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**Low-order conditional independence graphs for inferring genetic networks.** (English)

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Summary: As a powerful tool for analyzing full conditional (in-)dependencies between random variables, graphical models have become increasingly popular to infer genetic networks based on gene expression data. However, full (unconstrained) conditional relationships between random variables can be only estimated accurately if the number of observations is relatively large in comparison to the number of variables, which is usually not fulfilled for high-throughput genomic data.

Recently, simplified graphical modeling approaches have been proposed to determine dependencies between gene expression profiles. For sparse graphical models such as genetic networks, it is assumed that the zero- and first-order conditional independencies still reflect reasonably well the full conditional independence structure between variables. Moreover, low-order conditional independencies have the advantage that they can be accurately estimated even when having only a small number of observations. Therefore, using only zero- and first-order conditional dependencies to infer the complete graphical model can be very useful. Here, we analyze the statistical and probabilistic properties of these low-order conditional independence graphs (called 0 – 1 graphs). We find that for faithful graphical models, the 0 – 1 graph contains at least all edges of the full conditional independence graph (concentration graph). For simple structures such as Markov trees, the 0 – 1 graph even coincides with the concentration graph. Furthermore, we present some asymptotic results and we demonstrate in a simulation study that despite their simplicity, 0 – 1 graphs are generally good estimators of sparse graphical models. Finally, the biological relevance of some applications is summarized.

**MSC:**

- 62P10** Applications of statistics to biology and medical sciences; meta analysis
- 92D10** Genetics and epigenetics
- 05C90** Applications of graph theory

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