

DSB - 2020

Tuesday, Feb 4

- **9:15** Welcome all - few technical information
- **9:30** *Cost-optimal assignment of elements in genome-scale multi-way bucketed Cuckoo hash tables* Jens Zentgraf, Henning Timm and Sven Rahmann
- **10:00** *Faster Xenograft Sorting with 3-Way Bucketed Cuckoo Hashing of k-mers* Jens Zentgraf and Sven Rahmann
- **11:00** *Efficient and scalable representation of k-mer sets using simplitigs and spectrum-preserving string sets* Amatur Rahman, Paul Medvedev, Karel Brinda, Michael Baym and Gregory Kucherov
- **11:30** *REINDEER: efficient indexing of k-mer presence and abundance in sequencing datasets* Camille Marchet, Zamin Iqbal, Mikaël Salson and Rayan Chikhi
- **13:30** *Hierarchical Organization of Syntenic Blocks in Large Genomic Datasets* Daniel Doerr
- **14:00** *viaDBG - Fast and accurate approach for viralquasispecies inference* Borja Freire, Susana Ladra, José Ramón Paramá and Leena Salmela
- **14:30** *Space-efficient indexing of spaced seeds for accurate overlap computation of raw optical mapping data* Riku Walve, Simon Puglisi and Leena Salmela
- **15:30** *Computing longest common substring with k mismatches: Theory and practice* Garance Gourdel, Tomasz Kociumaka, Jakub Radoszewski and Tatiana Starikovskaya
- **16:00** [Work In Progress] *BCash: Best Compressible Hash* Antoine Limasset
- **16:30** [Work In Progress] *HowDeSBT and Simka wedding. What has been done and what we plan to do* Téo Lemane, Paul Medvedev, Rayan Chikhi, Pierre Peterlongo

Wednesday, Feb 5

- **9:00** *In-Place Bijective Burrows Wheeler Transformations* Dominik Köppl, Daiki Hashimoto, Diptarama Hendrian and Ayumi Shinohara
- **9:30** [Work In Progress] *Dynamic quasi-minimal perfect hash function for k-mers* Paola Bonizzoni, Luca Denti, Erik Garrison, Yuri Pirola and Marco Previtali
- **10:00** *Million sequences indexing* Antoine Limasset
- **11:00** *Optical map guided genome assembly* Miika Leinonen and Leena Salmela
- **11:30** *srnaMapper: a mapping tool for short-RNA sequencing* Matthias Zytnicki
- **12:00** *Shark: fishing in a sample to discard irrelevant RNA-Seq reads* Paola Bonizzoni,

Tamara Ceccato, Gianluca Della Vedova, Luca Denti, Yuri Pirola, Marco Previtali and Raffaella Rizzi

- **13:30** *HASLR: Fast Hybrid Assembly of Long Reads* Ehsan Haghshenas, Hossein Asghari, Jens Stoye, Cedric Chauve, Faraz Hach
- **14:00** *Reference independent somatic structural variant call* Taiki Yamada, Kenichi Chiba, Nozomi Hasegawa, Keisuke Kataoka, Yuichi Shiraishi and Kana Shimizu
- **14:30** [Work In Progress] *Superstring Graph in compact space* Bastien Cazaux and Eric Rivals