



The Hong Kong University of Science and Technology

Department of Mathematics

Seminar on Statistics

**On High-dimensional Misspecified Mixed Model Analysis and
Genome-wide Association Study**

By

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Abstract

We study behavior of the restricted maximum likelihood (REML) estimator under a misspecified linear mixed model (LMM) that has received much attention in recent genome-wide association studies. The asymptotic analysis establishes consistency of the REML estimator of the variance of the errors in the LMM, and convergence in probability of the REML estimator of the variance of the random effects in the LMM to a certain limit, which is equal to the true variance of the random effects multiplied by the limiting proportion of the nonzero random effects present in the LMM. The results also establish asymptotic normality of the REML estimators. The asymptotic results are fully supported by results of empirical studies, which include extensive simulation studies that compare the performance of the REML estimator (under the misspecified LMM) with other existing methods, and real data applications (only one example is presented) that have important genetic implications. More recent progress on estimation of the asymptotic variance of the REML estimator will be discussed. This work is joint with Cong Li of Takeda Pharmaceuticals International, Debashis Paul of the University of California, Davis, Can Yang of Hong Kong University of Science and Technology, and Hongyu Zhao of Yale University.

Date: Thursday, 28 December, 2017

Time: 11:00a.m.-12:00noon

***Venue: Room 2463, Academic Building,
(near Lifts 25&26), HKUST***

All are welcome!