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Bayesian Graphical Models for Gene Network Analysis in Large-Scale Problems

The detection of genetic interactions and inference about gene network topology can be a very valuable approach to understanding the joint basis of complex disease etiology. Network information is, unfortunately, extremely difficult to apprehend and only partially available. Bayesian Graphical models (BGMs) provide a probabilistic framework for making inference and representing our knowledge about these complex structured data. We discuss here the use of BGMs for gene network analysis in high-dimensional problems and how expert prior information and efficient algorithms can help inferring these complex networks. Applications to ongoing genetic and genomic problems in cancer research will be presented.