

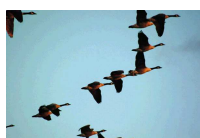
NiSIS / JCB / DFG International Spring School and Workshop Data Mining and Modelling in Systems Biology

International Workshop Data and Knowledge Based Biomolecular Network Reconstruction

16th March 2007, Jena/Germany

Technologie- und Innovationspark TIP Jena, 3rd 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 'Nature-inspired Smart Information Systems' NiSIS,
the Jena Centre for Bioinformatics JCB and the German Research Foundation DFG



Nature-inspired Smart Information Systems

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Programme (Part 1)

Morning

08.30 - 09.00 *Registration*

09.00 - 09.15 **Welcome, Introduction and Programme Overview**
M. Pfaff (BioControl Jena GmbH, Jena, Germany)
D.A. Linkens (University of Sheffield, England)

First Part

Network Inference
by '-omics' Data Analysis
and Knowledge Integration

09.15 - 09.35 **Biomolecular Network Inference by Information Fusion**
B. Olsson (University of Skovde, Sweden)

09.35 - 09.55 **Integrating Templates from Gene Ontology into an Evolutionary Algorithm for Deriving Gene Regulatory Networks**
B. Birkmeier (Technical University Darmstadt, Germany)

09.55 - 10.15 **Integrated Network Analysis Unravels the Osteoblast Differentiation Pathway**
E.P. van Someren (Radboud University Nijmegen, The Netherlands)

10.15 - 10.35 **Network Inference to Understand the Responsiveness to Antirheumatic Therapy**
M. Hecker (Hans Knoell Institute, Jena, Germany)

10.35 - 11.05 *Break*

11.05 - 11.25 **An Integrated Approach to Infer Gene Networks in the Context of Cell Communication**
F. Falciati (University of Birmingham, England)

11.25 - 11.45 **Microarray Data Analysis Focusing on Functional Modules**
K. Sameith (University of Birmingham, England)

11.45 - 12.05 **Application of Transcriptome and Proteome Profiling for Accelerated Process Optimisation of *E. coli* Host/Vector Systems**
T. Scharl, G. Striedner, K. Duerrschnid, K. Bayer (University of Natural Resources and Applied Life Sciences, Vienna, Austria)

12.05 - 12.25 **Network Inference Analysing Transcriptome and Proteome Time Series Data**
R. Guthke, W. Schmidt-Heck, K. Duerrschnid, K. Bayer (Hans Knoell Institute, Jena, Germany; University of Natural Resources and Applied Life Sciences, Vienna, Austria)

12.25 - 13.40 *Lunch Break*

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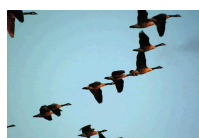
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Programme (Part 2)

Afternoon

Second Part

Biomolecular Data and Network Analysis

- 13.40 - 14.00 **Reconstruction of Signal Transduction Key Nodes**
N. Voss, A. Kel (BIOBASE GmbH, Wolfenbuettel, Germany)
- 14.00 - 14.20 **Promoter Models and Prediction of Transcription Factor Binding Sites for Gene Regulatory Network Reconstruction**
E. Shelest (Hans Knoell Institute, Jena, Germany)
- 14.20 - 14.40 **Modelling Biochemical Processes of Duchenne Muscular Dystrophy with Petri Nets**
I. Koch, S. Grunwald, J. Ackermann, A. Speer
(Technical University of Applied Sciences, Berlin, Germany;
Max Planck Institute for Molecular Genetics, Berlin, Germany;
FluT Biosystems GmbH, Sankt Augustin, Germany)
- 14.40 - 15.00 **Analysing the Robustness of Metabolic Networks**
S. Schuster (Friedrich Schiller University Jena, Germany)
- 15.00 - 15.30 *Break*
- 15.30 - 15.50 **Network Generation Based on Transcriptome Data Can Identify Novel Regulatory Mechanisms in Primary Hepatocytes**
S. Zellmer, W. Schmidt-Heck, R. Guthke, R. Gebhardt
(University of Leipzig, Germany; Hans Knoell Institute, Jena, Germany)
- 15.50- 16.10 **A Discovery Algorithm for Learning Causal Networks from Genomics Data**
K. Strimmer (University of Leipzig, Germany)
- 16.10 - 16.30 **Comparing Evolutionary Algorithms on the Parameter Optimisation of a Metabolic Network of *Corynebacterium glutamicum***
A. Draeger, J. Supper, H. Planatscher, A. Zell
(Eberhard Karls University Tuebingen, Germany)
- 16.30 - 17.00 *Break*
- 17.00 - 17.20 **Model Based Systems and Qualitative Reasoning for Systems Biology**
G.M. Coghill (University of Aberdeen, Scotland)
- 17.20 - 17.40 **Pattern Memory of Gene-Protein Interaction Networks**
R. Westra (University of Maastricht, The Netherlands)
- 17.40 - 18.00 **BioData Analysis and Network Reconstruction - Application Notes**
M. Pfaff, D. Driesch, D. Woetzel, S. Toepfer
(BioControl Jena GmbH, Jena, Germany)
- 18.00 - 18.15 **Closing Remarks**
R. Guthke (Hans Knoell Institute, Jena, Germany)
D.A. Linkens (University of Sheffield, England)