue-specific nuclear receptor deficiency using systems biology approaches

Pedro Rocha, Heiner Schrewe & Chris Bunce
M-P22 Erythroid progenitor cell development elucidated by a dynamic pathway model of MAP-kinase signaling

Marcel Schilling, Thomas Malwald, Jens Timmer & Ursula Klingmüller
M-P25 A mathematical model of Smad nucleocytoplasmic shuttling

Alexander Tournier, Bernhard Schmiere, Paul A. Bates & Caroline S. Hill

Towards Life: Principles and studies of simpler systems (Sunday posters)

L-P01 Regulation at the RNA level

Ilika Maria Axmann, Dennis Diens & Annett Wild

L-P04 Integration of signal transduction and firing behavior in neurons by means of multiscale modeling

Dirk Fey, Rajanikant Vadigepalli, Thomas Sauter & James Schwab

L-P07 Tobin - a toolbox for biochemical networks

Miguel Godinho & Victor Martins dos Santos

L-P10 Robustness of metabolic pathways leading to drug target identification. A systems biology approach

Sabrina S Khalil

L-P13 Bacterial control of growth, and adaptation to nutritional shifts in amino acid-limiting environments

Edward M. Matesescu & Terence Hua

L-P16 Control of noisy networks (P-P17)

Robert Platt, Frank Bruggeman, Herbert Sauro & Hans V. Westerhoff

L-P19 Systematic study of the Arabidopsis circadian clock and its entrained pathway (flowering)

Treuntun Sathong & Andrew J. Millar

L-P22 Spatiotemporal modeling of metabolic dynamics in human immune cells

Oliver Slaby, Mario S. Mommer, Ursula Kummer & Dirk Lebiedz

L-P25 Photoreception in *Bacillus subtilis*: light activates the general stress response.

Jeroen Bastiaans van der Steen, M. Avila-Perez & K.J. Hellingwerf

Tools and Methods for Systems Biology (Sunday posters)

T-P01 Symbolic control analysis for cellular systems

Timothy J. Akhurst, Jan-Hendrik S. Hofmeyr & Johann M. Rohwer

T-P04 Predicting functional modules in Arabidopsis thaliana root hairs that drive tip growth

Gordon Breen & Claire Groszer

T-P07 Database mining for systems biology with Taverna workflows and Weka

Luna De Ferrari

T-P10 Mitochondrial dysfunction in type 2 diabetes: a Systems Biology approach

Willemin Groenendaal

T-P13 Multiobjective mixed-integer optimization of metabolic systems

José Oscar Hernández-Sendín, Oliver Eiler & Julio Rodríguez Barga

T-P16 Bayesian methods for inferring protein function from diverse data

Jukka Kohonen, Elja Arjas, Petri Auvinen, Jukka Corander & Sanjit Talikoti

P-P10 Inferring the start-regulating gene network in *Arabidopsis thaliana*

Papapoti Inghasriwan, Sijin Megarac, Supaporn Cheevachanasak, Supatharee Netphan, Asawin Meechai, Sakon Prachittasaraes, Jeerayut Chajravanach, Morakot Tantibaroen & Sakarnir Bhumiratana

P-P13 A systems-biological approach to nuclear receptor signalling by PPARs: from model to experiment

Alexey Kolodkin, Katja Rybakova, Claudia Brudedgam, Marco Eijken, Frank Bruggeman, Hans van Leeuwen, Barbara Bakker & Hans V. Westerhoff

P-P16 Transcriptional regulation evolves around conserved and metabolically related genes

Kiran Raaschhe Palli, Prashant M Bapat, Ana Paula Oliveira & Jens Nielsen

P-P19 Underground metabolic routes in *E. coli*

Naomi Siew, Yizhak Pipel & Dan S. Tavrik

P-P22 Modeling Ca²⁺ calmodulin-dependent selective target activation

Najil Valayev, Nikolai Kotov, Ian Postlethwaite & Declan Bates

P-P25 no abstract

Jon Petre

P-P26 Central carbohydrate metabolism of the archaeon *Sulfolobus solfataricus*

Bettina Siebers & Christa Schlieper

P-P27 Adaptive response of a gene network to environmental changes by fitness-induced attractor selection

Tetsuya Yomo, Akiko Kashiwagi, Kunihiko Kaneko & Itaru Urabe

P-P28 Mathematical modeling of metabolic networks: From topology to dynamics of metabolic pathways

Ralf Steuer

Yeast Systems Biology (Sunday posters)

Y-P01 Robustness analysis of HOG pathway related genes in *Saccharomyces cerevisiae*

Dorjanel Ahmadpour, Lars-Göran Ottosson, Markus Krantz, Jonas Warringer, Anders Blomberg & Stefan Hohmann

Y-P04 Microarray investigation of pre-mRNA processing

David Barrass & Jean Beggs

Y-P07 Regulation of the glycolytic pathway during osmotic stress

Jilliau Bourman, Stanley Agbo, Alexander Lindenbergh, Karen van Eunen, Hans V. Westerhoff & Barbara M. Bakker

Y-P10 The effect of external oxygen conditions on the metabolic flux distribution of *Saccharomyces cerevisiae*

Paula Jouthen, Eija Rintala, Anne Huuskonen, Anu Tamminen, Mervi Toivari, Marjani Wiebe, Ari Rantanen, Laura Ruohonen, Merja Penttilä & Hannu Maeheno

Y-P13 Temperature stress in yeast

Femke Mensonides

Y-P16 A network identification of the mitotic exit in budding yeast *Saccharomyces cerevisiae*

van Orlandi & Lilla Alberghina

Y-P19 Modeling of translational efficiency in fission yeast based on genome sequence and microarray data

Falk Schubert, Daniel H. Lachner, Samuel Marguerat & Jürg Bahler

Y-P22 Robustness of *Saccharomyces cerevisiae* to deletion mutations and response to environmental stimuli as seen through the lens of high-throughput metabolic profiling

Ilya Vengler, Ilana Rogachev, Yizhak Pipel & Asaph Aharoni

Y-P25 Dynamic analysis of the LPR suggests a pathway controlling down-regulation in *Saccharomyces cerevisiae*

Theresa Yurazsek, David Raden, Anne Robinson & Francis J. Doyle III

Mammalian Systems Biology (Sunday posters)

M-P01 The role of CreM on circadian rhythm in the mouse model: a systems biology approach combining transcriptomics with metabolomics

Jure Aclimovic, Martina Fink, Ingemar Björkhem, Marko Golcinic & Damjana Rozman

M-P04 Activity of the vitamin D receptor during the cell cycle

Sebastiano Battaglia, James Thome & Moray J. Campbell

T-P19 Workshop: PottersWheel - MATLAB toolbox for model creation, analysis, multi-experiment fitting and experimental design

Thomas Malwald, Marcel Schilling, Ursula Klingmüller & Jens Timmer

T-P22 Modeling and simulation of fructo-oligosaccharides production

Orlando Rocha, Ana Domingues, Clarisse Nobre, Duarte Torres, Ligia Rodrigues, José Teixeira, Isabel Rocha & Eugénio Ferreira

T-P25 Stochastic and modular approach in cellular modeling

Egils Smilcizans

T-P28 Connectivity matrix method and atom mapping matrices

Jun Ohta

T-P29 No abstract

Shu Ye

Monday March 12: Symposium on Yeast (with YSBN)

Monday March 12: 8h30-23h00	
8h30 – 12h30:	Main lecture hall in 1
10h20-11h05:	Main lecture hall in 1, plus Yellow room, plus Gosau room
16h30-18h05:	Main lecture hall split in 3, plus Yellow room, plus Gosau room
18h20 – 19h25:	Main lecture hall in 1
21h00- 23h00:	Poster hall
Breakfast 7:00 - 8:30 am	
Yeast	
Lectures 8:30 am - 12:30 pm	
Chair: <i>Lilia Alberghina</i> Co-chair: <i>Jens Nielsen</i>	
Chairs introduction (plenary)	8:30 am - 8:35 am
Y-L01 <i>Barbara Bakker</i> [Main lecture hall] (plenary)	8:35 am - 9:20 am
Vertical Genomes (didactic lecture)	
Y-L03 <i>Jens Nielsen</i> [Main lecture hall] (plenary)	9:20 am – 9:40 am
Metabolic networks and fluxes (methodology)	
Y-L02 <i>Steve Oliver</i> [Main lecture hall] (plenary)	9:40 am – 10:00 am
How to deal with the complexity of a 'simple' eukaryotic cell (methodology)	
Coffee & Refreshment Break 10:00 am - 10:20 am	
Tutorials corresponding to lectures (3 in parallel) 10:20 am–11:05 am	
Barbara Bakker [Main lecture hall]	
Steve Oliver [Yellow room]	
Jens Nielsen [Gosau room]	
Coffee & Refreshment Break 11:05 am - 11:20 am	
Y-L03 <i>Jens Nielsen</i> [Main lecture hall] (plenary)	11:20 am – 11:40 am
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Metabolic networks and fluxes (results)	
Y -L02 <i>Steve Oliver</i> [Main lecture hall] (plenary)	11:40 am –12:00noon
How to deal with the complexity of a 'simple' eukaryotic cell (results)	
Chair's Resumé and students posing issues. General discussion [Main lecture hall]	12:00 noon – 12:30 am
Lunch & Afternoon Break 12:30 pm - 4:30 pm	
Coffee & Tea 4:00 pm - 4:30 pm	
Monday's Blackboard teaching / Computer practicals	
Session 1-Monday (parallel) 4:30 pm – 6:05 pm	
BB-01 <i>Frank J. Bruggeman & Hans V. Westerhoff</i> [Main lecture hall-A]	4:30 pm – 5:15 pm
Hierarchical regulation analysis of cellular adaptive responses (black board teaching)	
BB-02 <i>Edda Klipp</i> [Main lecture hall-B]	4:30 pm – 5:15 pm
Introduction to dynamic modeling of biochemical networks (black board teaching)	
BB-03 <i>Hans Meinhardt</i> [Main lecture hall-C]	4:30 pm – 5:15 pm
Model of biological pattern formation (black board teaching)	
BB-04 <i>Guy Shinar</i> [Gosau room]	4:30 pm – 5:15 pm
A Mechanism for Robust Biochemical Concentrations – 2 (black board teaching)	
CP-01 <i>Ursula Kummer</i> [Yellow room]	4:30 pm – 5:15 pm
CoPaSi (computer practical)	
Coffee & Refreshment Break 5:15 pm – 5:20 pm	
Session 2 - Sunday (parallel) 5:20 pm – 6:05 pm	
BB-05 <i>Jeroen Jeneson</i> [Main lecture hall-A]	5:20 pm – 6:05 pm
Physiological modeling (black board teaching)	
BB-06 <i>Uwe Sauer</i> [Main lecture hall-B]	5:20 pm – 6:05 pm
Metabolomics and Flux analysis (black board teaching)	
BB-07 <i>Johannes P. Schlöder</i> [Main lecture hall-C]	5:20 pm – 6:05 pm
Differential Equation Models: Parameter Estimation and Optimum Experimental Design (Black Board Teaching)	

CP-02 <i>Jacky L. Snoep</i> [Yellow room]	5:20 pm – 6:05 pm
Tools for Systems Biologists: using JWS Online for integration and storage of data and models (Computer Practicals)	
CP-03 <i>Igor Goryainov and Anatoly Sorokin</i> [Gosau room]	5:20 pm – 6:05 pm
Edinburgh Pathway Editor (Computer Practicals)	
Coffee & Refreshment Break 06:05 pm - 06:20 pm	
Monday's Yeast Short Talks and discussion (plenary) 06:20 pm - 07:05 pm	
Y-S01 <i>Matteo Barberis</i> [Main lecture hall] (plenary)	06:20 pm -06:35 pm
Cell size at S phase initiation: an emergent property of the G1/S network (short talk)	
Y-S02 <i>Juerg Baehler</i> [Main lecture hall] (plenary)	06:35 pm -06:50 pm
A Highly Connected Network of Multiple Regulatory Layers Shapes Gene Expression in Fission Yeast (short talk)	
Y-S03 <i>Stefan Hohmann</i> [Main lecture hall] (plenary)	06:50 pm -07:05 pm
Systems analysis of the yeast Snf1 pathway (short talk)	
Speaker's Panel addressing issues raised in the morning [Main lecture hall]	7:05 pm – 7:25 pm
Dinner 7:30 - 9:00 pm	
Poster Session 2 [Poster hall] 9:00 - 11:00 pm	
Viewing posters 9:00 - 9:45 pm	
Free poster wandering 9:45 - 10:30 pm	
Round table poster discussion (presenters and teachers only) 10:30 - 11:00 pm	
Today's (Monday's) Poster Presentations	
Poster session 2 (Monday)	
Principles of Systems Biology (Monday posters)	
P-P02 <i>Analysis and function of the two PRFP synthases in Lactococcus lactis</i> <i>Xiao Chen, Jan Martinussen & Mogens Kilstrup</i>	
P-P05 <i>Characterization of the role of PPARalpha in heart</i> <i>Anastasia Georgiadou</i>	
P-P08 <i>Genome-wide system identification and analysis reveals stable yet flexible network dynamics in yeast</i>	
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Mika Gustafsson, Michael Hornquist, Johan Björkregren, Jesper Tegner	
P-P11 <i>Correspondence between average and steady-state levels in some nonlinear models of calcium oscillations</i> <i>Beate Knoke, Marco Marhi, Matjaz Perc & Stefan Schuster</i>	
P-P14 <i>Towards a quantitative understanding of carbon source transitions</i> <i>Oliver Kotte & Matthias Heinemann</i>	
P-P17 <i>Control of noisy networks (ML-P16)</i> <i>Robert Platt, Frank Bruggeman, Herbert Sauro & Hans V. Westerhoff</i>	
P-P20 <i>Identification of gene regulatory networks by optimal experimental design in sparse linear models</i> <i>Florian Steinke, Matthias Seeger & Koji Taura</i>	
P-P23 <i>Database supported modelling</i> <i>Andreas Weidemann, Renate Kania, Ulrike Wittig, Martin Golebiewski, Olga Krebs, Saqib Mir, Sven Sahle, Ralph Gauges, Ursula Kummer & Isabel Rojas</i>	
Yeast Systems Biology (Monday posters)	
Y-P02 <i>RiboSys – systems biology of RNA metabolism in yeast</i> <i>Rosa Alexander, David Barras, Martin Koz, David Tollervad & Jean Beggs</i>	
Y-P05 <i>Genome-wide comparative analysis of physiological bottlenecks in multi-subunit protein production in Pichia pastoris</i> <i>Kristin Baumann, Diethard Mattanovich & Paul Ferrer</i>	
Y-P08 <i>Expression profiling studies of the network controlling S. cerevisiae</i> <i>Ayca Cankorur, Duygu Dikicoglu & Betül Kirdar</i>	
Y-P11 <i>Mathematical model for the DNA replication checkpoint</i> <i>Orosly Kapuy, Attila Csikasz-Nagy & Geza Novak</i>	
Y-P14 <i>Systems Biology of a simple eco-system: Saccharomyces cerevisiae and Gluconobacter oxydans</i> <i>Christiaan J. Malherbe, Johann M. Rohwer, Hans V. Westerhoff & Jacky L. Snoep</i>	
Y-P17 <i>Yeast cosmonegation – quantitative approach on a single cell level</i> <i>Elizbeta Petelenz, Emma Eriksson, Dag Hanström & Stefan Hohmann</i>	
Y-P20 <i>Date Management in Yeast Systems Biology</i> <i>Nell Swainston, Irena Spasic, Peter Li, Giles Velarde, Steve Oliver, Douglas Kell & Norman Paton</i>	
Y-P23 <i>Withdrawn</i>	
Y-P26 <i>Glucose metabolism and SNF1 kinase in Saccharomyces cerevisiae</i> <i>Jie Zhang</i>	
Y-P28 <i>Gene interaction networks and models of cation homeostasis in Saccharomyces cerevisiae</i> <i>Joaquin Arino & the Translucent Consortium</i>	
Mammalian Systems Biology (Monday posters)	
M-P02 <i>Towards a nucleocytoplasmic model of the G1 to S transition in mammalian cells</i> <i>Roberta Alfieri, Matteo Barberis, Ferdinando Chiaradonna, Daniela Gaglio, Luciano Milanesi, Marco Vanoni, Edda Klipp & Lilia Alberghina</i>	
M-P05 <i>A Systems biological approach unveils fast, yet energy efficient, reprogramming of the MAPK signal transduction cascade</i> <i>Nils Blüthgen, Szymon Kielbasa, Stefan Legewie, Anja Schramme, Oleg Tschernitsa, Reinhold Schefer, Christine Sars & Hanspeter Herzel</i>	
M-P08 <i>Human ribosomal protein S17 inhibits splicing of its own PRE-mRNA</i> <i>Ksenia Cherenitsina, Alexey Malayin & Galina Kapova</i>	
M-P11 <i>Graph based clustering approach for finding communities and clusters in signaling networks</i> <i>Sergii Ivakhno & Douglas Armstrong</i>	
M-P14 <i>Stereotyped cell networks in a mammalian endocrine organ</i> <i>Francis Molino, Nathalie Couty, Christel Lafont, Paul Le Tissier, Ian Robinson, Jacques Drouin, Philippe Trevenzol, Michael Unser & Patrice Molard</i>	
M-P17 <i>Potential cross-talk between VDR and PXR in regulating expression of several colonic CYP450 genes</i>	
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Tuesday March 13: Symposium Mammalian (with NucSys)

Tuesday March 13: 8h30-12h30	
8h30 – 12h30:	Main lecture hall in 1
10h20-11h05:	plus Yellow room, plus Gosau room
Breakfast 7:00 - 8:30 am	
Mammals Lectures 8:30 am - 12:30 pm	
Chair: <i>Hans van Leeuwen</i>	
Chairs introduction	8:30 am -8:35 am
M-L01 <i>Ursula Klingmüller & Jens Timmer</i> [Main lecture hall]	8:35 am - 9:20 am
Data based modeling and model based experimentation (didactic lecture)	
M-L02 <i>Bela Novak</i> [Main lecture hall] (plenary)	9:20 – 9:40 am
Reverse engineering of the yeast cell cycle control system (methodology)	
L-S04 <i>Takashi Nakakuki</i> [Main lecture hall] (plenary)	9:40 – 10:00 am
Integrative analyses of the Erb receptor signaling transcriptional network (methodology)	
Coffee & Refreshment Break 10:00-10:20 am	
Tutorials corresponding to lectures (3 in parallel) 10:20 – 11:05 am	
Ursula Klingmüller & Jens Timmer [Main lecture hall]	
Bela Novak [Yellow room]	
Takashi Nakakuki [Gosau room]	
Coffee & Refreshment Break 11:05 - 11:20 am	
Y-L04 <i>Bela Novak</i> [Main lecture hall] (plenary)	11:20 – 11:40 am
Reverse engineering of the yeast cell cycle control system (results)	
L-S04 <i>Takashi Nakakuki</i> [Main lecture hall] (plenary)	11:40 – 12:00 noon
Integrative analyses of the Erb receptor signaling transcriptional network (results)	
Chair's Resumé and students posing issues. General discussion	12:00 noon – 12:30 pm
Excursion and lunch 1:00 pm - 11:30 pm	

Thomas Nitke, Eniko Kállay & Heide S. Cross	
M-P20 <i>A systems-biological approach to nuclear receptor signaling by the glucocorticoid receptor: from model to experiment.</i> <i>Katja N. Rybakova, Alexey N. Kholodkin, Frank J. Bruggeman, Barbara M. Bakker, Marco Eijken, Hans V. Westerhoff & Hans van Leeuwen</i>	
M-P23 <i>A mathematical model of Small nucleocytoplasmic shuttling</i> <i>Bernhard Schmiere, Alexander L. Tournier, Paul A. Bates & Caroline S. Hill</i>	
M-P26 <i>Role of the aldoketoreductase AKR1C3 in leukemogenesis</i> <i>Pedro Velha & Christopher Bunce</i>	
Towards Life: Principles and studies of simpler systems (Monday posters)	
L-P02 <i>Dissection of the IFN-beta pathway in cervical carcinoma cell lines</i> <i>Anastasia Bachmann, Rainer Zawatzky & Frank Rösl</i>	
L-P05 <i>Key determinants of antibiotic stress response in Pseudomonas putida</i> <i>Sarah Frank, Oleg Reva, Christian Weinel & Burkhard Tümmler</i>	
L-P08 <i>Control and regulation analysis of phosphoglycerate kinase (PGK) RNA levels in Trypanosoma brucei</i> <i>Jürgen R. Haastria, Mhairi Stewart, Hans V. Westerhoff, Christine Clayton & Barbara M. Bakker</i>	
L-P11 <i>Global transcriptomics of genes modulated by antiviral drugs in yeast</i> <i>Nathalie Landstetter, Walter Glasner, Christa Gregor, Joachim Seipert & Kai Kueher</i>	
L-P14 <i>An automated approach to describe biological networks in terms of functional modules</i> <i>Ettore Murabito</i>	
L-P17 <i>Computability in Biology: Metabolic Networks</i> <i>Sabrina Reisman</i>	
L-P20 <i>Constraint-based prediction of intracellular fluxes in Escherichia coli</i> <i>Robert Schuetz, Lara Kuepfer & Uwe Sauer</i>	
L-P23 <i>Plant-virus system investigation for understanding a pathogenicity mechanism and for developing new plant-virus protection methods</i> <i>Anna Slavokhotova, Alexandr Shiyani & Emma Andreeva</i>	
L-P26 <i>Research intentions for Systems Biology</i> <i>Jennifer Wilbers</i>	
Tools and Methods for Systems Biology (Monday posters)	
T-P02 <i>Optimal Identification in Systems Biology: applications to cell signaling</i> <i>Eva Balsa-Canto, Antonio A. Alonso & Juli R. Banga</i>	
T-P05 <i>Network of interacting reactions in metabolic networks</i> <i>József Bruck & Oliver Eisenlohn</i>	
T-P08 <i>Fuzzy triplet periodicity as a footprint of coding regions evolution</i> <i>Felix E. Frenkel & Eugene V Korotkov</i>	
T-P11 <i>Screening the human interactome for novel disease complexes</i> <i>Niclas T. Hansen, Kasper Lage, Zenia M. Sterling, Olof E.L. Karlberg & Søren Brunak</i>	
T-P14 <i>Towards ordering genes into signaling pathways on a large-scale</i> <i>Peter Jovan, Gadi Shaulsky & Biz Zupan</i>	
T-P17 <i>Semantic SBML: computer-assisted construction, checking, and merging of biochemical models</i> <i>Wolfram Liebermeister</i>	
T-P20 <i>Dynamical and multiscale model of interacting populations of tzhikevich neurons: preliminary results</i> <i>Julien Modolo, Andre Gerenne, Jacques Henry & Anne Beuter</i>	
T-P23 <i>Handling reversible reactions in stochastic simulations</i> <i>Sven Sahle</i>	
T-P26 <i>Analyzing biological feedback with tools from control theory</i> <i>Stefen Waidherr, Thomas Eiding & Frank Allgower</i>	
Program	13

Wednesday March 14: Symposium Towards Life

Wednesday March 14: 8h30-23h00	
8h30 – 12h30:	Main lecture hall in 1
10h20-11h05:	Main lecture hall in 1, plus Yellow room, plus Gosau room
16h30-18h05:	Main lecture hall split in 3, plus Yellow room, plus Gosau room
18h20 – 19h25:	Main lecture hall in 1
21h00- 23h00:	Poster hall
Breakfast 7:00 am - 8:30 am	
Towards Life Lectures 8:30 am - 12:30 pm	
Chair: <i>Marta Cascante</i>	
Chairs introduction	8:30 am - 8:35 am
T-L01 <i>Erik Mosekild</i> [Main lecture hall] (plenary)	8:35 am-9:20 am
Nonlinear dynamics (didactic lecture)	
L-L02 <i>Judy Armitage</i> [Main lecture hall] (plenary)	9:20 am - 9:40 am
Nose diving into Systems Biology: Bacterial sensory networks (methodology)	
T-L02 <i>Jaroslav Stark</i> [Main lecture hall] (plenary)	9:40 am -10:00 am
Modeling methods: hormones and cells (methodology)	
Coffee & Refreshment Break 10:00 am - 10:20 am	
Tutorials corresponding to lectures (3 in parallel) 10:20 am – 11:05 am	
Máns Ehrenberg [Main lecture hall]	
Judy Armitage [Gosau room]	
Jaroslav Stark [Yellow room]	
Coffee & Refreshment Break 11:05 am - 11:20 am	
L-L02 <i>Judy Armitage</i> [Main lecture hall] (plenary)	11:20 am–11:40 am
Nose diving into Systems Biology: Bacterial sensory networks (results)	
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T-L02 <i>Jaroslav Stark</i> [Main lecture hall] (plenary)	11:40am-12:00noon
Modeling methods: hormones and cells (results)	
Chair's Resumé and students posing issues. General discussion	12:00 noon – 12:30 pm
Lunch & Afternoon Break 12:30 pm - 4:30 pm	
Coffee & Tea 4:00 pm - 4:30 pm	
Wednesday's Black Board Teaching / Computer practical (in parallel) 4:30 pm – 6:05 pm	
Session 1-Wednesday (parallel) 4:30 pm – 5:15 pm	
BB-01 <i>Frank J. Bruggeman & Hans V. Westerhoff</i> [Main lecture hall-A]	4:30 pm – 5:15 pm
Hierarchical regulation analysis of cellular adaptive responses (black board teaching)	
BB-02 <i>Edda Klipp</i> [Main lecture hall-B]	4:30 pm – 5:15 pm
Introduction to dynamic modeling of biochemical networks (black board teaching)	
BB-03 <i>Hans Meinhardt</i> [Main lecture hall-C]	4:30 pm – 5:15 pm
Model of biological pattern formation (black board teaching)	
BB-04 <i>Guy Shinar</i> [Gosau room]	4:30 pm – 5:15 pm
Kinetic proofreading (black board teaching)	
CP-01 <i>Ursula Kummer</i> [Yellow room]	4:30 pm – 5:15 pm
CoPaSi (computer practical)	
Coffee & Refreshment Break 5:15 pm – 5:20 pm	
Session 2 - Sunday (parallel) 5:20 pm – 6:05 pm	
BB-05 <i>Jeroen Jeneson</i> [Main lecture hall-A]	5:20 pm – 6:05 pm
Physiological modeling (black board teaching)	
BB-06 <i>Uwe Sauer</i> [Main lecture hall-B]	5:20 pm – 6:05 pm
Metabolomics and Flux analysis (black board teaching)	
BB-07 <i>Johannes P. Schlöder</i> [Main lecture hall-C]	5:20 pm – 6:05 pm
Differential Equation Models: Parameter Estimation and Optimum Experimental Design (Black Board Teaching)	
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CP-P2 Jacky L. Snoep	[Yellow room]	5:20 pm – 6:05 pm
Tools for Systems Biologists: using JWS Online for integration and storage of data and models (Computer Practicals)		
CP-03 Igor Goryanin and Anatoly Sorokin	[Gosau room]	5:20 pm – 6:05 pm
Edinburgh Pathway Editor (Computer Practicals)		
Coffee & Refreshment Break		06:05 pm-06:20 pm
Wednesday: Mammals	Short Talks and discussion (plenary)	06:20pm-07:05 pm
M-S01 Todor Vujanovic	[Main lecture hall]	(plenary) 6:20 pm -6:35 pm
Identification of new therapeutic strategies in immunology through the modeling of the Th1 lymphocyte response (short talk)		
M-S02 Hans van Beek	[Main lecture hall]	(plenary) 6:35 pm–6:50 pm
Dynamics of cardiac energy conversion: computational model for adaptation of oxidative phosphorylation to changing heartbeat rhythm (short talk)		
M-S03 Ksenija Drabek	[Main lecture hall]	(plenary) 6:50 pm–7:05 pm
A backbone to systems biology and multifactorial disease: systems biology of mineralization, bone formation and osteoporosis (short talk)		
Speaker's Panel addressing issues raised in the morning		7:05pm-7:25 pm
[Main lecture hall]		
Dinner		7:30 - 9:00 pm
Poster Session 3 [Poster hall]		9:00 - 11:00 pm
Viewing posters 9:00 - 9:45 am		
Free poster wandering 9:45 – 10:30 pm		
Round table poster discussion (presenters and teachers only) 10:30 – 11:00 pm		
Today's (Wednesday's) Poster Presentations		
Poster session 3		
P inciples of Systems Biology (Wednesday posters)		
P-P03	Using constraint-based modeling to estimate <i>E. coli's</i> capacity for redox-biocatalysis	Birgitte Ebert, Lars M. Eilers, Brian Bühler & Andreas Schmid
P-P06	SBABO-RK: a database for making biochemical kinetics accessible	Martin Golebiewski, Renate Kania, Olga Krebs, Saqib Mir, Jasmin Saric, Andreas Weidemann, Ulrike Wittig & Isabel Rojas
P-P09	Discovery of a dynamic mechanism of quantitative gene regulation	Feng He, Jan Buer, An-Ping Zeng & Rudi Baling
P-P12	Robustness analysis of the heat shock response in <i>Escherichia coli</i>	Heinz Koepl, Susanne Schindler & Elham Kashef
P-P15	Gene expression noise in motility and chemotaxis of <i>E. coli</i>	Linda Lövdick & Victor Soukup

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P-P18	A new <i>Bacillus thuringiensis</i> strain isolated in Tunisia is highly toxic to <i>Lepidopteran</i> larvae	Imen Saadoudi, Souad Rouas, Houba Boukris K. & Samir Jaoua
P-P21	Systematic investigation of the evolutionary conservation of genetic interactions using combinatorial RNA in <i>C. elegans</i>	Julia Tischler, Ben Lehner & Andrew Fraser
P-P24	Analyzing the robustness of cellular rhythms: from gene-regulatory to metabolic oscillations	Jana Wolf
Y east Systems Biology (Wednesday posters)		
Y-P03	Cell size at S phase initiation: an emergent property of the G1/S network	Matteo Barberis, Edda Klipp, Marco Vanoni & Lilla Alberghina
Y-P06	Computer analysis of xylose and arabinose pathways introduced in <i>Saccharomyces cerevisiae</i> for optimization of the co-utilization of glucose, xylose and arabinose for ethanol production	Bassi Bergdahl, Barbel Hahn-Hägerdal & Fernando Aranjó Torres
Y-P09	Modeling PDC1 and PDC5 expression as a function of thiamine availability in the yeast <i>S. cerevisiae</i>	Esa Pitkanen, Antti Tani, Ari Rantanen, Pauli Jouhonen, Jukka Roussu & Esko Ilkonen
Y-P12	Metabolic flux analysis of a glycerol-overproducing <i>Saccharomyces cerevisiae</i> strain based on GC-MS, LC-MS and 2D [¹³ C, ¹ H] COSY NMR derived ¹³ C-labeling data	Rooelco Kleijn, Jan-Maarten Geertman, Beckley Nfor, Dick Schipper, Cor Ras, Jack Pronk, Joseph Heynen, Ton van Maris & Wouter van Winden
Y-P15	Systems view of protein biosynthesis in <i>Saccharomyces cerevisiae</i>	Roberto Olivares, Kiran Pali & Jens Nielsen
Y-P18	Reconstructing structurally feasible metabolic networks	Esa Pitkanen, Antti Tani, Ari Rantanen, Pauli Jouhonen, Jukka Roussu & Esko Ilkonen
Y-P21	Development of a mathematical model for the occupancy of mRNA with ribosomes in <i>Saccharomyces cerevisiae</i>	Jannis Uthendorfer & Edda Klipp
Y-P24	Investigation of ceramides in wild type and deletion mutants of <i>Saccharomyces cerevisiae</i>	Esra Yucael & Kutilu Ulgun
Y-P27	Metabolic flux analysis of <i>Pichia pastoris</i> using stable isotopes and NMR techniques: a baseline study for metabolic engineering	Sandra Zinke & Paul Ferer
M ammalian Systems Biology (Wednesday posters)		
M-P03	Spatial modeling of the endothelial cell biochemical response to shear stress	Richard John Allen, Tae Yoon Kim, David Bagle, Roger Kamm & Anne Ridley
M-P06	Adaptation and regulation of the gp130-JAK1-STAT3 signaling pathway in primary hepatocytes	Sebastian Böhl, Thomas Malwald, Thomas Frahm, Jens Timmer & Ursula Klingmüller
M-P09	The system of pyruvate dehydrogenase kinases and PPAR signaling	Tatjana Degenhardt & Carsten Carlberg
M-P12	Mathematical modeling of the Wnt/beta-catenin pathway	Bernd Kolch, Gábor Rólf, Wolf Jans & Heinrich Reimhart
M-P15	Poster withdrawn	
M-P18	Towards a mathematical description of bone remodeling	Peter Prohaska, David Smith, Bruce Gardiner, Jonathan Good, Natalie Sims & Colin Durston
M-P21	Structural Analysis of Signal Transduction Networks. T-Cell/Receptor-Induced Signaling as a Case Study	Julio Saenz-Rodriguez, Luca Simeoni, Jonathan Lindquist, Rebecca Hemmawy, Ursula Sommerhart, Sebastian Mirschel, Martin Ginkel, Ernst Dieter Gilles, Burkhard Schraven & Steffen Klant
M-P24	Computational modeling of liver glucose homeostasis	Tom Samner
M-P27	Mathematical modeling explains the control mechanism of the Smad dependent TGF-β signaling pathway	Elzke Zi & Edda Klipp
M-P28	Light-induced chromatin modulation in <i>Arabidopsis thaliana</i>	Paul Franz

Coffee & Tea		4:00 pm - 4:30 pm
Thursday: Tools and Towards Life	Short Talks and discussion (plenary)	4:30 pm – 5:45 pm
L-S01 Robert Schuetz	[Main lecture hall]	(plenary) 4:30 pm -4:45 pm
Constraint-based prediction of intracellular fluxes in <i>Escherichia coli</i> (short talk)		
L-S02 Ilka Maria Axmann	[Main lecture hall]	(plenary) 4:45 pm -5:00 pm
Regulation at the RNA level (short talk)		
L-S03 Daniel Kahn	[Main lecture hall]	(plenary) 5:00 pm -5:15 pm
Towards an understanding of the interrelations between metabolic and gene regulation (short talk)		
T-S01 Paul K. Maciejewski	[Main lecture hall]	(plenary) 5:15 pm -5:30 pm
Systems biology to investigate biochemical pathways for metabolic functions <i>in vivo</i> (short talk)		
L-P08 Jurgen R. Haanstra	[Main lecture hall]	(plenary) 5:30 pm-5:45 pm
Control and regulation analysis of phosphorylase kinase (PGK) RNA levels in <i>Trypanosoma brucei</i>		
Coffee & Refreshment Break		5:45 pm-6:10 pm
General discussion		6:10 pm-6:45 pm
Closing lecture		
Chair: Karl Kuchler		
CL-01 Tom Kirkwood	[Main lecture hall]	7:00 pm - 8:00 pm
Systems Biology at last: ageing (keynote lecture)		
Banquet and Farewell Party		8:00 pm – am
Presentation of "Gosau YOUNG SysBio INVESTIGATOR AWARDS"		8:30 - 8:45 pm
María Cascaente and Lilla Alberghina		
Official Closure		8:45 - 9:00 pm
Hans Westerhoff and Karl Kuchler		

Program 21

M-P29	Stereotyped cell networks within a mammalian endocrine organ	Patrice Mollard, François Molino, Nathalie Coutry, Christine Lafont, Norbert Chauvet, Michael Unser, Philippe Thevenaz, Paul Le Tissier & Jacques Drouin
M-P30	Ras oncogene-driven MAPK pathway activation, nuclear targets and transformed phenotypes – a systematic study based on microarrays and RNA interference	Reinhold Schäfer, Oleg Tchemis, Anja Schramme & Christine Sers
T owards Life:		
Principles and studies of simpler systems (Wednesday posters)		
L-P03	Regulation of pxx mediated gene expression by coactivator ppc-1a	Marcin Buler, Olli Pelkonen & Jukka Haakola
L-P06	Genome-wide transcriptional response of the hyperthermophilic archaeon <i>Sulfolobus solfataricus</i> and of its virus SSV1 to UV-treatment	Sabrina Froels, Paul Gordon, Mayi Arcellana-Parillo, Christoph Sensen & Christa Schepner
L-P09	Research prospects in Systems Biology	Stachira Karamanli
L-P12	A framework for whole-body modeling	Mads F. Madsen, Sune Dana & Bjørn Gustorf
L-P15	A minimal model of cell size control	Benjamin Peurcy & Kurutoko Kaneko
L-P18	From modeling gene networks to prediction of chemotherapy efficacy for colorectal cancer	Benjamin Ribba, Nicolas Vorin, Jean Clairambaut & Santiago Schnell
L-P21	Research Intentions for Systems Biology	Alex Shaw
L-P24	No title submitted	Anatoly Sorokin
L-P28	Molecular analysis of chromatin changes involved in b1 paramutation, an allele-dependent transfer of epigenetic information	Matte Stam, Max Haring, Mariëke Louwers, Rechien Bader & Roel van Driel
L-P27	Analysis of temporal gene expression during <i>Bacillus subtilis</i> spore germination and outgrowth	Stanley Brul, Bart J.F. Keijser, Alex Ter Beek, Han Rauwerda, Frank Schuren, Roy Montijn & Hans van der Spiek
T ools and Methods for Systems Biology (Wednesday posters)		
T-P03	A data layout tool that associates the independent parameters of an experiment with the high content data generated from plate reading machines	Rod S.P. Benson
T-P06	Modeling networks of coupled enzymatic reactions using the total quasi-steady state approximation	Fabrizio Capuani & Andrea Ciliberto
T-P09	Parameterized kinetic modeling of metabolic networks	Sergio Grims, Joachim Seibig, Hermann-Gregor Holzhütter & Ralf Steuer
T-P12	Nonparametric bootstrap-based identifiability analysis of differential equations	Stefan Hengst, Clemens Kreutz, Jens Timmer & Thomas Malwald
T-P15	Genome-scale graphical model in metabolic level of <i>Mycobacterium tuberculosis</i>	Saowalak Kalapanitak, Anatoly Sorokin, Hongyu Ma & Igor Goryanin
T-P18	ReConn: connecting Cytoscape to the Reactome database	William P. A. Ligtensberg, Dragan Bozacki & Peter A.J. Hilbers
T-P21	Epigenome growth factor receptor inhibition, emergent network effects and cell fate decision	Nuno Aerns, Taimur Shah & Sylvia Nagl
T-P24	Identification of gene regulatory networks by optimal experimental design in sparse linear models	Matthias Seeger, Florian Steinke & Koji Tsuda
T-P27	Degradome project: building models for intracellular protein degradation	Duy E. Zinnar, Thomas S. Jensen & Søren Brunak

Program 19

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Program 23

Thursday March 15: Symposium Tools & Methods (with BioSim)

Thursday March 14: 8h30-23h00		
8h30 – 20h00:	Main lecture hall in 1	
Breakfast		7:00 - 8:30 am
T ools and Methods	L ectures	8:30 am - 12:30 pm
Chair: Uwe Sauer		
Co-chair: Erik Mosekilde		
C hairs introduction		8:30 am-8:35 am
L-L01 Måns Ehrenberg	[Main lecture hall] (plenary)	8:35 am - 9:20 am
Systems biology of growing bacteria: flows, concentrations, fluctuations and control systems (didactic lecture)		
L-L02 Marileen Dogterom	[Main lecture hall] (plenary)	9:20 am - 9:40 am
Towards macromolecular organization: assembly, forces and organization of the cytoskeleton (methodology)		
T-L04 Hans V. Westerhoff	[Main lecture hall] (plenary)	9:40 am - 10:00 am
Robust systems in control (methodology)		
Coffee & Refreshment Break		10:00am- 10:20am
T utorials corresponding to lectures (3 in parallel)		10:20 am - 11:05 am
Måns Ehrenberg	[Main lecture hall]	
Marileen Dogterom	[Gosau room]	
Hans V. Westerhoff	[Yellow room]	
Coffee & Refreshment Break		11:05 am - 11:20 am
L-L03 Marileen Dogterom	[Main lecture hall] (plenary)	11:20 am-11:40 am
Towards macromolecular organization: assembly, forces and organization of the cytoskeleton (results)		
T-L04 Hans V. Westerhoff	[Main lecture hall] (plenary)	11:40 am-12:00noon
Robust systems in control (results)		
Chair's Resumé and students posing issues. General discussion.		12:00 noon – 12:30 pm
Lunch & Afternoon Break		12:30 pm - 4:30 pm