Conference Agenda

RT Regular Talk **HT Highlight Talk**

Monday – September 4th

7:30 pm	**Registration**
8:15 am	**Opening Remarks**
	Session 1: Phylogenetics **Chair: Mohammed El-Kebir**
8:25 am	**Short welcome message by PC chairs**
8:30 am	**RT (WABI-[002]):** *EMMA: Adding Sequences into a Constraint Alignment with High Accuracy and Scalability.* Authors: Chengze Shen, Baqiao Liu, Kelly P. Williams, and Tandy Warnow
9:00 am	**RT (WABI-[003]):** *BATCH-SCAMPP: Scaling phylogenetic placement methods to place many sequences* Authors: Eleanor Wedell, Chengze Shen, and Tandy Warnow
9:30 am	**RT (WABI-[004]):** *Optimal Subtree Prune and Regraft for Quartet Score in Sub-quadratic Time* Authors: Shayesteh Arasti and Siavash Mirarab
10:00 am	**RT (WABI-[005]):** *Leveraging constraints plus dynamic programming for the large Dollo parsimony problem* Authors: Junyan Dai, Tobias Rubel, Yunheng Han, and Erin K. Molloy
10:30 am	**Break**
	Session 2: Networks – Cancer phylogenetics **Chair: Christina Boucher**
10:50am	**RT (WABI-[007]):** *Making a Network Orchard by Adding Leaves* Authors: Leo van Iersel, Mark Jones, Esther Julien, and Yukihiro Murakami
11:20 am	**RT (WABI-[008]):** *Quartets enable statistically consistent estimation of cell lineage trees under an unbiased error and missingness model* Authors: Yunheng Han and Erin K. Molloy
11:50 pm	**RT (WABI-[009]):** *Inferring Temporally Consistent Migration Histories* Authors: Mrinmoy Saha Roddur, Sagi Snir, and Mohammed El-Kebir
12:20 pm	**Lunch**
	Session 3: Reconciliation – Genome rearrangement - Planning **Chair: Yukihiro Murakami**
1:30 pm	**RT (WABI-[006]):** *Simultaneous reconstruction of duplication episodes and gene-species mappings* Authors: Paweł Górecki, Natalia Rutecka, Agnieszka Mykowiecka, and Jarosław Paszek
2:00 pm	**RT (WABI-[022]):** *Bridging Disparate Views on the DCJ-indel model for a Capping-free Solution to the Natural Distance Problem* Authors: Leonard Bohnenkämper
2:30 pm	**RT (WABI-[023]):** *Reinforcement Learning for Robotic Liquid Handler Planning* Authors: Mohsen Ferdosi, Yuejun Ge, and Carl Kingsford
3:00 pm	**Break**
3:30 pm	**Opening Keynote:** Teresa M. Przytycka. *Delineating relation between mutagenic signatures, cellular processes, and environment through computational approaches*
5:00 pm	**General assembly & SIGBIO General Meeting**
6:00 pm	**Poster Session & Reception**
8:00 pm	

Tuesday – September 5th

Session 4: Pattern Matching
Chair: Travis Gagie
8:15 am **RT (WABI-[010]):** *Finding Maximal Exact Matches in Graphs*
Authors: Nicola Rizzo, Manuel Cáceres, and Veli Mäkinen
8:45 am **RT (WABI-[011]):** *Revisiting the Complexity of and Algorithms for the Graph Traversal Edit Distance and Its Variants*
9:15 am Authors: Yutong Qiu, Yihang Shen, and Carl Kingsford
RT (WABI-[012]): *Co-linear Chaining on Pangenome Graphs*
Authors: Jyotshna Rajput, Ghanshyam Chandra, and Chirag Jain

Session of Highlights: Theory and Applications of r-index in Bioinformatics
Chair: Jens Stoye
9:45 am **HT:** *Pangenome Alignment via Recursive Prefix-free Parsing*
Authors: Ben Langmead, Travis Gagie, Marco Oliva, and Christina Boucher
10:15 am **HT:** *The r-index and friends*
Authors: Travis Gagie and friends

10:45 am **Break**

11:00 am **Keynote 2:** Nora Franceschini. *Genomics and Human Population Diversity*

12:00 pm **Lunch**
Session 5: Pattern Matching
Chair: Rob Patro
1:30pm **RT (WABI-[013]):** *Acceleration of FM-index Queries Through Prefix-free Parsing*
Authors: Aaron Hong, Marco Oliva, Dominik Köppl, Hideo Bannai, Christina Boucher, and Travis Gagie
RT (WABI-[014]): *Exact sketch-based read mapping*
2:00 pm Authors: Tizian Schulz and Paul Medvedev
RT (WABI-[015]): *Fractional Hitting Sets for Efficient and Lightweight Genomic Data Sketching*
2:30 pm Authors: Timothé Rouzé, Igor Martayan, Camille Marchet, and Antoine Limasset

3:00 pm **Break**

Session 6: Pattern Matching - Compression
Chair: Erin Molloy
3:30 pm **RT (WABI-[016]):** *Fast, Parallel, and Cache-friendly Suffix Array Construction*
Authors: Jamshed Khan, Tobias Rubel, Laxman Dhulipala, Erin Molloy, and Rob Patro
4:00 pm **RT (WABI-[017]):** *Compression algorithm for colored de Bruijn graphs*
Authors: Amatur Rahman, Yoann Dufresne, and Paul Medvedev
4:30 pm **RT (WABI-[018]):** *Fulgor: A fast and compact k-mer index for large-scale matching and color queries*
Authors: Jason Fan, Noor Pratap Singh, Jamshed Khan, Giulio Ermanno Pibiri, and Rob Patro

6:15 pm **Conference Banquet**
8:00 pm

Wednesday – September 6th

Session 7: RNA Bioinformatics
Chair: Jaroslaw Paszek

09:00 am **RT (WABI-[019]):** *SparseRNAFolD: Sparse RNA pseudoknot-free Folding including Dangles*
Authors: Mateo Gray, Sebastian Will, and Hosna Jabbari

09:30 am **RT (WABI-[020]):** *Automatic exploration of the natural variability of RNA non-canonical geometric patterns with a parameterized sampling technique*
Authors: Théo Boury, Yann Ponty, and Vladimir Reinharz

10:00 am **RT (WABI-[021]):** *Balancing Minimum Free Energy and Codon Adaptation Index for Pareto Optimal RNA Design*
Authors: Xinyu Gu, Yuanyuan Qi, and Mohammed El-Kebir

10:30 am **Break**

11:00 am **Closing Keynote:** Weida Tong. *The Ascent of AI: Predicting Drug-Induced Liver Injury*

12:00 pm **Lunch**

1:30 pm **Session 8: Future WABIs - Your inputs**
Chair: Jens Stoye
Information about WABI 2023; Future plans for WABI

Closing Ceremony

3:00 pm
3:30 pm