Saw Swee Hock Public Lecture in Statistics

Analysis of Massive Genome, Exposome and Phenome Data

by Professor Xihong LIN

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June 29, 2017 (Thursday)
6:00 p.m. - 7:00 p.m.
CPD-3.04, 3/F, Run Run Shaw Tower
(逸夫教學樓), Centennial Campus, HKU
Tea Reception at 5:30 p.m.

About the Talk

Massive 'ome data, including genome, exposome, and phenome data, are becoming available at an increasing rate with no apparent end in sight. Examples include Whole Genome Sequencing data, multiple metal data, digital phenotyping data, and Electronic Medical Records. Whole genome sequencing data and different types of genomics data have become rapidly available. Two large ongoing whole genome sequencing programs (Genome Sequencing Program (GSP) of NHGRI and Trans-omics for Precision Medicine Program (TOPMed) of NHLBI) plan to sequence 300,000-350,000 whole genomes. These massive genetic and genomic data, as well as exposure and phenotype data, present many exciting opportunities as well as challenges in data analysis and result interpretation. In this talk, I will discuss analysis strategies for some of these challenges, including rare variant analysis of whole-genome sequencing association studies; analysis of multiple phenotypes (pleiotropy), and integrative analysis of different types of genetic and genomic, environmental data using causal mediation analysis. Connection between mediation analysis and Mendelian Randomization will be discussed.

For online registration, please go to http://www.saasweb.hku.hk/seminar/20170629.html

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All interested are welcome

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