Statistical Methods in Genetic/Genomic Studies (03 –14 Jan 2022)

*Registration is required for this program.

Venue

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

ORGANIZING COMMITTEE

Co-Chairs

Jialiang Li
National University of Singapore

Jin Liu
National University of Singapore

Indranil Mukhopadhyay
Indian Statistical Institute

Members

Samsiddhi Bhattacharjee
National Institute of Biomedical Genomics

Jian Huang
The University of Iowa

Bani K. Mallick
Texas A&M University

Hongyu Zhao
Yale University

For more information: Click here

Statistical Methods in Genetic/Genomic Studies Workshop

(03 Jan 2022–14 Jan 2022)

All times are indicated in GMT+0.
For time zones conversion: Click Here

GMT Time Reference				
Greenwich Mean Time United Kingdom (+0)	Canada USA (-5)	India (+5:30)	China Hong Kong Singapore (+8)	Australia (+11)
0000	1900	0530	0800	1100
0700	0200	1230	1500	1800
***US Eastern Time is the day before the stated date, 1900 at start of the first talk.**				

Monday, 03 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0750–0800	Opening Remarks	Indranil Mukhopadhyay Indian Statistical Institute, India
0800	Session Chair: Jin Liu (National University of Singapore)	
0800–0900	*Distinguished Visitor Lecture Series* Integrative Analysis of Large-Scale Biobanks and Whole Genome Sequencing Studies	Xihong Lin Harvard University, USA
0900–1000	Methods for Integrating Phenome and Genome Across Electronic Health Records	Nancy Cox Vanderbilt University, USA
1000–1100	Analyzing high-dimensional mediators by mixed integer optimization	Peter Song University of Michigan, USA
1100–1200	Integrating multi-tissue multi-omics QTL with GWAS summary statistics for elucidation of the dynamic molecular mechanisms underlying disease genetics	Lin Chen University of Chicago, USA
1200–1600	*Group Photo & Break*	
1600	Session Chair: Jialiang Li (National University of Singapore)	
1600–1700	Probabilistic partial least squares methods for data integration	Jeanine Houwing-Duistermaat University of Leeds, UK

Monday, 03 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
1700–1800	Harness tumor heterogeneity and evolution for understanding ethnic differences and patient prognosis in cancer	Weiwei Zhai Chinese Academy of Science, China

Tuesday, 04 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Xiang Zhou (University of Michigan)	
0800–0900	Genetic Correlations across Traits and Populations	Hongyu Zhao Yale University, USA
0900–1000	MAST-Decon: Smooth Cell-type Deconvolution Method for Spatial Transcriptomics data	Yun Li University of North Carolina, China
1000–1100	A Deep Generative Approach to Conditional Sampling	Jian Huang University of Iowa, USA
1100–1200	Demystifying the drop-outs in single cell RNA-seq data	Mengjie Chen University of Chicago, USA
1200–1500	*Break*	
1500	Session Chair: Xingjie Shi (East China Normal University)	
1500–1600	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits	Can Yang Hong Kong University of Science and Technology, China
1600–1700	Detecting Local Genetic Correlations with Scan Statistics	Lin Hou Tsinghua University, China
1700–1800	Statistical method for integrative analysis in single-cell genomics	Zhixiang Lin Chinese University of Hong Kong, China

Wednesday, 05 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Mengjie Chen (University of Chicago)	
0800–0900	A Unified Approach to Robust Inference for Genetic Covariance	Hongzhe Lee University of Pennsylvania, USA
0900–1000	DAGBagM: Learning directed acyclic graphs of mixed variables with an application to identify protein biomarkers for treatment response in ovarian cancer	Pei Wang Icahn Medical School at Mount Sinai, USA

Wednesday, 05 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
1000–1100	Fair Generalized Linear Models	Judy Hua Zhong New York University, USA
1100–1200	Statistical analysis of spatial expression pattern for spatially resolved transcriptomic studies	Xiang Zhou University of Michigan, USA
1200–1500	*Break*	
1500	Session Chair: Yuling Jiao (Wuhan University)	
1500–1600	On Mendelian Randomisation Mixed-Scale Treatment Effect Robust Identification (MR MiSTERI) and Estimation for Causal Inference	Zhonghua Liu, Hong Kong University, China
1600–1700	Meta-clustering of Genomic Data	Yingying Wei Chinese University of Hong Kong, China
1700–1800	Spatial clustering for identifying tissue regions defined by spatial transcriptomics	Xingjie Shi East Normal University, China

Thursday, 06 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Pei Wang (Icahn School of Medicine at Mount Sinai)	
0800–0900	Gaussian graphical model-based heterogeneity analysis via penalized fusion	Shuangge Ma Yale University, USA
0900–1000	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomic Data	Li Hsu Fred Hutchinson Cancer Research Center, USA
1000–1100	A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples	Hongkai Ji Johns Hopkins University, USA
1100–1200	Robust Mendelian Randomization via Constrained Maximum Likelihood	Wei Pan University of Minnesota, USA
1200–1500	*Break*	
1500	Session Chair: Can Yang (The Hong Kong University of Science and Technology)	
1500–1600	Causal Inference with Truncation by Death in Observational Study	Andrew Xiaohua Zhou Peking University, China

Thursday, 06 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
1600–1700	A Bayesian network approach incorporating imputation of missing data enables exploratory analysis of complex causal biological relationships	Heather J. Cordell Newcastle University, UK
1700–1800	Deep Nonparametric Estimation	Yuling Jiao Wuhan University, China

Friday, 07 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Jialiang Li (National University of Singapore)	
0800–0900	Deciphering the Transcriptome of the World Trade Center Disaster-Related PTSD via RNA-Seq	Pei-Fen Kuan Stony Brook University, USA
0900–1000	Joint Gene Network Construction by Single-Cell RNA Sequencing Data	Fei Zou University of North Carolina, USA
1000–1100	Sparse Convoluted Rank Regression in High Dimensions	Hui Zou University of Minnesota, USA
1100–1200	Clipper: a general statistical framework for p-value-free FDR control in large-scale feature screening	Jingyi Jessica Li University of California, Los Angeles, USA

Monday, 10 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chairs: Indranil Mukhopadhyay (Indian Statistical Institute) Śaunak Sen (University of Tennessee Health Science Center)	
0800–0900	*Distinguished Visitor Lecture Series* Targeted Learning with Applications to Genomic Studies	Mark van der Laan University of California, Berkeley, USA
0900–1000	Empirical Bayes and the false discovery rate, revisited	Michael Newton University of Wisconsin-Madison, USA
1000–1100	Recent advances in p-value combination methods with emphasis on omics applications	George C. Tseng University of Pittsburgh, USA
1100–1200	Sparse bilinear models for structured high-throughput data	Śaunak Sen University of Tennessee Health Science Center, USA

Monday, 10 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
1200–1500	*Group Photo & Break*	
1500	Session Chair: Partha P. Majumder (National Institute of Biomedical Genomics)	
1500–1600	Statistical Approaches to Incorporating Prior Knowledge for Multiple-Testing and Variable-selection in Genomic Studies	Samsiddhi Bhattacharjee National Institute of Biomedical Genomics, India
1600–1700	Phenotypic and genetic profiling of exceptionally long-lived individuals	Anbupalam Thalamuthu University of New South Wales, Sydney, Australia
1700–1800	Joint analysis of multi-omics data: Some applications	Partha P. Majumder National Institute of Biomedical Genomics, India

Tuesday, 11 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Indranil Mukhopadhyay (Indian Statistical Institute)	
0800–0900	Ordinal Causal Discovery for Reverse-Engineering Gene Regulatory Networks	Yang Ni Texas A&M University, USA
0900–1000	A simple new approach to variable selection in regression, with application to genetic fine-mapping	Matthew Stephens University of Chicago, USA
1000–1100	Scalable Bayesian Variable Selection for Structured High-Dimensional Data	Suprateek Kundu The University of Texasat MD Anderson Cancer Center , USA
1100–1200	Fancy and powerful study design is cost beneficial only coupled with valid or versatile statistical approaches	Guolian Kang St. Jude Children's Research Hospital, USA
1200–1500	*Break*	
1500	Session Chair: Terry Speed (The Walter and Eliza Hall Institute of Medical Research)	
1500–1600	RUV-III: Removing Unwanted Variation in III steps	Terry Speed The Walter and Eliza Hall Institute of Medical Research, USA
1600–1700	RUV-III-NB: Normalization of single-cell RNA-seq Data	Agus Salim University of Melbourne, Australia
1700–1800	Removing unwanted variation from large-scale cancer RNA-sequencing data	Ramyar Molania The Walter and Eliza Hall Institute of Medical Research, USA

Wednesday, 12 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Eleanor Feingold (University of Pittsburgh)	
0800–0900	Are there still open statistical questions in modern genomics?	Eleanor Feingold University of Pittsburgh, USA
0900–1000	Personalized Integrated Network Estimation	Veera Baladandayuthapani University of Michigan, USA
1000–1100	Genomic Determination Index	Cheng Cheng St. Jude Children's Research Hospital, USA
1100–1200	Systematic spatial modeling of the heterogeneity in tumor signaling landscapes	Saumyadipta Pyne University of California, Santa Barbara, USA
1200–1500	*Break*	
1500	Session Chair: Mayetri Gupta (University of Glasgow)	
1500–1600	Bayesian structural equation modeling in multiple omics data integration with application to circadian genes	Arnab Kumar Maity Pfizer Inc., USA
1600–1700	Bayesian hierarchical mixture-based clustering for non-normal, noisy genomic datasets	Mayetri Gupta University of Glasgow, UK
1700–1800	Bayesian Nonlinear EM Based Approach for Analysis of Multi-Platform Genomics Data	Sounak Chakraborty University of Missouri, USA

Thursday, 13 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0800	Session Chair: Derek Gordon (Rutgers University)	
0800–0900	Top-Down Integrative Genomics for Colon Cancer Precision Therapeutics	Jeffrey S. Morris University of Pennsylvania, USA
0900–1000	Quantifying the reversible relationship between obesity and diabetes using bidirectional mediation models and Approaches for bi-directional Mendelian Randomization	Sanjay S. Shete M. D. Anderson Cancer Center, USA
1000–1100	High Throughput Proteomics to Basic and Clinic Research	Junmin Peng St. Jude Children's Research Hospital, USA

Thursday, 13 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
1100–1200	Impact of Heterogeneity on Genetic Association Sample size	Derek Gordon Rutgers University, USA

Friday, 14 Jan 2022		
Time* (GMT +8)	**Title**	**Speaker**
0830	Session Chair: Saonli Basu (University of Minnesota)	
0830–0900	Multi-omics data analysis in complex human diseases	Qi Yan Columbia University, USA
0900–1000	Statistical Analysis of single cell RNA sequencing (ScRNA-seq) data	Susmita Datta University of Florida, USA
1000–1100	Estimating SNP heritability in presence of population substructure in biobank-scale datasets	Saonli Basu University of Minnesota, USA
1100–1200	A joint nested random effects model for metagenomic trajectory analysis with disease outcome in matched sets	Qian Li St. Jude Children's Research Hospital, USA