Mathematics of Evolution-Phylogenetic Trees and Networks
(04 Sep 2023–29 Sep 2023)

Name & Affiliation	Talk Title
Elizabeth Allman University of Alaska Fairbanks, USA	Identifiability of species networks from multilocus data under the Network Multispecies Coalescent model
Siavash Mir Arabbaygi University of California at San Diego, USA	Non-parametric quartet-based estimation species tree inference
Hector Banos California State University, San Bernardino, USA	Tree of blobs inference under the coalescent model
Francois Bienvenu ETH Zurich, Switzerland	The emergence of branching structures in models of reticulated evolution
Alessandra Carbone Sorbonne Université-CNRS, France	*Keynote* Phylogenetic reconstructions based on chromosomal rearrangements as an alternative at the intrinsic complexity of protein evolution
Siyu Chen Oxford University, UK	Levels of SARS-CoV-2 population exposure are considerably higher than suggested by seroprevalence
Kwok Pui Choi National University of Singapore, Singapore	On the joint distribution of the numbers of cherries and pitchforks for the Ford model
James Degnan University of New Mexico, USA	Model selection for phylogenetic networks data with cross-validation
Vijaykrishna Dhanasekaran The University of Hong Kong, China	Phylodynamics of SARS-CoV-2 in Hong Kong, 2020–2022
Jie Feng Lanzhou University, China	Phylogenetic Supertree of Virus
Mareike Fischer University of Greifswald, Germany	How far is my network from being edge-based? Proximity measures for edgebasedness of unrooted phylogenetic networks
Andrew Francis Western Sydney University, Australia	Labellable phylogenetic networks
Michael Fuchs National Chengchi University, Taipei	Limit laws for patterns in ranked tree-child networks

Name & Affiliation	Talk Title
Philippe Gambette Université Gustave Eiffel, France	A database approach to solve the tree containment problem in phylogenetic networks
Mathieu Gascon Université de Montréal, Canada	Non-binary Tree Reconciliation with Endosymbiotic Gene Transfer
Olivier Gascuel ISYEB–CNRS Muséum National d'Histoire Naturelle, France	Transfer Bootstrap, Robustness of Branch Supports with Respect to Taxon Sampling *Keynote* Drug Resistance Mutations in HIV
Anupam Gautam University of Tübingen, Germany	Exploring the antibiotic resistance potential of the virome in infant metagenome
Bernhard Gittenberger TU Wien, Austria	On the Sackin index of galled trees
Paweł Górecki University of Warsaw, Poland	Inferring phylogenetic networks via minimizing deep coalescence cost
Elizabeth Gross University of Hawaii at Mānoa, USA	Distinguishing level-1 phylogenetic network-based Markov models
Momoko Hayamizu Waseda University, Japan	The structure theorem for rooted binary phylogenetic networks: theory, applications, and challenges
Katharina T. Huber University of East Anglia, UK	Ploidy profiles
Daniel Huson University of Tübingen, Germany	SplitsTree - phylogenetic trees, rooted networks and unrooted networks all in one
Mark Jones TU Delft, Netherlands	Reconstructing semi-directed network topology under Markov models
Elahe Khayatian National University of Singapore, Singapore	The k-Robinson-Foulds distance for comparison of labelled trees
Mark P. Khurana University of Copenhagen, Denmark	The value of high coverage whole genome sequencing of SARS-CoV-2 in Denmark
Tsz Ho Kwan The Chinese University of Hong Kong, China	A network approach for studying HIV molecular epidemiology
Manuel Lafond Université de Sherbrooke, Canada	Inferring horizontal gene transfers on a species phylogeny using character traits

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Jue Tao Lim Nanyang Technological University, Singapore	Synthetic control methods for infectious disease epidemiology: applications to Wolbachia interventions
Simone Linz University of Auckland, New Zealand	Pre-process before computing distances between phylogenetic trees!
Jian Lu Peking University, China	Evolutionary dynamics and lineage designation of SARS-CoV-2 genomes
Bui Quang Minh Australian National University, Australia	MAST: Phylogenetic inference with mixtures across sites and trees
Swapnil Mishra National University of Singapore, Singapore	Genomic characterization and epidemiology of P.1 and Delta SARS-CoV-2 Variants Swapnil
Vincent Moulton University of East Anglia, UK	Computing a consensus for 1-nested phylogenetic networks
Luay Nakhleh Rice University, USA	*Keynote* Beyond Simple Trees: Trees of Clusters (Clonal Trees) and Clusters of Trees (Phylogenetic Networks)
Joan Carles Pons University of the Balearic Islands, Spain	Extended μ-representation for the identification and comparison of orchard phylogenetic networks
Sebastien Roch University of Wisconsin-Madison, USA	Recovering the species tree under lateral gene transfer
Neil Scheidwasser University of Copenhagen, Denmark	Leaping through tree space: continuous inference for phylogenies
Charles Semple University of Canterbury, New Zealand	Finding redundancy in phylogenetic networks
October M. Sessions National University of Singapore, Singapore	Zika virus transmission dynamics and characterisation of naturally occurring mutations in a paediatric cohort during the 2016 Nicaragua epidemic
Jessica E Stockdale Simon Fraser University, Canada	Genomic epidemiology for estimation of serial intervals in COVID-19 transmission clusters
Benedikt Stufler TU Wien, Austria	A branching process approach to level-k phylogenetic networks
Mark M. Tanaka University of New South Wales, Australia	Estimating viral mutation rates in the post-genomic era

Name & Affiliation	Talk Title
Michael Wallner TU Wien, Austria	Stretched exponentials in the asymptotics of phylogenetic networks
Lusheng Wang City University of Hong Kong, China	Computing a Consensus Phylogeny via Leaf Removal
Kristina Wicke New Jersey Institute of Technology, USA	Exploring spaces of semi-directed phylogenetic networks
Aiping Wu, Chinese Academy of Medical Sciences Peking Union Medical College & Suzhou Institute of Systems Medicine, China	Detection and surveillance for genomic variation of SARS-CoV-2
Taoyang Wu University of East Anglia, UK	Planar Phylogenetic Networks
Yufeng Wu University of Connecticut, USA	Algorithms for Inferring the Ancestry of an Admixed Individual
Yifei Xu Shandong University, China	The origin tracing and tracking of emerging influenza A virus and SARS-CoV-2
Barnaby Edward Young National Centre for Infectious Diseases, Singapore	*Keynote* Clinical research during the COVID-19 pandemic. What do we need to do better next time?
Guan-Ru Yu, National Kaohsiung Normal University, Kaohsiung	Bijections for phylogenetic networks
Louxin Zhang National University of Singapore, Singapore	Network Classes and Their Mathematical Properties A Scalable Method for Inferring Phylogenetic Networks from Trees