

Program of the 23th TBI Winterseminar in Bled 2008

(Session 1 from 16:00-18:00; Session 2 from 20:00-21:30)

Mo	1	Lehmann, Jörg	Near intron positions are reliable phylogenetic markers: application to holometabolous insects.
	1	Eisenhardt, Carina	NIPs: Analysis of unsequenced holometabolic groups.
	1	Bernhart, Stephan	Improving the performance of RNAalifold.
	1	Munteanu, Andreea	Gene networks and Development. Neutrality in EvoDevo?
	2	Gorodkin, Jan	Tails from the Road to better Bacon.
	2	Matthias Bernt	Identifying Sorting Tandem Duplication Random Loss Events.
Di	1	Hiller, Michael	Pre-mRNA secondary structures influence exon recognition.
	1	Margraf, Thomas	Multiple protein structure alignments.
	1	Wirth, Stefan	On Life, the Universe and (almost) Everything: New ncRNAs using Tiling-Arrays & C/D Box snoRNA target prediction.
	1	Stefan Seemann	PETfold: About RNAs which do not fold into the lowest free energy structure.
	2	Miramontes, Pedro	Genomic large-scale inhomogeneities.
	2	Veiko Krauss	Trans-splicing in Drosophila.
	2	Andrew Torda	What everybody is doing wrong in the RNA World.
Mi	1	Marc Hellmuth	The Strong Graph Product.
	1	Werner Klöckl	Decompositions of Directed Graphs with respect to the Direct Product.
	1	Dilmurat Yusuf	Automatic detection of rnpB genes in bacteria genomes.
	1	Schutt, Katharina	Analysis of microRNA-targets: bioinformatical prediction and experimental validation using differential expression of microRNAs.
	2	Ullmann, Kerstin	Identification, Validation and Characterization of novel Prostate Cancer specific microRNAs.
	2	Schulz, Christine	Search for novel non-coding RNAs in Prostate Carcinoma cells.
	2	Heine, Christian	Visualisation of RNA Secondary Structures with Pseudoknots.
	2	Rohrschneider, Markus	Understanding KEGG - An Interactive Approach to Visualizing Metabolic Pathway Networks.
	Do		11:00-20:00
A		Tafer, Hakim	Prediction of RNA-RNA interaction target sites.
B		Merkle, Daniel	An Algorithm for Inferring Genome Rearrangements on Phylogenetic Trees.
C		Donath, Alexander	TIR domain containing proteins
D		Backofen, Rolf	LocARNA, a tool for high-quality multiple alignment of RNA sequences.
Fr	1	Mann, Martin	Memory efficient basin flooding.
	1	Will, Sebastian	Cookbook for RNA Alignments.
	1	Heyne, Steffen	Pairwise Comparison of RNA Secondary Structures <i>via</i> Exact Sequence-Structure Patterns.
	2	Isabel-Bermudez-Santana, Clara	tRNA-pair arrangement: Does it mean something?
	2	Gesell, Tanja	SISSIZ: Dinucleotide Controlled Null Models for Comparative RNA Gene Prediction.
	2	Chen, Doris	RNA Polymerase II Binding Elements (part 1).
	2	Zimmermann, Bob	RNA Polymerase II Binding Elements and SELEX (part 2).
Sa	1	Thurner, Caro	Kinwalker: Prediction of folding pathways of large RNAs.
	1	Hernandez-Rosales, Maribel	Phylogenetics + Phylogenomics = Cophylogen_what?
	1	Mückstein, Ulrike	Thermodynamics of Microarray Hybridisation.
	1	Gruber, Andreas	RNAz refurbished: some ideas.
	1	Lorenz, Ronny	Secondary Structure Prediction for circular RNA.