

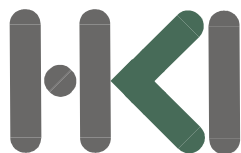
# NiSIS/JCB Workshop

## Reverse Engineering in Systems Biology

10<sup>th</sup> June 2005, Jena/Germany

Technologie- und Innovationspark TIP Jena, 3<sup>rd</sup> Floor,  
Beutenberg-Campus, Wildenbruchstr. 15, D-07745 Jena

Organized by the Leibniz Institute for Natural Product Research and Infection Biology - Hans Knoell Institute and BioControl Jena GmbH with Support from the European Co-ordination Action NiSIS 'Nature-inspired Smart Information Systems' and the Jena Centre for Bioinformatics JCB



### Programme

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|---------------|---|
| 08.30 - 09.00 | <i>Registration</i>   |
| 09.00 - 09.10 | <b>Welcome, Introduction and Programme Overview</b><br><u>M. Pfaff</u> (Jena/Germany)   |
| 09.10 - 09.30 | <b>NiSIS Nature-inspired Smart Information Systems – Reconstructing Nature's Principles</b><br><u>D.A. Linkens</u> (Sheffield/England)  |
| 09.30 - 10.00 | <b>Monitoring of Stress Response during Recombinant Protein Production in <i>E. coli</i> on Transcriptome and Proteome Level</b><br>H. Reischer, K. Duerrschmid, <u>K. Bayer</u> , W. Schmidt-Heck, R. Guthke (Vienna/Austria, Jena/Germany)  |
| 10.00 - 10.30 | <b>Network Reconstruction from Gene Expression during Recombinant Protein Production in <i>E. coli</i></b><br>W. Schmidt-Heck, <u>R. Guthke</u> , S. Toepfer, H. Reischer, K. Duerrschmid, K. Bayer (Jena/Germany, Vienna/Austria)  |
| 10.30 - 11.00 | <i>Break</i>  |
| 11.00 - 11.30 | <b>Three-dimensional Bioartificial Liver Cell Systems: Tools for <i>in vitro</i> Studies of Human Liver Cell Functions</b><br>K. Zeilinger, <u>H. Stachelscheid</u> , G. Pless, M. Pfaff, S. Toepfer, D. Driesch, W. Schmidt-Heck, R. Guthke, P. Neuhaus, J.C. Gerlach (Berlin/Germany, Jena/Germany, Pittsburgh/USA) |
| 11.30 - 12.00 | <b>Analysis of Bioartificial Liver Cell Systems by Network Reconstruction Methods</b><br><u>M. Pfaff</u> , S. Toepfer, D. Driesch, K. Zeilinger, H. Stachelscheid, P. Neuhaus, J.C. Gerlach, W. Schmidt-Heck, R. Guthke (Jena/Germany, Berlin/Germany, Pittsburgh/USA)  |
| 12.00 - 13.15 | <i>Lunch Break</i>  |
| 13.15 - 13.45 | <b>Use of Gene Expression Data for Modelling Networks describing the LiCl-induced Expression of Glutamine Synthetase in Hepatocytes</b><br><u>S. Zellmer</u> , W. Schmidt-Heck, F. Gaunitz, A. Baldysiak-Figiel, R. Guthke, R. Gebhardt (Leipzig/Germany, Jena/Germany)   |
| 13.45 - 14.15 | <b>Elucidation of Transcriptional Networks Regulated by KRAB Zinc Finger Proteins</b><br>P. Lorenz, D. Koczan, R. Guthke, <u>H.-J. Thiesen</u> (Rostock/Germany, Jena/Germany)  |
| 14.15 - 14.45 | <i>Break</i>  |
| 14.45 - 15.15 | <b>Unravelling the Osteoblast Differentiation Pathway through Least Absolute Regression Network Analysis</b><br><u>E.P. van Someren</u> , B.L.T. Vaes, W.T. Steegenga, A.M. Sijbers, K.J. Decherig, M.J.T. Reinders (Delft, The Netherlands)  |
| 15.15 - 15.45 | <b>On the Identifiability of Hierarchic, Sparse and Piecewise Linear Gene-Protein Interaction Networks Relative to Stochastic Fluctuations and Deterministic Chaos</b><br><u>R.L. Westra</u> (Maastricht, The Netherlands)  |
| 15.45 - 16.15 | <b>A Novel 4-valued Discrete Network for the Analysis of Signalling Events</b><br><u>S. Ziagos</u> , S. Woelfl (Jena/Germany, Heidelberg/Germany)   |
| 16.15 - 16.45 | <i>Break</i>  |
| 16.45 - 17.15 | <b>Small Sample Statistical Modelling and Inference of Genetic Networks</b><br><u>J. Schaefer</u> (Munich/Germany)  |
| 17.15 - 17.45 | <b>Simplification of Complex Data Analysis by Integration of Gene Ontology Annotations</b><br><u>N.C. Hauser</u> (Stuttgart/Germany)  |
| 17.45 - 18.15 | <b>Integrated Time Series Metabolomic and Transcriptomic Analysis of a Systematically Perturbed Plant System</b><br><u>H. Kanani</u> , B. Dutta, J. Quackenbush, M.I. Klapa (Maryland/USA, Patra/Greece)  |
| 18.15 - 18.30 | <b>Closing Remarks</b><br><u>M. Pfaff</u> (Jena/Germany), <u>D.A. Linkens</u> (Sheffield/England)   |