Program DSB 2020 - Rennes - France

Monday, Feb 3

• Welcome evening, from 6.30 pm <u>Shamrock</u> pub <u>http://www.leshamrockrennes.com</u>

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

- 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

- 12:00 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

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, Pierre Peterlongo

- **17:00** Time for discussion
- 19:00 Diner at restaurant "Origines" Hotel Dieu http://origines-rennes.fr/

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

• 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

• 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

Superstring Graph in compact space

Bastien Cazaux and Eric Rivals

• **15:00** Final Coffee break and *ad libitum* discussions