

SCHOOL OF DATA SCIENCE

SEMINAR SERIES

High-Throughput Biotechnologies and Data Analysis

Date: 21 December 2018 (Friday)
Time: 2:30pm to 3:30pm
Venue: P7303, 7/F, Yeung Kin Man Academic Building (YEUNG),
City University of Hong Kong

Professor Zhang, Xiaohua Douglas
Faculty of Health Sciences
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Guest Speaker's profile

Prof. Xiaohua Douglas Zhang is a professor in University of Macau, a fellow in the American Statistical Association and an elected member of International Statistical Institute. He earned his Ph.D. in statistics from Carnegie-Mellon University, PA, USA, an MS in Genetics and a BS in Biology from Beijing Normal University. Before joining UM in 2016, Dr. Zhang was a Senior Principal Scientist in Merck Research Laboratories, West Point, USA and had worked there for more than 14 years, had established/managed (as a director) a biostatistics team supporting projects in drug discovery, clinical trials and clinical biomarkers 2012 — 2014 and mentored junior staff and summer interns in both USA and China. He is conducting research on digital health/medicine including wearable medical device and medical big data, and has also been working in quantitative genomics and statistical omics. Dr. Zhang is the single author of a book "Optimal High-Throughput Screening" published by Cambridge University Press in 2011. He has published numerous first-authored, single-authored or co-authored articles in prestigious peer-reviewed journals. The novel methods developed by Dr. Zhang and his colleagues along with their applications have a profound impact on the high throughput screening (HTS) research field, especially in RNAi HTS research. One of his first-authored articles has been listed among the top 50 most-cited articles in Bioinformatics in 2013. Five of his articles (3 single authored, 1 first-authored and 1 second-authored) have been listed among the top 50 most-cited articles in Journal of Biomolecular Screening for many years. One of his co-authored articles had been highlighted in Nature Medicine's year-end review on Notable Advances in 2008. Dr. Zhang has been invited to serve as a critical reviewer for papers submitted to Nature, Nature Methods and so on, as an Expert Evaluator for grant proposals for multiple panels in the European Union (EU) 2020 Horizon Program, the EU 7th Framework Programme Health Theme, and as a reviewer for the NIH Study Section.



Abstract

In 2003, the Human Genome Project was completed. By laying out in order the 3.2 billion units of our DNA, researchers sparked a firestorm of discovery and an explosion of genomic knowledge. Accompanied with them are the rapidly emerging novel genomic technologies including microarrays, whole-genome single nucleotide polymorphism chips, RNA interference high-throughput screening etc. All these launch the high-throughput genotyping era. Recently, besides high-throughput (HT) genomics technologies, the rapid development of large data storage technologies, mobile network technology and portable medical devices makes it possible to measure, record, store, and track analysis of the genome and physiological dynamics of an individual. Portable non-invasive medical devices are crucial to capture individual characteristics of biological dynamics. In fact, the rapid development of wearable, mobile, automatic, continuous, HT medical device for measuring human biological parameters heralds a new era --- high throughput phenotyping era. In this new era, the wearable non-invasive medical devices and the analysis/management of related digital medical data will revolutionize the management of health and treatment of diseases. In this presentation, I will first describe my work in data analysis for HT genotyping with focus on HT RNAi screens. I will then describe my recent work in data science for HT phenotyping with application in diabetes and respiratory diseases. Finally, I will present my thoughts on how to use both HT genotyping and HT phenotyping data for biomedical research.

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All are welcome