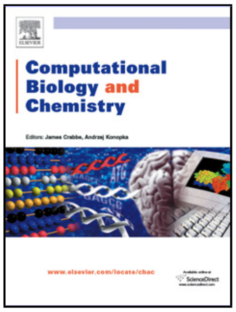

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Statistical methods to detect novel genetic variants using publicly available GWAS summary data

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Abstract

We propose statistical methods to detect novel genetic variants just using genome-wide association studies (GWAS) summary data without access to raw genotype and phenotype data. With more and more summary data being posted for public access in the post GWAS era, the proposed methods are practically very useful to identify additional interesting genetic variants and shed lights on the underlying disease mechanism. We illustrate the utility of our proposed methods with application to GWAS meta-analysis results of fasting glucose from the international MAGIC consortium. We found several novel genome-wide significant loci that are worth further study.

Key words: GWAS; SNP-set association test; Summary statistics

1 Introduction

In the past decade, the genome-wide association studies (GWAS) have been very successful in identifying thousands of common genetic variants that are associated with various traits

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