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Gradient directed regularization for sparse Gaussian concentration graphs, with applications to inference of genetic networks. (English) [Zbl 1169.62378](#)
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Summary: Large-scale microarray gene expression data provide the possibility of constructing genetic networks or biological pathways. Gaussian graphical models have been suggested to provide an effective method for constructing such genetic networks. However, most of the available methods for constructing Gaussian graphs do not account for the sparsity of the networks and are computationally more demanding or infeasible, especially in the settings of high dimension and low sample size. We introduce a threshold gradient descent (TGD) regularization procedure for estimating the sparse precision matrix in the setting of Gaussian graphical models and demonstrate its application to identifying genetic networks. Such a procedure is computationally feasible and can easily incorporate prior biological knowledge about the network structure. Simulation results indicate that the proposed method yields a better estimate of the precision matrix than the procedures that fail to account for the sparsity of the graphs. We also present the results on inference of a gene network for isoprenoid biosynthesis in *Arabidopsis thaliana*. These results demonstrate that the proposed procedure can indeed identify biologically meaningful genetic networks based on microarray gene expression data.

MSC:

- 62P10 Applications of statistics to biology and medical sciences; meta analysis
- 62C12 Empirical decision procedures; empirical Bayes procedures
- 05C90 Applications of graph theory

Cited in **29** Documents

Keywords:

Empirical Bayes thresholding; Graphical models; Microarray; Threshold gradient descent

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