AlCoB 2020 & 2021

International Conference on Algorithms for Computational Biology

Missoula, November 9-11, 2021 (virtual)

Tuesday, November 9

09:30 - 09:40 Opening

09:40 - 10:30 **Tamar Schlick**. Biomolecular Modeling and Simulation Thriving in the Age of Technology - Invited lecture

10:50 - 12:05
Hannah Brown, Lei Zuo, and Dan Gusfield. Comparing Integer Linear Programming to SAT-solving for Hard Problems in Computational and Systems Biology

Md Momin Al Aziz, Parimala Thulasiraman, and Noman Mohammed. Parallel Generalized Suffix Tree Construction for Genomic Data

Andre Rodrigues Oliveira, Géraldine Jean, Guillaume Fertin, **Klairton Lima Brito**, Ulisses Dias, and Zanoni Dias. A 3.5-Approximation Algorithm for Sorting by Intergenic Transpositions

12:25 - 13:40
Gabriel Siqueira, **Klairton Lima Brito**, **Ulisses Dias**, and Zanoni Dias. Heuristics for Reversal Distance between Genomes with Duplicated Genes

Lucia Williams and **Brendan Mumey**. Extending Maximal Perfect Haplotype Blocks to the Realm of Pangenomics

Zhe Yu, Chunfang Zheng, and **David Sankoff**. Gaps and Runs in Syntenic Alignments a

14:00 - 15:15

Remie Janssen, Mark Jones, and **Yukihiro Murakami**. Combining Networks Using Cherry Picking Sequences

Remie Janssen and **Yukihiro Murakami**. Linear Time Algorithm for Tree-child Network Containment

Mohsen Katebi, Pedro Feijao, Julius Booth, Mehrdad Mansouri, Sean La, **Alex Sweeten**, Reza Miraskarshahi, Matthew Nguyen, Johnathan Wong, William Hsiao, Cedric Chauve, and Leonid Chindelevitch. PathOGiST: A Novel Method for Clustering Pathogen Isolates by Combining Multiple Genotyping Signals

15:35 - 16:05

Tathagata Debnath and **Mingzhou Song**. Local Clustering inside a Genome

Matthew Hayes, Derrick Mullins, and Angela Nguyen. Complex Germline Structural Variant Discovery via Discordant Cluster Normalization

<mark>Nick Steinauer, Chun Guo, and **Jinsong Zhang**. Deciphering Gene Regulatory Networks via Logistic Regression of Cistromic and Transcriptomic Features in Disease Models</mark>

(published in Steinauer N, et al. (2021) *Computational modeling of gene-specific transcriptional repression, activation and chromatin interactions in leukemogenesis by LASSO-regularized logistic regression.* **IEEE/ACM Transactions on Computational Biology and Bioinformatics.** 2021 May 7;PP. doi: 10.1109/TCBB.2021.3078128. Online ahead of print)