HIGH-THROUGHPUT DETECTION OF EPISTASIS IN STUDIES OF THE GENETICS OF COMPLEX TRAITS

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Gene interactions are thought to be important in shaping complex trait variation in agricultural, model organism and human disease genetics. They have been poorly explored, however, because of the lack of high throughput tools to analyze many different traits. In this poster we present a novel tool that has been developed to allow routine high throughput analysis of epistasis in complex traits in populations genotyped with high density single nucleotide polymorphism (SNP) markers. Such population data have been commonly used in genome-wide association studies in different species but barely analyzed for epistasis at the genome-wide level. The key challenge is how to effectively reduce the search space without losing power of detection so that one trait can be analysed in CPU hours. To tackle the challenge, we propose Epicluster, a novel method that can quickly select candidate SNPs with consistent genotype distribution patterns differentiating phenotypes of interest and then perform comprehensive epistasis analysis among the candidate SNPs. The developed method is based on a bi-clustering data mining algorithm named Mining Attribute Profiles that has been successfully applied in gene expression data analyses. In the future we plan to implement the developed algorithm as a distributed computing tool to allow multiple traits to be analyzed simultaneously.

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