## 38th TBI WINTERSEMINAR

#### Day1 - 2023/02/12

5pm-12pm Arrival

### Day2 - 2023/02/13

11am-12pm Welcome notes and dinner planning

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3pm-6pm Session I – Computational Biology / RNA Structure

Chair: Stephan Bernhart

3pm-3:20pm PEVO basket trial, combining immunotherapy with an epidrug in squamous

 $\begin{array}{c} \textbf{cell carcinomas} \\ \textit{Gabor Balogh} \end{array}$ 

3:20pm-3:40pm CRISPR-Cas and associated RNA secondary structures

 $Maximilian\ Feussner$ 

3:55pm-4:15pm Computational estimation of energy parameters

 $Thomas\ Spicher$ 

4:15pm-4:35pm The effect of modified nucleotides on secondary structure prediction in tRNA

Yuliia Varenyk

5pm-5:20pm RNA-RNA interaction dynamics

Maria Waldl

5:20pm-5:40pm Salt concentration correction in ViennaRNA package

Hua-Ting Yao

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8pm-10pm Session II - Graph Theory

Chair: Daniel Merkle

8pm-8:20pm Approximate Graph Products

Wilfried Imrich

 $8:20 \mathrm{pm} - 8:40 \mathrm{pm}$  Nut graphs are not edge transitive

Nino Bašić

8:40pm-9pm On vertex-transitive nut graphs that are noticrculant graphs

Tomaž Pisanski

9:15pm-9:35pm k-Median Graphs

 $Sandhya\ Thekkumpadan\ Puthiyaveedu$ 

#### Day3 - 2023/02/14

3pm-6:15pm Session III – Phylogeny / Transcriptomics

Chair: Jan Gorodkin

3pm-3:25pm A quartet-based approach to infer phylogenetically informative characters

from phenotypic data

Ben Luis Hack

3:25pm-3:35pm	A quartet-based approach to inferphylogenetically informative characters from phenotypic data  Vivian Brandenburg	
3:35pm-3:55pm	Evolution of Neuropeptide Y/R Famide-likereceptors in Nematodes $\it Franziska\ Reinhardt$	
4:10pm-4:30pm	Evolution of the CCA-adding Enzyme in early-branchingMetazoa Elisa Israel	
4:30pm-4:50pm	Magnipore: Differential single nucleotide changes of ONT signals  Jannes Spangenberg	
4:50pm-5:10pm	DNA methylation analysis using Nanopore sequencing  Daria Meyer	
5:30pm-5:55pm	Locus-specific expression analysis of TransposableElements Robert Schwarz	
5:55pm-6:15pm	The impact of methylation patterns in lymphoma onallele-specific expression Christiane Gärtner	
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8pm-10pm	Session IV – Graph Theory / Cheminfo Chair: Peter Stadler	
8pm-8:10pm	TACsy: Training Alliance for Comput-ational SystemsChemistry  Daniel Merkle	
8:10pm-8:30pm	Atom Transition Networks for Atom Tracing  Nora Beier	
8:30pm-8:50pm	A Petri-Net Based Framework for Atom-Tracingin Chemical Networks  Casper Asbjørn Eriksen	
9:05pm-9:25pm	Synthesizability of molecules Nico Domschke	
9:25pm-9:45pm	Comparison of Atom Maps  Marcos Laffitte	
9:45pm-10pm	An Application of Graph Products in Rule Inference $Akbar\ Davoodi$	
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# $\underline{D_{AY4} - 2023/02/15}$

8pm-10pm	Session V – Genomics / Other Chair: Sven Findeiß
8pm-8:20pm	Nonretroviral RNA viruses integrated into the humangenome
	Muriel Ritsch
8:20 pm - 8:40 pm	Bashing irreproducibility with shournal
	Tycho Kirchner
9 pm - 9:30 pm	Theory is Dead! Long Live Theory!
	Axel Mosig

# Day5 - 2023/02/16

3pm-6pm	Session VI – Graph Theory Chair: Josef Leydold
3pm-3:20pm	Promoters revisited
	Elina Wiechens
3:20 pm - 3:30 pm	Bubble Structures in Digraphs
	Lena Gladbach

Annachiara Korchmaros 4:10pm-4:30pm Directed Permutation Graphs Bruno Schmidt 4:30pm-4:50pm **Nesting of Polygons** Carsten R. Seemann 4:50pm-5:10pm CORENET: Complex chemical reaction networks for breakthrough scalable reservoir computing Mehmet Aziz Yirik 5:30pm-6pm Randomization of chemical reaction networks Christoph Flamm \* \* \* 8pm-10:10pm Session VII – Bioinformatics Chair: Ivo Hofacker 8pm-8:20pm Bashbone: NGS Bash library Konstantin Riege 8:20pm-8:30pm VirJenDB: the virus genome database based at FSUJena  $Shahram\ Saghaei$ 8:30pm-8:55pm Automated gating of flow cytometry data Carmen Bruckmann 9:10pm-9:30pm Differential analysis of RNA cross-linkedHTS reads with RNAswarm  $Gabriel\ Lencioni\ Lovate$ 9:30pm-9:50pm Approaching RNA-protein interaction predictionsfrom an evolutionary perspective using co-alignments Sarah Krautwurst 9:50pm-10:10pm Prediction of base editing outcomes by deep learning Ying Sun Day6 - 2023/02/1710am-1pm Session VII – Genomics Chair: Steve Hoffmann 10am-10:20am Screen for conserved RNA structures in cyanobacteria Adrian Geissler 10:20am-10:40am De-novo canonical microRNA annotation: Insightsusing iterative models Cristian Velandia 10:40am-11am Genome regulation by tumor suppressors and oncoproteins Martin Fischer 11:15am-11:30am Deciphering the molecular causes of exceptional aging phenomens in the animal kingdom by applying multi-omics Arne Sahm 11:30am-11:50am Annotation-free Identification of Synteny Anchors Karl Kaether 11:50pm-12:10pm Genomics on a Shoestring Budget Thomas Gatter

3:30pm-3:50pm Quasi Best Match Graphs