Keynote Speaker



Xihong Lin, Ph.D., 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 is the former Chair of the COPSS (2010-2012) and a former member of the Committee of Applied and Theoretical Statistics (CATS) of

the National Academy of Science. She co-launched the new Section of Statistical Genetics and Genomics of the ASA and served as a former section chair. She is the former Coordinating Editor of Biometrics and the founding co-editor of Statistics in Biosciences. She has served on a large number of committees of many statistical societies, and numerous NIH and NSF review panels. Dr. Lin's research interests lie in development and application of scalable statistical and computational methods for analysis of massive data from genome, exposome and phenome, and scalable statistical inference and learning for big health and genomic data. Her theoretical and computational statistical research includes statistical methods for testing a large number of complex hypotheses, statistical inference for large covariance matrices, prediction models using high-dimensional data, and cloud-based statistical computing.

Time: December 14 (Monday): 9:00-10:00AM (Central Time)

Host: Jianguo Sun, Ph.D., ICSA President and Professor, Department of Statistics, University of Missouri

Title: Learning from COVID-19 Data in Wuhan, USA and the World on Transmission, Health Outcomes and Interventions

Abstract: COVID-19 is an emerging respiratory infectious disease that has become a pandemic. In this talk, I will first provide a historical overview of the epidemic in Wuhan. I will provide the analysis results of 32,000 lab-confirmed COVID-19 cases in Wuhan to estimate transmission rates, the multi-faceted public health intervention effects that helped Wuhan control the COVID-19 outbreak, and epidemiological characteristics of the cases. I will present the results using the transmission dynamic model that show two features of the COVID-19 epidemic: high transmissibility and high covertness, and a high proportion of undetected cases, including asymptomatic and mildly symptomatic cases, and the chances of resurgence in different scenarios. I will next present the epidemic models to estimate the transmission rates in USA and other countries and intervention effects, as well as the prevalence and the total number of infections. I will present methods and analysis results of >500,000 participants of the HowWeFeel project on symptoms and health conditions in US, and discuss the factors associated with who have been tested in US and the factors associated with positive PRC tests/COVID-19 infection. I will provide several takeaways learned from the pandemic and discuss priorities.