19th Herbstseminar - Schedule

Monday 2023-10-02

Arrival and Registration			
14:00-18:00		Arrival and Registration	

18:00-20:00 Dinner

Opening Remarks		Chair: Nora Beier	
20:00-20:15	Nora Beier	Welcome	15
20:15-21:00	Peter F Stadler	Above, Below, or Equal? Identifying Horizontal Gene Transfer with Graph Theory	45

Tuesday 2023-10-03

Introduction to Pandas and other tools for Data Analysis in Python (Nono Saha Cyrille Merleau)			
10:00-12:30			

non-coding RNAs and Genomics		Chair: Ronny Lorenz	
14:00-14:05	Dulce I. Valdivia	Lost in tRNAslation: causes and consequences of tRNA abundance variation	5
14:05-14:25	Julie Ozerova	Weird mt-tRNAs and where to find them	15
14:25-14:45	Christopher Klapproth	A computational search for Telomere Template RNAs (TRs) in Nematodes	15
14:45-15:05	Yuliia Varenyk	Modified nucleotides in tRNA structure	15
15:05-15:25	Die Hu	Viral and prokaryotic genomes recovered from metagenomes as bioindicators of children with atopic eczema	15

30 min Break with Coffee and Tea

MISC		Chair: Peter F Stadler	
16:00-16:20	Gennuo Wang	Influence of Bromoxynil on virus-prokaryote host interactions in grassland soil: insights from a genome-centric analysis of metagenomes in a microcosm succession study	15
16:20-16:40	Martin Bole	Loss of knowledge and what does metadata have to do with it	15
16:40-17:00	Sanchita Kamath	Exploring the functional annotation of MAGs from terrestrial environment based on their Orthogroups.	15
17:00-17:20	Dhouha Grissa	Probe design for pathogen detection by strand displacement	15
17:20-17:40	Franziska Reinhardt	Analysis of allosteric networks of receptor states	15

18:00-20:00 Dinner

non-coding RNAs		Chair: Hua-Ting Yao	
20:20-20:40	Xueer Han	The structural impact of SNPs on the secondary RNA structure of long non-coding RNAs	15
20:40-21:00	Geissler Adrian	Computational screen for conserved RNA structure motifs in cyanobacteria	15
21:00-21:20	Thomas Spicher	Free energy calculation for modified nucleotides by molecular dynamics simulations	15

Powerpoint Karaoke			
21:30-22:30			

Wednesday 2023-10-04

Genomics		Chair: Harald Ringbauer	
14:00-14:20	Christian Anthon	Fair reporting of Deep Learning results in CRISPR	15
14:20-14:40	Ziyi Sheng	Incorporating scaffold structure information for gRNA efficiency prediction by deep learning	15
14:40-15:00	Ying Sun	Enhanced CRISPR base editing design from data generation and deep learning	15
15:00-15:20	Wenhao Gao	A benchmark of CRISPRoff2 for assessing CRISPR off-target with mismatches and indels	15

30 min Break with Coffee and Tea

Group Photo	Chair: Bruno Johann Schmidt

Genomics		Chair: Geissler Adrian	
16:15-16:35	Dhvani Vora	A binding energy model for CRISPR/Cas12a off-target analysis	15
16:35-16:55	Amos Onn	Single Cell Lineage Reconstruction using Short Tandem Repeats	15
16:55-17:15	Christiane Gärtner	Sex-specific gene expression in Burkitt lymphoma	15
17:15-17:45	Harald Ringbauer	Long shared haplotypes in ancient DNA - Inferring relatives and demography	25

18:00-20:00 Dinner

Escape Room			
20:00-23:00			

Thursday 2023-10-05

Hiking Tour			
10:00-13:00			

Graph theory and networks		Chair: Nicola Vassena	
14:00-14:05	Richard Golnik	Modelling isotope labeling in atom transition networks	5
14:05-14:10	Manuel Uhlir	Predicting mass spectra using theoretically derived graph transformation rules	5
14:10-14:30	Guillaume Scholz	Consensus Segmentation: Part 2.	15
14:30-14:35	Maximilian Salomon	Predicting intermediate GPCR conformations	5
14:35-14:55	Annachiara Korchmaros	Orthology pipeline: project and realization	15
14:55-15:15	Bruno Johann Schmidt	Weighted Fitch Graph Optimization	15

30 min Break with Coffee and Tea

Genomics		Chair: Stephan Bernhart	
16:00-16:20	Sarah von Löhneysen	Phylogenetic Information as Soft Constraints in RNA Secondary Structure Prediction	15
16:20-16:40	Ella Cassidy	Integrative analysis of Human Papillomavirus (HPV) detection, integration sites and transcriptome profiling using RNA-Seq.	15
16:40-17:00	Gabor Balogh	Automated analysis of epigenetic and transcriptomic biomarkers from public data to assist individualised treatment success predictions for patients with SCCs	15
17:00-17:20	Ulisses Nunes da Rocha	Doctoral double degrees between Germany and the Global South	15
17:20-17:40	Faith Oni	Genome-centric analysis of an aromatics-degrading sulfate-reducing microbial community	15

18:00-20:00 Conference Dinner

Party and Escape Room			
20:00-23:00			

Friday 2023-10-06

Graph theory and networks		Chair: Bruno Iha	
14:00-14:20	Marcos Laffitte	Progressive Graph Alignment	15
14:20-14:40	Nora Beier	RCLASS and how a database stands in your way to actually use their data (Graph reconstruction story)	15
14:40-15:00	Casper Asbjørn Eriksen	StructRecon: Reconciling Inconsistent Molecular Structures from Biochemical Databases	15
15:00-15:20	Nicola Vassena	Instability is the new autocatalysis	15

45 min Break with Coffee and Tea

Graph theory and networks		Chair: Annachiara Korchmaros	
16:15-16:35	Grover Enrique Castro Guzman	Spectral density for graphs with short cycles	15
16:35-16:55	Bruno Iha	Dealing with uncertainties in bacterial metabolic simulations	15
16:55-17:15	Sissel Banke	Detecting Hypercycles	15
17:15-17:35	Carsten R. Seemann	Something about graphs ;)	15
17:35-17:55	Nico Domschke	Machine learning in chemistry and graph bipartitioning of molecules	15

18:00-20:00 Dinner

Saturday 2023-10-07

Departure			
10:00-14:30		Departure	