G&I Genomics & Informatics

eISSN 2234-0742
Genomics Inform 2016;14(4):137
https://doi.org/10.5808/GI.2016.14.4.137

EDITORIAL

Editor's Introduction to This Issue

Taesung Park*

Department of Statistics, Seoul National University, Seoul 08826, Korea

With the recent development of high-throughput DNA microarray and next-generation sequencing techniques for detecting various genomic variants, genome-wide association studies (GWASs) have become a popular strategy to discover genetic factors affecting common complex diseases. Many GWASs have successfully identified genetic risk factors associated with common diseases and have achieved substantial success in unveiling the genomic regions that are responsible for various aspects of the resulting phenotypes. However, identifying the underlying mechanism of disease-susceptible loci has proven to be difficult due to the complex genetic architecture of common diseases. The previously associated variants that have been revealed through GWASs explain only a small portion of the genetic factors in complex diseases. This rather limited finding is partly ascribed to the lack of intensive analysis on undiscovered genetic determinants, such as rare variants. In this context, the analysis of association studies has been steered from a common variant approach toward a rare variant approach to understand the complexity of genotype-phenotype associations. However, there is still room to improve the statistical analysis of GWAS data.

This special issue introduces more advanced statistical analysis methods for GWAS data and has successfully demonstrated that important biological insights can be inferred from GWAS data through an appropriate statistical method. Despite the development of an enormous amount of analyses, however, the analysis of high-dimensional omics data is still very challenging. This special issue covers these challenging issues for GWAS data, such as the multiple testing problem, gene-gene interactions, and prediction. Dr. Hokeun Sun (Pusan National University) introduces a new efficient multiple-group testing procedure for high-dimensional genomic data. Dr. Mira Park's group (Eunji Medical University) introduces a new test based on the generalized index of dissimilarity measure for genetic association studies. Dr. Yun Joo Yoo (Seoul National University) investigates the effects of SNP marker density on haplotype block partition.

There are interesting papers on gene-gene interaction analyses. Dr. Sunho Won's group (Seoul national University) and Seungyoeun Lee's group (Sejong University) propose efficient gene-gene interaction analyses for case-control study and survival data, respectively. Although they are focusing on the same topic, their approaches are quite different. Dr. Buhm Han (Asan Medical Center) compares the performance of two meta-analysis methods based on inverse variance-weighted average and weighted sum of z-scores, respectively. Also, there are two manuscripts on the prediction of traits using genetic markers. Prediction becomes more and more important in this era of precision medicine.

For further details, please visit the G&I homepage (http://www.genominfo.org/).

***Corresponding author:** Tel: +82-2-880-8924, Fax: +82-2-883-6144, E-mail: tspark@stats.snu.ac.kr