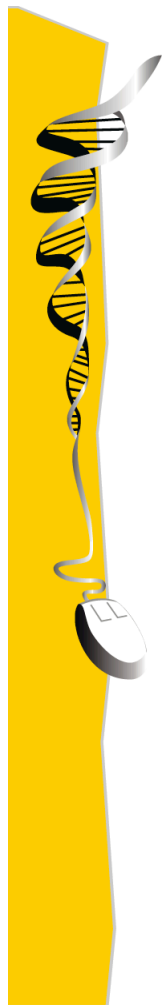


GCB 2011 - German Conference on Bioinformatics 2011

Weihenstephan
September 7-9, 2011



Home	<u>Preliminary Program</u>
Program	Wednesday, September 7
	08:00- Registration
	08:30-08:40 Opening GCB Junior Conference
Call for Papers	08:40-09:00 <i>J. Patrick Pett, Daniel H. Mehnert, Jonas Ibn-Salem, Ole Eigenbrod, Raik Otto, Stephan Knorr, Stina-Stephanie M. Richter and Roland Krause</i> Identification of shared components of protein complexes
Invited Speakers	09:00-09:20 <i>Eva Vennmann, Nadine Schneider and Matthias Rarey</i> Discrimination of permanent and transient heterodimers: The real challenge in the classification of protein-protein interactions
Registration	09:20-09:40 <i>Florian Erhard and Ralf Zimmer</i> Detecting outlier peptides in quantitative High-Troughput mass spectrometry
Venue & Map	09:40-10:00 <i>Thomas Hoffmann and Iris Antes</i> Modeling the variable regions of T-Cell Receptors
Accommodation	10:00-10:20 <i>Manuel Andreas Glaser and Iris Antes</i> Docking Peptides into MHC Class II Complexes
Social Event	10:20-10:50 Coffee Break 10:50-11:10 <i>Sebastian Dümcke, Martin Seizl, Nicole Pirkl, Steffanie Etzold, Dietmar Martin and Achim Tresch</i> One Hand Clapping: Detection of condition-specific Transcription Factor Interactions from genome-wide gene activity Data
Organizing Committee	11:10-11:30 <i>Matthias Böck, Constanze Schmitt and Stefan Kramer</i> A Study of Dynamic Time Warping for the Inference of Gene Regulatory Relationships
Program Committee	11:30-11:50 <i>Robert Pesch and Ralf Zimmer</i> To transfer or not to transfer - Complementing the eukaryotic protein-protein interactome
Supporters and Sponsors	11:50-12:10 <i>Lukas Windhager, Jonas Zierer and Ralf Zimmer</i> Module Extraction from Ensembles of Networks
Contact	12:10-12:30 <i>Alena Mysickova and Martin Vingron</i> Detection of interacting transcription factors in human tissues using predicted DNA binding affinity
Imprint	12:30-13:30 Lunch 13:30-13:50 <i>Huy Dinh, Ortrun Mittelsten Scheid and Arndt Von Haeseler</i> MethColor: a computational approach to uncover DNA methylation heterogeneity
	13:50-14:10 <i>Haroon Naeem, Ralf Zimmer and Robert Küffner</i> Rigorous assessment of gene set enrichment tests
	14:10-14:30 <i>Sabine Hug, Daniel Schmidl, Wei Bo Li, Matthias Greiter and Fabian J. Theis</i> Bayesian Model Selection for Zirconium Processing in the Human Body after Ingestion
	14:30-15:50 <i>Michael Schwarzfischer, Carsten Marr, Jan Krumsiek, Philipp S. Hoppe, Adam Filipczyk, Timm Schroeder and Fabian J. Theis</i> Automated cell quantification allows inference of protein half-life from single cell time-lapse microscopy
	14:50-15:10 <i>Martin Preusse, Andreas Kowarsch, Carsten Marr and Fabian J. Theis</i> miTALOS: Analyzing the tissue-specific regulation of signaling pathways by human and mouse microRNAs
	15:10-15:30 <i>Andre Dau and Johannes Krugel</i> tt-analyze and tt-generate: Tools to Analyze and Generate Sequences with Trained Statistical Properties
	15:30-16:00 Coffee Break
	16:00- Welcome Address Opening Event GCB 2011: 10 Years Bioinformatics Munich (BIM) Opening Lecture: Pavel Pevzner (UC San Diego): De Novo Sequencing of Antibiotics: Metabolomics Meets Graph Theory
	19:00- Welcome Reception
	Thursday, September 8
	08:30-09:15 <i>Matthias Mann (MPI Biochemistry, Martinsried)</i>