

Pangenome sequencing and analysis

Program

Monday, September 5

10:10 - 11:10 WABI Session on k-mer Sets

14:00 - 15:00 WABI Session on Succinct Data Structures

Tuesday, September 6

8:50 - 9:50 WABI Session on BWT-like Data Structures

Wednesday, September 7

8:50 - 9:50 WABI Session on Indexing Genomes

11:30 - 12:30 Leena Salmela: Efficient solutions to biological problems using de Bruijn graphs

14:00 - 15:00 Knut Reinert: Hierarchical Interleaved Bloom Filter: Enabling ultrafast, approximate sequence queries

and ALPACA business meeting (Alexander Schönhuth)

15:20 - 16:20 PANGAIA network meeting, part I (Paola Bonizzoni)

16:30 - 21:30 Social event: Boat tour including dinner and drinks
(register by email to jens.stoye@uni-bielefeld.de)

Thursday, September 8

8:50 - 9:50 PANGAIA network meeting, part II (Paola Bonizzoni)

10:10 - 11:10 Camille Marchet: Round table discussion: how to improve communication with your advisors, and a few other items about wellness at work

and **Mathias Weller:** Peer Community in bioinformatics: a new approach to reviewing and publishing

11:30 - 12:30 Christina Boucher: Computational Problems in Metagenomic Amplification

14:00 - 15:00 Erin K. Molloy: Recent advances and open challenges in estimating evolutionary histories from low-homoplasy markers

and **Rayan Chikhi:** Metagenome assembly and analysis

15:20 - 16:20 Paul Medvedev: The theoretical analysis of sequencing bioinformatic algorithms

16:40 - 18:00 Open problems session (Travis Gagie)

Friday, September 9

8:50 - 9:50 Hackathon, part I (Rayan Chikhi)

10:10 - 11:10 Hackathon, part II (Rayan Chikhi)

11:30 - 12:30 Gene Myers: High Fidelity Genome Sequencing: What have we been missing?
Closing remarks