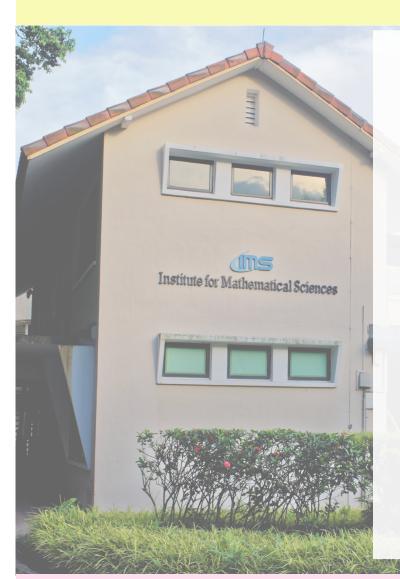# Computational Approaches to the Analysis of Biomolecular Sequences, Structures and Their Functions and Applications to Biotechnology and Clinical Data Studies

(26 - 27 Mar 2020)

ORGANIZING COMMITTEE

Co-Chairs

Igor N. Berezovsky
Bioinformatics Institute (BII) - A*Star

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Computational Approaches to the Analysis of Biomolecular Sequences, Structures and Their Functions and Applications to Biotechnology and Clinical Data Studies

(23 - 27 Mar 2020)

conducted via Zoom

Thursday, 26 Mar 2020

Time	Title	Speaker
1100	Chair: Lars Nordenskiöld, Nanyang Technological University, Singapore	
1100 - 1200	Multiscale modelling approaches to large systems in biology: understanding infectious diseases and the host response	Peter J. Bond Bioinformatics Institute - A*Star, Singapore
1200 - 1330	Lunch Break	
1330	Chair: Chair: Igor N. Berezovsky, Bioinformatics Institute - A*Star, Singapore	
1330 - 1430	Multiscale modeling of macromolecular systems by structure-based coarse-graining	Alexander Lyubartsev Stockholm University, Sweden
1430 - 1500	Coffee Break	
1500 - 1600	Whole viral particle metastability and dynamics by HDX mass spectrometry	Ganesh Srinivasan Anand National University of Singapore, Singapore
1600 - 1615	To bind or not to bind: IgM versus IgG in Pertuzumab and Trastuzumab	Firdaus Samsudin Bioinformatics Institute - A*Star, Singapore

Friday, 27 Mar 2020

Time	Title	Speaker
0930	Chair: Frank Eisenhaber, Bioinformatics Institute - A*Star, Singapore	
0930 - 1030	Amino acid sequence insertions or deletions inside Mycobacterium tuberculosis's respiratory complexes provide fitness for the pathogen and new pathways for TB-drug development"	Gerhard Grüber Nanyang Technological University, Singapore
1030 - 1100	Coffee Break	
1100 - 1200	A genome assembly quality assessment measure that integrates contiguity, completeness, and correctness	Lim Soon Wong National University of Singapore, Singapore

Friday, 27 Mar 2020		
Time	Title	Speaker
1230 - 1330	Lunch Break	
1330	Chair: Frank Eisenhaber,Bioinformatics Institute - A*Star, Singapore	
1330 - 1430	Tutorial: Reinforcement learning and its biomedical applications	Mahsa Paknezhad Bioinformatics Institute - A*Star, Singapore
1430 - 1500	Coffee Break	
1500 - 1600	Tutorial: Computational imaging with deep learning: biomedical focus	Kaicheng Liang Bioinformatics Institute - A*Star, Singapore
1600 - 1615	Sequence similarity networks: a working model for defining the 'known-unknowns' of gene function in microbiomes	Rohan Williams National University of Singapore, Singapore