

DISTINGUISHED LECTURE SERIES

Integrative Analysis of Large-Scale Biobanks and Whole Genome Sequencing Studies

Big data from genome, exposome, and phenome are becoming available at a rapidly increasing rate with no apparent end in sight. Examples include Whole Genome Sequencing data, digital data, and Electronic Health Records (EHRs). A rapidly increasing number of large scale national and institutional biobanks have emerged worldwide. Biobanks integrate genotype, electronic health records, and epidemiological and biomarker data, and is the trend of health science research. In this talk, I will discuss opportunities, analytic tools and resources, and challenges presented by analyzing large scale biobanks and population-based Whole Genome Sequencing (WGS) studies of common and rare genetic variants and EHRs by integrating WGS data with functional multi-omic data. The discussions are illustrated using ongoing large scale whole genome sequencing studies of the Genome Sequencing Program of the National Human Genome Research Institute and the Trans-Omics Precision Medicine Program from the National Heart, Lung and Blood Institute, and the UK Biobank and FinnGen, as well as rare-variant meta-analysis. I will also discuss integrative analysis of different types of data using whole genome causal mediation analysis.



Professor Xihong Lin
Harvard University, USA

2 January 2022, Sunday
7–8pm (GMT-5, Boston USA)

3 January 2022, Monday
8–9am (GMT+8, Singapore)

Virtual via Zoom



Dr. Xihong Lin is Professor and former Chair of the Department of Biostatistics, Coordinating Director of the Program in Quantitative Genomics at the Harvard T. H. Chan School of Public Health, and Professor of the Department of Statistics at the Faculty of Arts and Sciences of Harvard University, and Associate Member of the Broad Institute of Harvard and MIT. Dr. Lin is an elected member of the National Academy of Medicine. She received the 2002 Mortimer Spiegelman Award from the American Public Health Association, and the 2006 Committee of Presidents of Statistical Societies (COPSS) Presidents' Award and the 2017 COPSS FN David Award. She is an elected fellow of American Statistical Association (ASA), Institute of Mathematical Statistics, and International Statistical Institute. Dr. Lin's research interests lie in development and application of statistical and computational methods for analysis of massive data from genome, exposome and phenome, and scalable statistical inference and learning for big genomic, epidemiological and health data.

Online event. Registration required
<https://tinyurl.com/ImStatisticalReg>

Program webpage
<https://tinyurl.com/imgeneJan2022>

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