



Joint likelihood calculation for intervention and observational data from a Gaussian Bayesian network

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Methodological development for the inference of gene regulatory networks from transcriptomic data is an active and important research area. Several approaches have been proposed to infer relationships among genes from observational steady-state expression data alone, mainly based on the use of graphical Gaussian models. However, these methods rely on the estimation of partial correlations and are only able to provide undirected graphs that cannot highlight causal relationships among genes. A major upcoming challenge is to jointly analyze observational transcriptomic data and intervention data obtained by performing knock-out or knock-down experiments in order to uncover causal gene regulatory relationships. To this end, in this technical note we present an explicit formula for the likelihood function for any complex intervention design in the context of Gaussian Bayesian networks, as well as its analytical maximization. This allows a direct calculation of the causal effects for known graph structure. We also show how to obtain the Fisher information in this context, which will be extremely useful for the choice of optimal intervention designs in the future.

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