Inferring gene regulatory networks from gene expression data by path consistency algorithm based on conditional mutual information

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Résumé en anglais	Motivation: Reconstruction of gene regulatory networks (GRNs), which explicitly represent the causality of developmental or regulatory process, is of utmost interest and has become a challenging computational problem for understanding the complex regulatory mechanisms in cellular systems. However, all existing methods of inferring GRNs from gene expression profiles have their strengths and weaknesses. In particular, many properties of GRNs, such as topology sparseness and non-linear dependence, are generally in regulation mechanism but seldom are taken into account simultaneously in one computational method.Results: In this work, we present a novel method for inferring GRNs from gene expression data considering the non-linear dependence and topological structure of GRNs by employing path consistency algorithm (PCA) based on conditional mutual information (CMI). In this algorithm, the conditional dependence between a pair of genes is represented by the CMI between them. With the general hypothesis of Gaussian distribution underlying gene expression data, CMI between a pair of genes is computed by a concise formula involving the covariance matrices of the related gene expression profiles. The method is validated on the benchmark GRNs from the DREAM challenge and the widely used SOS DNA repair network in Escherichia coli. The cross-validation results confirmed the effectiveness of our method (PCA-CMI), which outperforms significantly other previous methods. Besides its high accuracy, our method is able to distinguish direct (or causal) interactions from indirect associations.
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