Network-based Analysis of eQTL Data

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Abstract

Genetical genomics experiments have now been routinely conducted to measure both the genetic variants and gene expression data on the same subjects. The gene expression levels are often treated as quantitative traits and are subject to standard genetic analysis in order to identify the gene expression quantitative loci (eQTL). However, the genetic architectures for many gene expressions may be complex, and poorly estimated genetic architectures may compromise the inferences of the dependency structures of the genes at the transcriptional levels. I will present several statistical methods for analysis of eQTL data, including a sparse seemingly unrelated regression model for joint inferences of genetic effects and genetic association networks and a penalized likelihood approach for dynamic co-expression analysis.