

## Statistical Methods in Genetic/Genomic Studies (3–14 January 2022)

Name and Affiliation	Talk Title
Veera Baladandayuthapani University of Michigan, USA	Personalized Integrated Network Estimation ( <a href="#">Video</a> )
Saonli Basu University of Minnesota, USA	Estimating SNP heritability in presence of population substructure in biobank-scale datasets ( <a href="#">Video</a> )
Samsiddhi Bhattacharjee National Institute of Biomedical Genomics, India	Statistical Approaches to Incorporating Prior Knowledge for Multiple-Testing and Variable-selection in Genomic Studies
Sounak Chakraborty University of Missouri, USA	Bayesian Nonlinear EM Based Approach for Analysis of Multi-Platform Genomics Data ( <a href="#">Video</a> )
Lin Chen University of Chicago, USA	Integrating multi-tissue multi-omics QTL with GWAS summary statistics for elucidation of the dynamic molecular mechanisms underlying disease genetics ( <a href="#">Video</a> )
Mengjie Chen University of Chicago, USA	Demystifying the drop-outs in single cell RNA-seq data ( <a href="#">Video</a> )
Cheng Cheng St. Jude Children's Research Hospital, USA	Genomic Determination Index ( <a href="#">Video</a> )
Heather J. Cordell Newcastle University, UK	A Bayesian network approach incorporating imputation of missing data enables exploratory analysis of complex causal biological relationships ( <a href="#">Video</a> )
Nancy Cox Vanderbilt University, USA	Methods for Integrating Phenome and Genome Across Electronic Health Records ( <a href="#">Video</a> )
Susmita Datta University of Florida, USA	Statistical Analysis of single cell RNA sequencing (ScRNA-seq) data ( <a href="#">Video</a> )
Eleanor Feingold University of Pittsburgh, USA	Are there still open statistical questions in modern genomics? ( <a href="#">Video</a> )
Derek Gordon Rutgers University, USA	Impact of Heterogeneity on Genetic Association Sample size ( <a href="#">Video</a> )

Name and Affiliation	Talk Title
Mayetri Gupta University of Glasgow, UK	Bayesian hierarchical mixture-based clustering for non-normal, noisy genomic datasets <a href="#">(Video)</a>
Lin Hou Tsinghua University, China	Detecting Local Genetic Correlations with Scan Statistics <a href="#">(Video)</a>
Jeanine Houwing-Duistermaat University of Leeds, UK	Probabilistic partial least squares methods for data integration <a href="#">(Video)</a>
Li Hsu Fred Hutchinson Cancer Research Center, USA	A Mixed-Effects Model for Powerful Association Tests in Integrative Functional Genomic Data <a href="#">(Video)</a>
Jian Huang The University of Iowa, USA	A Deep Generative Approach to Conditional Sampling <a href="#">(Video)</a>
Hongkai Ji Johns Hopkins University, USA	A statistical framework for differential pseudotime analysis with multiple single-cell RNA-seq samples <a href="#">(Video)</a>
Yuling Jiao Wuhan University, China	Deep Nonparametric Estimation <a href="#">(Video)</a>
Guolian Kang St. Jude Children's Research Hospital, USA	Fancy and powerful study design is cost beneficial only coupled with valid or versatile statistical approaches <a href="#">(Video)</a>
Pei-Fen Kuan Stony Brook University, USA	Deciphering the Transcriptome of the World Trade Center Disaster-Related PTSD via RNA-Seq <a href="#">(Video)</a>
Suprateek Kundu The University of Texas at MD Anderson Cancer Center, USA	Scalable Bayesian Variable Selection for Structured High-Dimensional Data <a href="#">(Video)</a>
Mark van der Laan University of California, Berkeley, USA	<i>Distinguished Visitor Lecture Series</i> Targeted Learning with Applications to Genomic Studies <a href="#">(Video)</a>
Hongzhe Lee University of Pennsylvania, USA	A Unified Approach to Robust Inference for Genetic Covariance <a href="#">(Video)</a>
Jingyi Jessica Li University of California, Los Angeles, USA	Clipper: a general statistical framework for p-value-free FDR control in large-scale feature screening <a href="#">(Video)</a>
Qian Li St. Jude Children's Research Hospital, USA	A joint nested random effects model for metagenomic trajectory analysis with disease outcome in matched sets <a href="#">(Video)</a>

Name and Affiliation	Talk Title
Yun Li The University of North Carolina at Chapel Hill, USA	MAST-Decon: Smooth Cell-type Deconvolution Method for Spatial Transcriptomics data <a href="#">(Video)</a>
Xihong Lin Harvard University, USA	<i>Distinguished Visitor Lecture Series</i> Scalable Analysis of Large Multi Ethnic Biobanks and Whole Genome Sequencing Studies <a href="#">(Video)</a>
Zhixiang Lin The Chinese University of Hong Kong, China	Statistical method for integrative analysis in single-cell genomics <a href="#">(Video)</a>
Zhonghua Liu University of Hong Kong, China	On Mendelian Randomisation Mixed-Scale Treatment Effect Robust Identification (MR MiSTERI) and Estimation for Causal Inference <a href="#">(Video)</a>
Shuangge Ma Yale University, USA	Gaussian graphical model-based heterogeneity analysis via penalized fusion <a href="#">(Video)</a>
Arnab Kumar Maity Pfizer Inc., USA	Bayesian structural equation modeling in multiple omics data integration with application to circadian genes <a href="#">(Video)</a>
Partha P. Majumder National Institute of Biomedical Genomics, India	Joint analysis of multi-omics data: Some applications <a href="#">(Video)</a>
Ramyar Molania The Walter and Eliza Hall Institute of Medical Research, USA	Removing unwanted variation from large-scale cancer RNA-sequencing data <a href="#">(Video)</a>
Jeffrey S Morris University of Pennsylvania, USA	Top-Down Integrative Genomics for Colon Cancer Precision Therapeutics <a href="#">(Video)</a>
Michael Newton University of Wisconsin–Madison, USA	Empirical Bayes and the false discovery rate, revisited <a href="#">(Video)</a>
Yang Ni Texas A&M University, USA	Ordinal Causal Discovery for Reverse-Engineering Gene Regulatory Networks <a href="#">(Video)</a>
Wei Pan University of Minnesota, USA	Robust Mendelian Randomization via Constrained Maximum Likelihood <a href="#">(Video)</a>
Junmin Peng St. Jude Children’s Research Hospital, USA	High Throughput Proteomics to Basic and Clinic Research <a href="#">(Video)</a>

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Saumyadipta Pyne University of Pittsburgh, USA	Systematic spatial modeling of the heterogeneity in tumor signaling landscapes ( <a href="#">Slides</a> )
Agus Salim University of Melbourne, Australia	RUV-III-NB: Normalization of single-cell RNA-seq Data ( <a href="#">Video</a> )
Śaunak Sen University of Tennessee Health Science Center, USA	Sparse bilinear models for structured high-throughput data ( <a href="#">Video</a> )
Sanjay S. Shete M. D. Anderson Cancer Center, USA	Quantifying the reversible relationship between obesity and diabetes using bidirectional mediation models and Approaches for bi-directional Mendelian Randomization ( <a href="#">Video</a> )
Xingjie Shi East China Normal University, China	Spatial clustering for identifying tissue regions defined by spatial transcriptomics ( <a href="#">Video</a> )
Peter Song University of Michigan, USA	Analyzing high-dimensional mediators by mixed integer optimization ( <a href="#">Video</a> )
Terry Speed The Walter and Eliza Hall Institute of Medical Research, USA	RUV-III: Removing Unwanted Variation in III steps ( <a href="#">Video</a> )
Mathew Stephens The University of Chicago, USA	A simple new approach to variable selection in regression, with application to genetic fine-mapping ( <a href="#">Video</a> )
Anbupalam Thalamuthu University of New South Wales, Sydney, Australia	Phenotypic and genetic profiling of exceptionally long-lived individuals ( <a href="#">Video</a> )
George C. Tseng University of Pittsburgh, USA	Recent advances in p-value combination methods with emphasis on omics applications ( <a href="#">Video</a> )
Pei Wang Icahn School of Medicine at Mount Sinai, USA	DAGBagM: Learning directed acyclic graphs of mixed variables with an application to identify protein biomarkers for treatment response in ovarian cancer ( <a href="#">Video</a> )
Yingying Wei The Chinese University of Hong Kong, China	Meta-clustering of Genomic Data ( <a href="#">Video</a> )
Qi Yan Columbia University, USA	Multi-omics data analysis in complex human diseases ( <a href="#">Video</a> )

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Can Yang The Hong Kong University of Science and Technology, China	A unified framework for cross-population trait prediction by leveraging the genetic correlation of polygenic traits ( <a href="#">Video</a> )
Weiwei Zhai Chinese Academy of Science, China	Harness tumor heterogeneity and evolution for understanding ethnic differences and patient prognosis in cancer ( <a href="#">Video</a> )
Hongyu Zhao Yale School of Public Health, USA	Genetic Correlations across Traits and Populations ( <a href="#">Video</a> )
Judy Hua Zhong New York University, USA	Fair Generalized Linear Models ( <a href="#">Video</a> )
Andrew Xiaohua Zhou Peking University, China	Causal Inference with Truncation by Death in Observational Study ( <a href="#">Video</a> )
Xiang Zhou University of Michigan, USA	Statistical analysis of spatial expression pattern for spatially resolved transcriptomic studies ( <a href="#">Video</a> )
Fei Zou The University of North Carolina at Chapel Hill, USA	Joint Gene Network Construction by Single-Cell RNA Sequencing Data ( <a href="#">Video</a> )
Hui Zou University of Minnesota, USA	Sparse Convoluted Rank Regression in High Dimensions ( <a href="#">Video</a> )