THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

SEMINAR ON STATISTICS

The Method of Limits and Its Application to The Analysis of Count Data in Genome-wide Association Studies

By

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Abstract

We propose a new method of statistical inference, called the method of limits (MoL), which may be viewed as an extension of the method of moments. This method is motivated by the need to analyze count data for genome wide association studies (GWAS), where the existing methods are hindered in statistical inference due to computational challenges. We establish consistency and asymptotic normality of the MoL estimator of heritability from GWAS data, which is seen as an advantage over the existing PQLseq method. Furthermore, we derived a consistent estimator of the proportion of causal SNPs. MoL also showed an advantage of both statistical and computational eIiciency measured by relative average statistical eIiciency (RASE) in our simulation studies compared to PQLseq. We also illustrate the usefulness of MoL through its application to the UK Biobank data to infer the heritability of week champagne consumption and week red wine consumption using the count data. This work is joint with Leqi Xu, Yiliang Zhang, and Hongyu Zhao of Yale University.

Date : 30 July 2024 (Tuesday)
Time : 3:00pm
Venue : Room 5506 (Lift 25/26)

All are Welcome!