

## Combinatorial Problems of Strings and Graphs and Their Applications in Bioinformatics Part 2 (04–15 Apr 2022)

Name and Affiliation	Talk Title
Md. Shamsuzzoha Bayzid Bangladesh University of Engineering and Technology, Bangladesh	Genome-scale species tree estimation from quartets ( <a href="#">Video</a> )
Sankardeep Chakraborty The University of Tokyo, Japan	Succinct data structures for automata with optimal membership query ( <a href="#">Video</a> )
Roberto Grossi Università di Pisa, Italy	Fast assessment of Eulerian trails in graphs, and its relation to sequences ( <a href="#">Video</a> )
Wing-Kai Hon National Tsing Hua University, Hsinchu	FM-Indexing grammars induced by suffix sorting ( <a href="#">Video</a> )
Yu Lin Australian National University, Australia	Binning metagenomic sequences ( <a href="#">Video</a> )
Bernard Moret École Polytechnique Fédérale de Lausanne, Switzerland	Randomized algorithms in computational biology ( <a href="#">Video</a> )
Md. Saidur Rahman Bangladesh University of Engineering and Technology, Bangladesh	Research on pairwise compatibility graphs: current state and open problems ( <a href="#">Video</a> )
Sohel Rahman Bangladesh University of Engineering and Technology, Bangladesh	Phylogeny-aware MO optimization approach for computing MSA ( <a href="#">Video</a> )
Mingfu Shao Pennsylvania State University, USA	SubseqHash and its applications in error-prone long reads analysis ( <a href="#">Video</a> )

Name and Affiliation	Talk Title
Tetsuo Shibuya The University of Tokyo, Japan	Differentially private methods in bioinformatics ( <a href="#">Video</a> )
Yanni Sun City University of Hong Kong, China	Charactering viral haplotypes using long reads ( <a href="#">Video</a> )
Krister Swenson LIRMM and CNRS, France	Using quadrangulations and planar trees for weighted genome rearrangement ( <a href="#">Video</a> )
Yufeng Wu University of Connecticut, USA	Probability computation for trees and networks under coalescent theory ( <a href="#">Video</a> )
Han Xu MD Anderson Cancer Center, USA	Modeling and prediction of CRISPR/Cas9 sensitivity and specificity ( <a href="#">Video</a> )
Louxin Zhang National University of Singapore, Singapore	The Sackin index of simplex networks ( <a href="#">Video</a> )
Xiuwei Zhang Georgia Institute of Technology, USA	Reconstructing cell lineage tree using single cell lineage barcode and gene expression data ( <a href="#">Video</a> )