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University of Science and Technology of China, Hefei, Anhui, P.R.China

Coauthors: Jiahua Chen

## **GENOME-WIDE ASSOCIATION STUDIES: CHALLENGES FACING STATISTICIANS**

ZEHUA CHEN

Many diseases and quantitative traits are attributable to genetic variants. Disease gene mapping and quantitative trait loci mapping are of extreme scientific and medical importance. With the availability of the densely spaced SNPs (single nucleotide polymorphisms) over the whole genome, genome-wide association studies for disease gene mapping and quantitative trait loci mapping become feasible and promising. The data from a typical genome-wide association study consists of genotypes of tens of thousands, even hundreds of thousands, SNPs with a relatively small sample size. A genome-wide association study can be cast as a variable selection problem in statistics. However, the sheer number of the SNPs and the relatively small sample size pose great challenges to statisticians. To take on the challenges, we proposed a novel approach to variable selection which is particularly tailored for the genome-wide association studies. The approach constitutes two components: a tournament screening process and an extended Bayesian information criterion. The tournament screening process mimics rounds of competitions in a tournament and screens covariates in stages by using a penalized likelihood procedure. Since the ordinary Bayesian information criterion is inappropriate in the case of huge number of covariates, it is extended in the way that, in the penalty to balances the log likelihood, not only the number of the unknown parameters but also the complexity of the model space is taken into account. In this talk, we discuss the details of the tournament process, the extended Bayesian information criterion and its consistency. We also provide the results of some numerical studies to demonstrate the desirable properties of the new approach.

NATIONAL UNIVERSITY OF SINGAPORE  
*E-mail address:* `stachenz@nus.edu.sg`