Bayesian Graphical Models for Computational Network Biology

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ABSTRACT
We first review the use of Bayesian graphical models to model complex molecular networks with an emphasis on reciprocal graphical models (RG) which remain curiously under-used in biostatistics and bioinformatics literature. RG’s strictly contain chain graphs as a special case and are suitable to model reciprocal causality such as feedback mechanism in molecular networks. We then extend the RG approach in [1] to modeling molecular networks by integrating DNA-, RNA- and protein-level data. We apply the extended RG method to The Cancer Genome Atlas (TCGA) multi-platform ovarian cancer data and reveal several interesting findings.

KEYWORDS
Directed graph, undirected graph, chain graph, reciprocal graph, causality.

REFERENCES
[1] Yang Ni, Yuan Ji, and Peter Mueller. 2016. Reciprocal Graphical Models for Integrative Gene Regulatory Network Analysis. arXiv preprint arXiv:1607.06849 (2016).