Program of the 26$^{\text{th}}$ TBI Winterseminar in Bled 2011

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

Day	Speaker	Title
Mon	Parikesit, Arli	Transcripton Factor Domain Co-occurrence Distribution.
	Eggenhofer, Florian	Webserver for small RNA target prediction.
	Fasold, Mario	Learning about RNA Degradation from Microarray Data.
	Höner, Christian	A Folding Algorithm for Extended RNA Secondary Structures.
	Erb, Ionas	Improved promotor-alignments using pro-COFFEE.
	Wehner, Stefanie	Bacteria-wide detection of 6S RNAs.
	Lechner, Marcus	Fragment based pipeline for ncRNAs.
	Lorenz, Ronny	Update on the status of `ViennaRNA v2.0`
Tue	Klavžar, Sandi	Convex Excess and Inequalities for Partial Cubes.
	Imrich, Wilfried	Product Graphs and Large Networks.
	Ostermeier,Lydia	Twisted Cartesian products.
	Andersen, Jakob	Finding chemical patterns in reaction networks.
	Costa, Fabricio	Graph kernels and machine learning.
	Mann, Martin	Does it smell? Aromaticity prediction in molecule graphs.
	Widder, Stefanie	FFLs: Linking Function, Plasticity, Evolvability and Abundance.
	Thomma, Anton	Metagenomics and ancient DNA.
Wed	Alkhanbashi, Omer	Analysis of CRISPR-repeat structure.
	Jühling,Frank	Mitochondrial tRNAs.
	Kleinkauf, Robert	Ligand-binding RNA Design.
	Bernt, Matthias	Phylogeny Reconstruction and Incompatible Characters.
	Keller-Schmidt, Stephanie	Simulation of Cophylogenies using the age model.
	Wieseke, Nicolas	An extended event model for coevolution.
	Hellmuth, Marc	Relation θ and reconciliation trees.
	Hernandez-Rosales, Maribel	Generation of Gene Family Histories.
Thu	Ullrich, Alexander	Robustness and Modularity in Metabolic Networks.
	Ghanbarnejad, Fakhteh	Predicting nodes influence in Boolean networks.
	Smith, Martin	Measuring purifying selection in 2D.
	Rose, Dominic	Long non-coding RNAs.
	Siebauer, Michael	Proceedings of Locarna-Scan.
	Radhakrishnan, Sabari	Finding locally disrupted RNA structure from SNPs.
	Pundhir, Sachin	Identification and Classification of ncRNAusing deep sequencing data.
	Croft, Larry	miRNAs and networks.
	Anthon, Christian	ncRNAs in the piggenom.
Fri	Hertel, Jana	The Expansion of the let-7 miRNA family from Acon worm to human.
	Badelt, Stefan	Barrier-heights in pseudoknot space.
	Seemann, Stefan	Structured RNAs are everywhere in the mouse brain.
	Tippmann, Sylvia	The relative contribution of transcriptional and post-transcriptional regulation to mRNA levels
	Langenberger, David	DARIO (web-service for deep sequencing data)
	Lange, Sita	Are plant microRNA really so simple?
	Otto, Christian	Mapping of bisulfite sequencing data.
	Steiner, Lydia	Identify Homologous Words.
Sat	Stadler, Peter	Folding with Fancy Constraints Secondary Structures from Probing Data.
	Fallmann, Jörg	RNA-Protein interaction prediction.
	Hopp, Lydia	Gene expression in artificial genomes after perturbations: gene insertion and knock -out.
	Marz, Manja	Friends.
	Vierna, Joaquín	Evolutionary analysis of 5S ribosomal DNA in metazoans