

Program GCB2005

Hamburg, 5.-7. October 2005

Wednesday, 5. October 2005

9:00–13:00 Registration

9:00–12:00 Tutorials

- Ines Liebich: Experiences with Integrated Databases
- Ulrich Meier: Solutions for Grid Computing in Life Sciences
- Florian Markowitz: Computational Inference of Cellular Networks

12:30–13:45 Lunch

13:45–14:00 Welcome Address

Session 1: RNA Structures

(Chair: Robert Giegerich)

14:00–14:45 IT

Peter Schuster (University of Vienna, Austria)

Landscapes in RNA folding and evolution

14:45–15:15 RP

Ulrike Mückstein, Hakim Tafer, Jörg Hackermüller, Stephan H. Bernhart, Peter F. Stadler, Ivo L. Hofacker

Thermodynamics of RNA-RNA Binding

15:15–15:45 RP

Ivo L. Hofacker, Peter F. Stadler

Memory Efficient Folding Algorithms for Circular RNA Secondary Structures

15:45–16:25 Coffee break

Session 2: Sequence Analysis

(Chair: Hans-Werner Mewes)

16:25–17:10 IT

Tom Slezak (Lawrence Livermore National Laboratory, Livermore, USA)

A large-scale application of comparative genomics for biodefense

17:10–17:40 RP

Christian Wawra, Mohamed I. Abouelhoda, Enno Ohlebusch

Efficient mapping of large cDNA/EST databases to genomes: A comparison of two different strategies

17:40–18:10 RP

Annette Höglund, Pierre Dönnès, Torsten Blum, Hans-Werner Adolph, Oliver Kohlbacher

Using N-terminal targeting sequences, amino acid composition, and sequence motifs for predicting protein subcellular localization

18:10–18:30 DN

J.O. Korbel, T. Doerks, L.J. Jensen, C. Perez-Iratxeta, S. Kaczanowski, S. Hooper, M. Andrade, P. Bork

Systematic Association of Genes and Phenotypes Using Literature and Genome Mining Indicates Novel Pathogenicity-Factors

18:30–20:45 Poster Session A

Thursday, 6. October 2005

Session 3: Microarrays

(Chair: Martin Vingron)

8:30–9:15 IT

Guo-Ping Zhao (Chinese National Genome Center, Shanghai, China)

SARS molecular epidemiology and SARS-CoV evolution: Combating an emerging infectious disease with the regimen of genomics and bioinformatics

9:15–9:45 RP

Alexander Kel, Tatiana Konovalova, Tagir Valeev, Evgeny Cheremushkin, Olga Kel-Margoulis, Edgar Wingender

Composite Module Analyst: A Fitness-Based Tool for Prediction of Transcription Regulation

9:45–10:15 RP

Katrin Fundel, Robert Küffner, Thomas Aigner, Ralf Zimmer

Data Processing Effects on the Interpretation of Microarray Gene Expression Experiments

10:15–10:45 RP

Alexey V. Antonov, Igor V. Tetko, Denis Kosykh, Dmitriy Surmeli, Hans-Werner Mewes

Exploiting scale-free information from expression data for cancer classification

10:45–11:25 Coffee break

Session 4: Structure and Docking

(Chair: Jeremy Smith)

11:25–12:10 IT

Rolf Hilgenfeld (University of Lübeck, Germany)

Proteins of SARS coronavirus - experimental and theoretical studies

12:10–12:40 RP

Jean-Christophe Nebel

Generation of 3D templates of active sites of proteins with rigid prosthetic groups

12:40–13:10 RP

Axel Griewel, Matthias Rarey

From greedy to branch & bound and back: Assessing optimization strategies for incremental construction molecular docking tools

13:10–14:10 Lunch

Session 5: Populations and Evolution

(Chair: Peter F. Stadler)

14:10–14:55 IT

Li Jin (Fudan University, Shanghai, China)

Linkage Disequilibrium Sharing and TagSNP Portability Between Populations

14:55–15:25 RP

Hannes Luz, Martin Vingron

Family specific rates of protein evolution

15:25–15:45 DN

Ming Zhang, Anne-Kathrin Schultz, Burkhard Morgenstern, Mario Stanke, Bette Korber, Thomas Leitner

Greater HIV Genome Diversities Inferred From Re-subtyping of HIV Database Sequences

15:45–16:05 DN

Csaba Pál, Balázs Papp, Martin J. Lercher

Evolution of metabolic networks in bacteria

16:05–18:20 Coffee Break and Poster Session B

16:15 Society Meetings (Dechema, GI, GBM)

19:15 Social Event

Friday, 7. October 2005

Session 6: Protein Structures and Interactions

(Chair: Oliver Kohlbacher)

8:30–9:15 IT

David A. Case (Scripps Research Institute, La Jolla, USA)

Macromolecular Simulations Using Continuum Solvent Models

9:15–9:45 RP

Alexander Seifert, Michael Krahn, Stephan Tatzel, Rolf D. Schmid, Jürgen Pleiss

A Model of Specificity and Selectivity of Mammalian Cytochrome P450 Monooxygenases

9:45–10:15 RP

Bingding Huang, Michael Schroeder

Using residue propensities and tightness of fit to improve rigid-body protein-protein docking

10:15–10:35 DN

Oliver Martin

Consensus scoring of Protein-Protein Docking Solutions

10:35–11:15 Coffee break

Session 7: Metabolic Networks

(Chair: Dietmar Schomburg)

11:15–12:00 IT

Hugo Kubinyi (University of Heidelberg, Germany)

Chemistry meets Biology: Chemogenomics in Drug Discovery

12:00–12:30 RP

Ari Rantanen, Taneli Mielikäinen, Juho Rousu, Esko Ukkonen
Planning isotopomer measurements for estimation of metabolic fluxes

12:30–13:00 RP

Christian Spieth, Felix Streichert, Nora Speer, Andreas Zell
Inferring Regulatory Systems with Noisy Pathway Information

13:00–13:20 DN

M. Oldiges, M. Kunze, J. Magnus, R. Takors
Microbial Metabolome Analysis: A Source of in-vivo Metabolite Data for Metabolic Modelling

13:20 Final Remarks

Abbreviations: IT = invited talk, DN = discovery note, RP = regular paper