

AMENDMENT



The Hong Kong University of Science and Technology

Department of Mathematics

Seminar on Statistics

**A Comprehensive Framework for Genomewide Mendelian
Randomization under Pervasive Pleiotropy**

By

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Abstract

Mendelian randomization (MR) is a method of exploiting genetic variation to unbiasedly estimate a causal effect in presence of unmeasured confounding. MR is being widely used in epidemiology and other related areas of population science. One major challenge of applying MR to infer the causal relationship between complex traits is that the selected genetic variations can easily become invalid Instrumental Variables (IVs) with the presence of pleiotropy, which has recently been shown to be pervasive for complex traits. We develop a new statistical approach RAPS for MR using GWAS data, which brings up the importance of using a large number of weakly effective genetic variants to deal with pleiotropy. With theoretical guarantees, RAPS can correctly estimate the causal relationship under several common pleiotropy scenarios. The performance of RAPS is further evaluated through known causal relationships of complex traits. Finally, RAPS is applied to several case studies, including understanding the relationship between lipid traits with coronary heart disease, and the relationship between autoimmune disease and Psychiatric disease.

Date: Thursday, 21 June, 2018

Time: 3:30p.m.-4:30p.m.

Venue: Room 5562, Academic Building,
(Lifts 27, 28), HKUST

All are welcome!