

17th Herbstseminar - Schedule

Monday 2019-09-30

Arrival and Registration			
14:00-18:30		Arrival and Registration	

18:30-20:00 Dinner

Opening	Chair: Iris Eckert		
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Opening ceremony of the 17th Herbstseminar			
20:00-20:20			

Tuesday 2019-10-01

Proteomics		Chair: Stephanie Kehr	
15:25-15:45	Florian Eggenhofer	Something about small proteins	15
15:45-16:00	Franziska Reinhardt	Ancestor Reconstruction of Gammaproteoacterial Poly(A) Polymerases	15
16:00-16:20	Florian Mock	protein classification with Deep Learning	15

20 min Break with Coffee and Tea

RNA		Chair: Joerg Fallmann	
16:40-16:45	Sarah Strobel	Terminator Prediction	5
16:45-16:50	Christiane Gärtner	Something about Nanopore RNA sequencing	5
16:50-16:55	Viola Braunmüller	something about self-splicing introns	5
16:55-17:15	Grzegorz Lach	Forbidden motives in RNA structures	15

10 min Break

Genomics		Chair: Jakob Havgaard	
17:25-17:45	Geissler Adrian Sven	BSGatlas: Annotation of genes and transcripts for the Bacillus subtilis genome	15
17:45-18:05	Enrique Gonzalez-Tortuero	Differential gene expression of Bacillus subtilis during fermentation	15
18:05-18:25	Giulia Corsi	Transcriptomic data analysis of neurons (iPSCs) carrying PSEN1 fAD mutations	15
18:25-18:30	Veerendra Gadekar	Total RNA-seq challenges/workflow	5

18:30-20:00 Dinner

Fun with Slides	Chair: Iris Eckert		
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Wednesday 2019-10-02

Workshop: Introduction to the RNAlib interface			
10:00-11:30		Please install the ViennaPackage from https://www.tbi.univie.ac.at/RNA/#download and make sure it is python compatible on your computer system. Further information on the workshop will be given at time.	

Genomics		Chair: Natasha Jorge	
14:55-15:15	Sebastian Krautwurst	RNA modification detection with nanopore sequencing	15
15:15-15:20	Lisa-Marie Barf	Viruses from ancient samples using nanopore sequencing	5
15:20-15:40	Kevin Lamkiewicz	Even EVE has to stand in LINE	15
15:40-16:00	Gabor Balogh	Technical solutions based on a prospective basket trial with combination-therapy for SCC	15

Group Picture	Chair: Nicolas Wieseke
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20 min Break with Coffee and Tea

Graph theory and networks		Chair: Marc Hellmuth	
16:40-17:00	Zhongjie Han	Interpreting the Dynamics of Binding Interactions of snRNA and U1A Using a Coarse-Grained Model	15
17:00-17:20	Carmen Bruckmann	Constructing Event-Labeled Rooted Median Graphs from Generalized Orthology Relations	15
17:20-17:40	Carsten R. Seemann	Characterization of Generalized Fitch Relations, Introducing R-Metrics, and Further Fields	15
17:40-18:00	Tom Hartmann	Edge-Colored Permutations Graphs	15

18:00-20:00 Dinner

non-coding RNAs		Chair: Joerg Fallmann	
20:00-20:20	Iwona Nowak	Structure-specific regulation of RNA expression by MCPIP1 protein	15
20:20-20:40	Cristian Arley Velandia Huerto	Key Structural Patterns of miRNA Family Reconstruction	15
20:40-20:45	Jeong-Eun Lee	A path to find human-specific non-coding RNAs	5
20:45-20:50	Marie Lataretu	scRNAseq analysis of FAPs	5
20:50-20:55	Justus Täger	RNA identification via CNN	5
20:55-21:15	Irene K. Beckmann	RNA-RNA Interaction in 3D - Constrained folding simulations	15

Thursday 2019-10-03

Workshop: Introduction to the RNAlib interface			
10:00-11:30		Please install the ViennaPackage from https://www.tbi.univie.ac.at/RNA/#download and make sure it is python compatible on your computer system. Further information on the workshop will be given at time.	

non-coding RNAs		Chair: Stephan Bernhart	
15:15-15:45	Michal Boniecki	SimRNA: a coarse-grained method for RNA 3D structure modeling - new ideas accounting for non-canonical base pairing	25
15:45-16:05	Maria Waldl	Bi-alignments as models of incongruent evolution of RNA sequence and structure	15
16:05-16:25	Milad Miladi	Something about RNA dotplots	15

20 min Break with Coffee and Tea

Genomics		Chair: Ronny Lorenz	
16:45-17:15	Ulisses Rocha	From hypothesis to microbial community omics data and back	25
17:15-17:35	Joao Pedro Saraiva	OrtAn ? improving functional annotation of clusters of ortholog groups	15
17:35-17:55	Felipe Borim Corrêa	From microbial big data to functional capacity of microbial communities	15
17:55-18:00	Nora Grieb	Method evaluation of clustering of transcriptomic fingerprints	5

18:00-22:00 Conference Dinner

Friday 2019-10-04

240 min Hiking

Graph theory and networks		Chair: Tom Hartmann	
14:55-15:10	Stefan Kraemer	Linking chemical exposure to transcriptomic effects	15
15:10-15:30	David Schaller	Inference of Best Matches from Evolutionary Distance Data	15
15:30-15:50	Angel Eduardo Rodríguez Fernández	To be announced	15

20 min Break with Coffee and Tea

Algorithmics		Chair: Nicolas Wieseke	
16:10-16:30	Felix Kühnl	BarMap-QA: cotranscriptional folding with quality assurance	15
16:30-17:00	Thomas Gatter	New Strategies in Assembly	25
17:00-17:30	Peter Stadler	Aligning stuff that is not just a sequence or a tree	25

18:00-20:00 Dinner

Saturday 2019-10-05

Departure			
08:00-11:00		Departure	