

Tuesday 05.10.2010

15:00 - 19:00			Registration at Penzion Zvonecek
19:00 - 20:00			Dinner
20:15 - 21:00	Findeiss	Sven	Opening Session

Wednesday 06.10.2010

Session I: Mathematical Models & RNA Motif Prediction

Chair: Sven Findeiss

15:00	Keller-Schmidt	Stephanie	growth models	15
15:30	Pundhir	Sachin	Read Patterns	15
5min break				
15:55	Badelt	Stefan	Design & Future aspects of artificial RNA switches for synthetic biology	25
16:25	Hertel	Jana	Detecting motifs with GotohScan	15
5min break				
17:10	Fallmann	Joerg	Proteins that bind ARE-motifs	15
17:30	Wintsche	Axel	Paraspeckles, A to I editing, and discriminative motifs	25

DINNER: 18:15 - 19:15

Session II: Transcripts and their evolution

Chair: Manja Marz

19:15	Wiuf	Carsten	Mathematical modeling and some results for signaling cascades of length n	25
19:45	Juehling	Frank	t-RNA	15
5min break				
20:10	Otto	Christian	Tiling Array data	15
20:30	Ongyerth	Matthias	splice site evolution in primates	15
20:50	Nitsche	Anne	splice sites	15
5min break				
21:15	Parikesit	Arli	Domain Prediction in Eukaryote Genomes	25
21:45	Nowick	Katja	Evolution of transcription factors in primates	25

Thursday 07.10.2010

Session III: Phylogeny

Chair: Hackermueller Joerg

14:30	Hernandez Rosales	Maribel	Phylogenomics	25
15:00	Wieseke	Nicolas	How to evaluate co-phylogenetic reconstructions?	15
5min break				
15:25	Donath	Alex	detection of local rate variation by ML optimization	25
15:55	Lechner	Marcus	ncRNA prediction and protein based phylogeny	15

15 Min Break

Session IV: Epigenetics

Chair: Steve Hoffmann

16:30	Krinner	Axel	agent based cell simulation	15
16:50	Galle	Joerg	Modelling of epigenetic regulation	15
17:10	Steiner	Lydia	histone modifications	15
5min break				
17:35	Prohaska	Sonja	Inheritance of Histone marks	15
17:55	Arnold	Christian	Mechanisms of epigenetic inheritance	15
18:15	Cakir	Mehmet Volkan	Random Genome Model and Epigenetic Regulation	15
5min break				
18:40	Rohlf	Thimo	Gene networks in time and space: modeling combinatorial geometry of genomes	30

DINNER: 19:30 - OpenEnd

Friday 08.10.2010**Session V: Graphs and Dynamics**

Chair: Marc Hellmuth

14:00	Ostermeier	Philipp-Jens	MCBs of the Lexicographic Product	25
14:30	Ostermeier	Lydia	Cartesian graph product	25
5min break				
15:05	Long	Yangjing	relations between graphs	15
15:25	Gu	Jiao	The distance among species using eigenvalues	15
15:45	Ghanbarnejad	Fakhteh	Stability of Boolean dynamics	25
5min break				
16:20	Giri	Varun	Modelling the chemical dynamics of autocatalytic networks in a pre-biotic scenario	30
5min break				
16:55	Rohrschneider	Markus	Visual Network Analysis of Dynamic Metabolic Pathways	25
17:25	Scherf	Nico	quo vadis? Analysis of single cell behaviour in time lapse movies	25

*DINNER: 18:00 - 19:15***Session VI: RNA Tools**

Chair: Ivo Hofacker

19:15	Engelhardt	Jan	local structure-based clustering	15
19:35	Siebauer	Michael	Master Thesis: Homology search with Locarna-Scan	15
19:55	Eggenhofer	Florian	A webserver for bacterial sRNA target prediction	15
5min break				
20:20	Lorenz	Ronny	ViennaRNA Package 2.0	25
20:50	Puton	Tomasz	CompaRNA: a server for continuous benchmarking of automated methods for RNA structure prediction.	25
5min break				
21:25	Seemann	Stefan	RNA-RNA interaction	25

Saturday 09.10.2010

Session VII: Evolution and RNA

Chair: Andreas Gruber

15:00	Lozada	Alejandro	Evolution of viral genomes from a Quasispecies perspective	25
15:30	Lozada-Chavez	Irma	Evolution of ncRNAs and their contribution to the biological complexity of life: PART I	25
5min break				
16:05	Tafer	Hakim	RNAplex	15
16:25	Bartschat	Sebastian	snoRNAs	15
16:45	Kehr	Stephanie	Target prediction for C/D-box snoRNAs	15
5min break				
17:10	Wehner	Steffi	paRNA: waste and vast	15
17:30	Hoener zu Siederdisen	Christian	Discriminatory Power of RNA Family Models	25

DINNER: 18:15 - 19:15

Session VIII: RNA world

Chair: Sven Findeiss

19:15	Flamm	Christoph	RNA world hypothesis: An old story with new findings	30
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