Program of the 27th TBI Winterseminar in Bled 2012

Discussion groups and computer labs 10:00–12:00 and 13:00–15:00;
Session 1 from 16:00–18:00; Session 2 from 20:00–22:00

Day	S	Name	Title
Mon	1	Stadler,P	Long non-coding RNAs are well conserved.
	1	Nebel, M	Enumerating RNA pseudoknot structures.
	1	Fabian, A	Translation initiation modelling and its application in sRNA target prediction.
	2	Pace, B	Axelrod's discrete model for the dissemination of Cultures: from dynamics on a network to its landscape.
	2	Hoener, C	Fusion Power
	2	Seemann,S	Sequence and expression analysis of gaps in human chromosome 20 & RIlogo.
Tue	1	Zimmermann, B	Analysis of high-throughput data from genomic SELEX.
	1	Lange, S	Global or local? Predicting secondary structure in mRNAs.
	1	Fallmann, J	Who ARE you? In search for novel AUBP targets.
	1	Eggenhofer, F	CM-compare Webserver.
	2	Langenberger, D	W.W.D.D.: What Would DICER Do?
	2	Duarte, LR	Impact of Global Change on Ancient Environments: What can we achieve with a Genomics-Transcriptomics Approach?
	2	Wieseke, N	TBA: The Bingo Adaption.
	2	Kehr, S	Target conservation of snoRNAs.
Wed	1	Tanzer, A	Insights from within the ENCODE project - The interplay of small and long RNAs.
	1	Will, S	Structure-based Whole Genome Realignment Reveals Many Novel Non-coding RNAs.
	1	Heyne, S	GraphClust: structural clustering of local RNA secondary structures.
	1	Costa, F	Extracting Sense from Structure: an application to functional non-coding RNA polymers.
	2	Kleinkauf, R	Ligand conditional synthetic riboswitches.
	2	Behrens, S	Small RNAs in Listeria.
	2	Pudhir, S	Comparative analysis of read processing patterns across 11 RNA-seq datasets.
	2	Radhakrishnan, S	Measures to detect the effect of SNPs on RNA secondary structure.
	2	Findeiß, S	Theo Controls Stop and Go.
Thu	1	CONFERENCE DINNER	BLED CASTLE
	2	Backofen, R	Bioinformatic analysis of Crispr elements.
	2	Andersen, JL	MedØlDatschgerl and Beyond.
	2	Peters, Ph	Exploring Chemistry Using Satisfiability Modulo Theories.
	2	Reiche, K	Molecular signatures of long ncRNAs in breast cancer patients.
	2	Gu, J	The spectral analysis on biology networks.
	2	Long, Y	Relation between graphs.
Fri	1	Schaefer, A	Edge Clustering in Human Brain Graphs.
	1	Wintsche, A	Leontis Westhof Notation for RNA-Protein Complexes?
	1	Theis, C	An open question – Can RNA 3D motifs enhence ncRNA prediction?
	1	Lorenz, R	In silico RNA folding kinetics using 2DKin.
	2	Parikesit, A	Evolution and Quantitative Comparison of Genome-Wide Protein Domain Distributions.
	2	Sahyoun, A	Nucleotide frequency distribution in mitochondrial genomes.
	2	Kaur,Simranjeet	Sequence analysis of human UTRs.
	2	Wenzel, A & Rudebeck, AF	RIsearch.
	2	Ostermeier, Ph-J	Dihypergraphs.
Sat	1	Ostermeier, L	Square property.
	1	Kerpedjiev, P	Approaching RNA 3D modeling.
	1	Kucharik, M	RNA folding kinetics.
	1	Badelt, S	Conformational design of self-organizing ribozymes.