## Modular Analysis of the Weighted Genetic Interaction Network

Minghua Deng School of Mathematical Sciences Peking University Beijing, 100871 China dengmh@pku.edu.cn

## Abstract

Epistasis Miniarray Profiles (EMAP) has enabled the mapping of large-scale genetic interaction networks; however, sophisticated computational strategies of analyzing such networks are yet to be developed. Towards this goal, we adopted a mixture modeling procedure to construct a weighted genetic interaction network, and then implemented a probabilistic scheme to identify densely interacting modules in the network. The mixture modeling is demonstrated as a soft-threshold technique of EMAP measures. Furthermore, we utilized our approach on an early secretory pathway EMAP data set to predict 254 modules. Among these modules, 88 are enriched in a Gene ontology (GO) category, seven are enriched in a Kyoto Encyclopedia of Genes and Genomes < http:://www.genome.jp/kegg/ > (KEGG) pathway, and six are enriched in the Munich Information Center for Protein Sequences (MIPS) protein complex.