

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

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