

Program DSB 2020 - Rennes - France

Monday, Feb 3

- Welcome evening, from 6.30 pm [Shamrock](http://www.leshamrockrennes.com) pub <http://www.leshamrockrennes.com>

Tuesday, Feb 4 [Inria/Irisa Campus de Beaulieu](http://www.irisa.fr/en/access-map) - Room Petri/Turing <http://www.irisa.fr/en/access-map>

- **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
- **10:30 Coffee break**
- **11:00**
Optical map guided genome assembly
Miika Leinonen and Leena Salmela
- **11:30** (two combined talks) *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
- **12:30 Lunch**
- **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
- **15:00 Coffee break**
- **15:30** [WIP] *HowDeSBT and Simka wedding. What has been done and what we plan to do* Téo Lemane, Paul Medvedev, Pierre Peterlongo
- **16:00** [WIP]
BCash: Best Compressible Hash Antoine Limasset
- **16:30** *TBA* Tatiana Starikovskaya
- **17:00** Time for discussion
- **19:00** Diner at restaurant "[Origines](http://origines-rennes.fr/)" Hotel Dieu <http://origines-rennes.fr/>

Tuesday, Feb 5 [Inria/Irisa Campus de Beaulieu](http://www.irisa.fr/en/access-map) - Room Petri/Turing <http://www.irisa.fr/en/access-map>

- **9:00** *In-Place Bijective Burrows Wheeler Transformations* Dominik Köppl, Daiki Hashimoto, Diptarama Hendrian and Ayumi Shinohara
- **9:30** *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
- **10:30 Coffee break**
- **11:00**
REINDEER: efficient indexing of k-mer presence and abundance in sequencing datasets
Camille Marchet, Zamin Iqbal, Mikaël Salson and Rayan Chikhi
- **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
- **12:30 Lunch**
- **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** TBA
Bastien Cazau
- **15:00** Final Coffee break and *ad libitum* discussions