

**Combinatorial Problems of Strings and Graphs  
and Their Applications in Bioinformatics  
Part 2  
Workshop  
(6–7 April 2022)**



\*[Registration](#) is required for this program.

**Venue**

Hybrid

Virtual: The details and link will be sent to you before the program commences after registration has been processed.



**ORGANIZING  
COMMITTEE**

**Co-Chairs**

**Kwok Pui Choi**  
National University of Singapore

**Sohel Rahman**  
Bangladesh University of Engineering &  
Technology

**Vaibhav Rajan**  
National University of Singapore

**Kunihiko Sadakane**  
The University of Tokyo

**Wing-Kin Sung, Ken**  
National University of Singapore

For more information: [Click here](#)

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All times are indicated in **GMT+8**.  
For time zones conversion: [Click Here](#)

GMT Time Reference						
Greenwich Mean Time (GMT+0)	USA (Hawaii) (GMT -10)*	France Italy Switzerland (GMT +2)	Bangladesh (GMT +6)	China Singapore Taiwan (GMT +8)	Japan (GMT +9)	Australia (GMT +10)
0100	1500	0300	0700	0900	1000	1100
0600	2000	0800	1200	1400	1500	1600

\*(GMT -10) is the day before the stated date of the morning talks (GMT+8).

Wednesday, 06 April 2022		
Time (GMT +8)	Title	Speaker
<b>0900</b>	<b>Session Chair: Vaibhav Rajan (National University of Singapore)</b>	
0900–0930	Randomized algorithms in computational biology	Bernard Moret École Polytechnique Fédérale de Lausanne, Switzerland
0930–1000	Binning metagenomic sequences	Yu Lin Australian National University, Australia
1000–1030	Modeling and prediction of CRISPR/Cas9 sensitivity and specificity	Han Xu MD Anderson Cancer Center, USA
1030–1100	Succinct data structures for automata with optimal membership query	Sankardeep Chakraborty The University of Tokyo, Japan
1100–1130	Differentially private methods in bioinformatics	Tetsuo Shibuya The University of Tokyo, Japan
1130–1430	Lunch Break	
<b>1430</b>	<b>Session Chair: Wing-Kin Sung, Ken (National University of Singapore)</b>	
1430–1500	Phylogeny-aware MO optimization approach for computing MSA	Sohel Rahman Bangladesh University of Engineering and Technology, Bangladesh

Wednesday, 06 April 2022		
Time (GMT +8)	Title	Speaker
1500–1530	FM-Indexing grammars induced by suffix sorting	Wing-Kai Hon National Tsing Hua University, Hsinchu
1530–1600	Fast assessment of Eulerian trails in graphs, and its relation to sequences	Roberto Grossi Università di Pisa, Italy
1600–1630	Charactering viral haplotypes using long reads	Yanni Sun City University of Hong Kong, China

Thursday, 07 April 2022		
Time (GMT +8)	Title	Speaker
<b>0900</b>	<b>Session Chair: Wing-Kin Sung, Ken (National University of Singapore)</b>	
0900–0930	Reconstructing cell lineage tree using single cell lineage barcode and gene expression data	Xiuwei Zhang Georgia Institute of Technology, USA
0930–1000	SubseqHash and its applications in error-prone long reads analysis	Mingfu Shao Pennsylvania State University, USA
1000–1030	Probability computation for trees and networks under coalescent theory	Yufeng Wu University of Connecticut, USA
1030–1100	Using quadrangulations and planar trees for weighted genome rearrangement	Krister Swenson LIRMM and CNRS, France
1100–1130	The Sackin index of simplex networks	Louxin Zhang National University of Singapore, Singapore
1130–1400	Lunch Break	
<b>1400</b>	<b>Session Chair: Sohel Rahman (Bangladesh University of Engineering &amp; Technology)</b>	
1400–1430	Research on pairwise compatibility graphs: current state and open problems	Md. Saidur Rahman Bangladesh University of Engineering and Technology, Bangladesh
1430–1500	Genome-scale species tree estimation from quartets	Md. Shamsuzzoha Bayzid Bangladesh University of Engineering and Technology, Bangladesh