

15th Herbstseminar - Schedule

Monday 2017-10-2

Arrival and registration	
14:00-18:30	Registration

Dinner 19:00-20:30

Opening		
20:30-20:45	Felix Kuehnl	Opening ceremony of the 15th Herbstseminar
20:45-21:00	Joerg Fallmann & Matthias Bernt	Introduction Galaxy Workshop
21:00-21:45	Marc Hellmuth	The Matroid Structure of Representative Triple Sets

Tuesday 2017-10-3

<i>Galaxy Workshop</i>	
12:00-13:30	Installation of necessary software [optional]

Session 1: Genomics		Chair: Irma Lozada-Chvez	
14:00-14:30	Valerie De Anda	MEBS: A new software platform to evaluate and classify omic samples according to their metabolic machinery	25
14:30-14:50	Cristian A. Velandia Huerto	Study of the genomic organization of ancestral domains of the immune system of basal chordates	15
14:50-14:55	Marie Lataretu	Something about fungi and mitochondria	5

20 min break with coffee and tea

Session 2: Algorithmics		Chair: Nicolas Wieseke	
15:15-15:35	Dominik Otto	Independent Component Analysis as Signal Deconvolution	15
15:35-15:55	Halima Saker	Multidimensional segmentation	15
15:55-16:15	Thomas Gatter	New Methods for Transcript Isoform Assembly	15
16:15-16:20	Falco Kirchner	Partially Local Multi-Way Alignments	5

15 min break

Session 3: Algorithmics for 3D structure		Chair: Ronny Lorenz	
16:35-17:05	Christoph Leberecht	SiNGA: Harnessing three-dimensional molecular structure data using graphs	25
17:05-17:35	Bernhard Thiel	How to properly sample 3-way junctions in coarse-grained RNA 3D structure prediction	25
17:35-17:40	Irene Beckmann	Predicting Pseudoknots in RNA 3D structures	5

Dinner 18:00-20:00

Powerpoint Karaoke		Chair: Stephan Bernhart	
20:00-22:00			

Wednesday 2017-10-5

<i>Galaxy Workshop</i>	
10:00-13:00	How to use the Galaxy environment.

Session 4: Non-coding RNAs I		Chair: Florian Eggenhofer	
15:00-15:20	Stefan Hammer	An universal RNA design pipeline	15
15:20-15:40	Felix Kuehnl	The design of transcriptional neomycin riboswitches	15
15:40-16:00	Adrian Geissler	Bioinformatics pipeline for analyzing ncRNA in transcriptomics data	15
16:00-16:20	Michael Rade	Long non-coding RNAs related to MAPK-inhibitor resistance in melanoma	15
16:20-16:25	Sarah Krautwurst	How Does Ligand Binding Influence Local Conformation?	5

20 min break with coffee and tea

Session 5: Non-coding RNAs II		Chair: Stephan Bernhart	
16:45-17:15	Siegfried Zöttsche	Training and evaluation of a support vector regression model for standardized RNA folding energies	25
17:15-17:35	Gregor Entzian	High precision RNA folding kinetics	15
17:35-17:55	Sarah Berkemer	SMORE - prep roast eat	15
17:55-18:00	Maria Waldl	something on RNA Interactions (seed kinetics or 3D structures)	5
18:00-18:05	Florian Mock	Virus host prediction machine learning	5

Dinner 18:00-20:00

Session 6: Visualization & Tools		Chair: Nancy Retzlaff	
20:00-20:30	Pavankumar Videm	An integrated framework for annotation and visualization of chimeric reads	25
20:30-21:00	Daniel Gerighausen	RNApuzzler IV	25
21:00-21:20	Florian Eggenhofer	CMV - Visualisation for RNA and Protein family models and their comparisons	15

Thursday 2017-10-6

<i>Galaxy Workshop</i>	
10:00-13:00	How to integrate tools into the Galaxy environment.

Session 7: Graph theory and networks		Chair: Christoph Leberecht	
15:00-15:30	John Anders	Xenology relations in phylogenetic gene trees	25
15:30-15:50	Manuela Geiss	Reconstructing Gene Trees From Fitch's Xenology Relation	15
15:50-16:10	Sebastian Krautwurst	De novo viral quasispecies reconstruction from long noisy reads using de Bruijn graphs	15
16:10-16:15	Patrick Braun	Random-graph-models for chemical reaction-networks	5
16:15-16:20	Angel E. Rodriguez F.	Neutrality and Ruggedness in Fitness Landscapes	5

20 min break with coffee and tea

Session 8: Transcriptomics I		Chair: Joerg Fallmann	
16:40-17:00	Emanuel Barth	Something about Transcriptome Data Statistics	15
17:00-17:20	Anne Hoffmann	Accurate Mapping of tRNA Reads	15
17:20-17:40	Lasse Feldhahn	A novel approach of transcriptome de novo assembly	15
17:40-17:45	Simon Rasmussen	Querying many RNA-seq data sets	5

15 min break

Session 9: Proteins		Chair: Henrike Indrischek	
18:00-18:20	Jan Engelhardt	Something about DNA methylation	15
18:20-18:40	Nico Herbig	Fun and Trouble with Histone Modifications	15
18:40-19:00	Maximilian Collatz	In Silico enrichment of immunodominant proteins	15

Dinner 19:00 - open end

Friday 2017-10-7

Session 10: Non-coding RNAs and viruses		Chair: Peter Stadler	
15:00-15:20	Anne Wenzel	"RNA tools registry and ontologies"	15
15:20-15:40	Roman Ochsenreiter	Identifying Homolog and Analog Viral ncRNAs	15
15:40-16:00	Kevin Lamkiewicz	A machine-learning approach to identify viral miRNAs	15
16:00-16:20	Daniel Desir	Influenza A Packaging	15

20 min break with coffee and tea

Session 12: Omics		Chair: Sonja Prohaska	
16:40-17:00	Nadezhda Doncheva	Tissue-specific, orthology-based pathway comparison between human and animal models	15
17:00-17:20	Mariam Farman	Modulated SubPath Finder	15
17:20-17:50	Ivo Grosse	Phylogenetic footprinting with intra-motif dependencies	25

Dinner 18:00 - open end

Saturday 2017-10-8

Goodbye and departure	
until 10:00	Check-out