Comparative Evaluation of Different Graphical Models for the Analysis of Gene Expression Data

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Abstract: An important problem in systems biology is to infer the architecture of gene regulatory networks and biochemical pathways from postgenomic data. Various reverse engineering methods have been developed and proposed in the Statistics and Bioinformatics literature, and it is important to understand their relative merits and shortcomings. To shed light onto this problem, the learning performances of three widely-used Machine Learning methodologies: Relevance Networks, Graphical Gaussian models, and Bayesian Networks are evaluated and compared on different real and synthetic test data sets taken from the RAF signalling network which describes the interactions between eleven phosphorylated proteins and phospholipids in human immune system cells.