

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**
REINDEER: efficient indexing of k-mer presence and abundance in sequencing datasets*
Camille Marchet, Zamin Iqbal, Mikaël Salson and Rayan Chikhi
- **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**

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

- **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