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Node-Based Learning of Multiple Gaussian Graphical Models

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We consider the problem of estimating high-dimensional Gaussian graphical models corresponding to a single set of variables under several distinct conditions. This problem is motivated by the task of recovering transcriptional regulatory networks on the basis of gene expression data. We assume that most aspects of the conditional dependence networks are shared, but that there are some structured differences between them. Rather than assuming that similarities and differences between networks are driven by individual edges, we take a node-based approach. We consider estimation under two distinct assumptions: (1) differences between the K networks are due to individual nodes that are perturbed across conditions, or (2) similarities among the K networks are due to the presence of common hub nodes that are shared across all K networks. Using a row-column overlap norm penalty function, we formulate two convex optimization problems that correspond to these two assumptions. We solve these problems using an alternating directions method of multipliers algorithm, and we derive a set of necessary and sufficient conditions that allows us to decompose the problem into independent sub-problems so that our algorithm can be scaled to high-dimensional settings. Our proposal is illustrated on synthetic data and on a brain cancer gene expression data set.

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