

Program of the 25th TBI Winterseminar in Bled 2010

(Session 1 from 16:00-18:00; Session 2 from 20:00-22:00)

Day	Speaker	Title
Sun	Flamm, Christoph	Synthetic Biology a brief overview.
Mon	Gorodkin, Jan Menzel, Peter Seemann, Stefan	Non-coding RNAs in pig and other mammalian genomes. Sequence reconstruction by Maximum Likelihood. In silico screen for structured RNAs, neuronal RNA co-expression and co-folding.
	Dilimulat, Yusuf Kehr, Stephanie Bartschat, Sebastian Donath, Alexander	rnpB in metagenomes and the analysis of rnpB promoter-terminator. SnoBoard: A database for snoRNAs (part 1). SnoBoard: A database for snoRNAs (part 2). Don't believe the RefSeq.
Tue	Langenberger, David	Detecting new miRNAs from deep sequencing data: A field-study in worm.
	Bermudez-Santana, Clara Isabel Otto, Christian Wirth, Henry	Searching for tRNA motive from Transcriptome sequence data. Statistical detection of expressed segments on Tiling Arrays. Colors of Gene Expression.
	Höner, Christian Ostermeier, Philipp-Jens Gringmann, Lydia Hellmuth, Marc	Semantics and Ambiguity of Stochastic RNA Family Models. Cycle Bases. Hypergraphs. A general approach for the recognition of approximate graph products.
Wed	Merkle, Daniel Lorenz, Ronny Mann, Martin	Barrier Trees for Continuous Landscapes. Coarse-grained RNA folding Dynamics. Transition rate sampling in energy landscapes.
	Busch, Anke Ullrich, Alexander Ekker, Heinz	Exon duplication - common or rare? Analysis of metabolic networks. Automated Atom Mapping of Biochemical Reactions.
Thu	Arnold, Christian Steiner, Lydia Krauß, Veiko Keller-Schmidt, Stephanie	Chromatin Computation. An Example for Chromatin Regulation. Evolution of DNA methylation in metazoans. Efficient Likelihood Estimation for 'Growth Models'.
	Zarzer, Clemens Wintsche, Axel Gruber, Andreas	Inverse analysis of ODE models from Systems Biology. Improved Sequence Motif finding. Introducing Paperpile.
Fri	Parikesit, Arli Heyne, Steffen Jüling, Frank Lehmann, Jörg	Domain Distribution of Transcription Factor. RFam clans. Tertiary interactions in mitochondrial tRNAs. NIP search and analysis in Metazoans.
	Amman, Fabian Beyer, Wolfgang Badelt, Stefan Machne, Rainer	Small RNA Target Prediction. Predicting RNA pseudoknots by modifying RNAPlex. Design of artificial RNA triggered RNA-switches. Yeast redox-oscillations.
Sat	Marz, Manja Lechner, Marcus Hoffman, Steve Findeiß, Sven	The 100 days of Marburg. Proteinortho – Orthology detection. ULCER and friends. What others call transcriptomics.