

Annual Colloquium of the DFG Priority Program

„Informatics Methods for the Analysis and Interpretation of Large Genomic Datasets“

Thursday and Friday November 20 and 21, 2003, Schloss Dagstuhl, Wadern

Preliminary Program

Thursday, November 20, 2003

12:00-13:30 **Registration (Ruth Christmann) and Lunch**

13:40 Welcome address

13:45 **Opening Lecture: Genetics of Cancer (Working Title)**
(Eckart Meese, Saarbrücken)

Protein Structure

14:45 **Constraint-based alignment and classification of genomes**
(Jan Gewehr and Alessandro Macri, München)

15:25 **Predicting protein structure classes from function predictions**
(Ingolf Sommer, Saarbrücken)

15:50 **Protein Structure Prediction: Application Studies**
(Mario Albrecht, Saarbrücken)

16:05 – 16:30 **Coffee Break**

Sequence and Genome Analysis

16:30 **Software for multiple genome comparison**
(Enno Ohlebusch, Ulm)

17:00 **Improving scoring functions for multiple sequence alignment**
(Jan Weyer-Menkhoff, Bielefeld)

17:30 **Genome duplication and the evolution of duplicated gene regulatory elements**
(Dirk Steinke, Konstanz)

18:00 **Searching for noncoding RNA families in large genomic sequence data**
(Stefan Gräf, Düsseldorf)

18:30 **Dinner**

Friday, November 21, 2003

Protein Function

- 09:00 **Integration of genomic data to improve automatic functional annotation**
(Dimitrij Surmeli, Neuherberg)
- 09:30 **Overcoming semantical and technical heterogeneity using SEMEDA and the BioData Server**
(Jakob Köhler, Bielefeld)
- 10:00 **Improving solvation free energy calculations by nonlocal electrostatics**
(Andreas Hildebrandt, Saarbrücken)
- 10:30-11:00 Coffee Break**

Pathways

- 11:00 **Modeling of metabolic networks based on in vivo, in vitro, and in silico data**
(Ralf Takors, Jülich; Wolfgang Wiechert, Siegen)
- 11.40 **An interactive annotation and validation system for transcriptional and post-transcriptional networks**
(Holger Maier, Neuherberg)
- 12:10 - 13:30 Lunch**

Pathways and HIV

- 13:30 **Metabolic pathway analysis of Mycoplasma pneumoniae metabolism**
(Mikhail Pachkov, Jena)
- 14:00 **Toward genotyping/bioinformatics assisted HIV/AIDS therapy optimization: new developments and results**
(Martin Däumer, Köln; Niko Beerenwinkel, Saarbrücken)
- 14:40 Closing Remarks and End of Meeting**