

**Tuesday 2012-10-02**

<i>Arrival and registration</i>				
	15:00-19:00			Registration
	19:00-20:30			Dinner
<i>Opening session</i>				
	20:30-20:45	Wintsche	Axel	Opening of the 10. Herbstseminar: introduction and announcements
	20:45-21:30	Mosig	Axel	The Benefits of Procrastination in Image Analysis

**Wednesday 2012-10-03**

<i>Session 1: Evolution and Networks</i>				
Chair	Katja Nowick			
	15:00-15:20	Tincopa Marca	Luz rosalina	Transcription factors in primates
	15:20-15:40	Parikesit	Arli Aditya	Eukaryotes Protein Domain Distribution
	15:40-16:00	Machne	Rainer	Dynamic chromosomal domain organization of an archaic eukaryotic growth program
<i>15min break</i>				
	16:15-16:35	Wieseke	Nicolas	Anchored Multiple Sequence Alignment
	16:35-16:55	Steiner	Lydia	something about chromatin
	16:55-17:25	Lozada-Chávez	Irma	Differential evolution of non-coding DNA across eukaryotes and its relationship with multicellular complexity
<i>15min break</i>				
	17:40-18:00	Wehner	Stefanie	Results of the practical course "Methods for HT-sequencing"
	18:00-18:20	Riege	Konstantin	Automatization of ncRNA annotation - an outlook
<i>Dinner</i>				
	18:30-19:30			
<i>Session 2: ncRNAs</i>				
Chair	Jana Hertel			
	19:30-19:50	Bartschat	Sebastian	snoRNAs in fungi
	19:50-20:10	Kehr	Stephanie	snoRNAs in the Cajal Body
	20:10-20:30	Weinholdt	Claus	A mRNA region-model for miRNA target prediction
<i>10min break</i>				
	20:40-21:00	Lach	Grzegorz	RNA design with smart mutations
	21:00-21:20	Tanzer	Andrea	Over Short or Long

**Thursday 2012-10-04**

<i>Session 1: RNA folding</i>				
Chair	Ronny Lorenz			
	15:00-15:20	Riechert	Maik	Predicting pseudoknots without hacking in C
	15:20-15:40	Kucharik	Marcel	RNA folding kinetics
	15:40-16:00	Kato	Yuki	RNA structural alignment using dual decomposition
<i>15min break</i>				
	16:15-16:35	Kerpedjiev	Peter	Coarse Grained 3D RNA Folding
	16:35-16:55	Boniecki	Michal	SimRNA - program for RNA folding simulations
	16:55-17:15	Marcin	Magnus	Prediction of accuracy of RNA 3D models
<i>15min break</i>				
<i>Session 2: Modeling of chemical reactions and cells</i>				
Chair	Daniel Merkle			
	17:30-17:50	Andersen	Jakob L.	Even more on Analysis of Chemical Reaction Networks
	17:50-18:10	Jiao	Gu	something about spectrum
	18:10-18:40	Waldmann	Johannes	sth. about Constraint Programming/SAT encoding/Haskell
<i>10min break</i>				
	18:50-19:10	Johann	Tim	An integrated modular software framework for cellular simulations.
	19:10-19:30	Neitsch	Johannes	Modeling of cells in liver

Conference Dinner 19:30-Open end

**Friday 2012-10-05**

<i>Session 1: Biology</i>					
Chair	Manja Marz				
	15:00-15:20	Fricke	Markus	Bioinformatic analysis of the coronavirus - an outlook	15
	15:20-15:40	Sahyoun	Abdullah	Mitochondrial genomes	15
	15:40-16:00	Amman	Fabian	bacterial translation initiation and sRNA	15
<i>15min break</i>					
	16:15-16:35	Rivarola D.	Lorena	NGS and Ecotoxicology	15
	16:35-16:55	Liu	Xuanshi	The role of parent-of-origin in obesity using haplotype phasing	15
<i>15min break</i>					
<i>Session 2: Sequence analysis</i>					
Chair	David Langenberger				
	17:10-17:30	Fasold	Mario	SNP detection in deep sequencing data	15
	17:30-17:50	Radhakrishnan	Sabarinathan	RNAseq - features and application	15
	17:50-18:10	Otto	Christian	something about segemehl and its features	15
	18:10-18:30	Moritz	Ruby	Annotation Guided Local Similarity Search in Multiple Sequences and its Application to Mitochondrial Genomes	15
<i>Dinner</i>					
	18:30-19:30				
<i>Session 3: interactive RNA</i>					
Chair	Stephan Bernhart				
	19:30-19:50	Wenzel	Anne	something about RNA-RNA interactions	15
	19:50-20:10	Chojnowski	Grzegorz	Structural analysis of RNA-RNA interactions	15
	20:10-20:30	Wild	Sebastian	RNA-RNA Interaction Prediction with Stochastic Grammars	15
<i>10min break</i>					
	20:40-21:00	Fallmann	Joerg	protein-RNA interactions, ARE elements, ....	15
	21:00-21:20	Lorenz	Ronny	G-Quadruplexes	15

**Saturday 2012-10-06**

<i>Session 1: Miscellaneous math</i>					
Chair	Alexander Schäfer				
	15:00-15:20	Ostermeier	Lydia	sth about graphs	15
	15:20-15:40	Ostermeier	Philipp-Jens	xy ungelöst	15
	15:40-16:00	Peters	Philipp	Exploring chemistry with SMT	15
<i>10min break</i>					
	16:10-16:30	Qin	Jing	Landscapes	15
	16:30-16:50	Arnold	Christian	Chromatin Rules and Complexity	15
<i>15min break</i>					
<i>Session 2: image analysis, RNA probing and everything</i>					
Chair:	Stefan Seemann				
	17:05-17:25	Friebel	Adrian	Image Analysis	15
	17:25-17:45	Kaempfer	Christoph	Understanding RNA probing	15
	17:45-18:05	Badelt	Stefan	Design of self-processing ribozymes	15
<i>10min break</i>					
	18:11-18:35	Janssen	Stefan	Fun with covariance models	15
	18:35-18:55	Eggenhofer	Florian	cmcompare webservice	15
	18:55-19:15	Matelska	Dorota	RNA motifs in ribosomal protein operons	15

*Dinner* 19:30-Open end