

# Inferring gene regulatory networks using time series microarray data

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## **Abstract:**

Although microarray data have been successfully used for gene clustering and classification, the use of time series microarray data for constructing gene regulatory networks remains a particularly difficult task. The challenge lies in reliably inferring gene regulatory relationships from time series microarray datasets that normally possess a large gene dimensional space and a small sample dimensional space. In addition to the challenge from microarray data, the enormous complexity and dynamic properties of transcriptional regulation also impede the progress of inferring gene regulatory relationships. Based on the current transcriptional model and some features of gene regulation, we developed a new approach for inferring gene regulatory relationships by combining target-target pattern recognition and examining the presence of regulator-specific binding sites in the promoter regions of putative target genes. As we implemented the approach to yeast microarray data, we detected hundreds of new regulatory relationships, among which 17% are rediscovered, experimentally validated ones. An even larger number of inferred relationships can be reasonably explained in the biological context of the regulation. Since the regulatory relationships are inferred from pattern recognition between target genes and target genes rather than between regulators and target genes, the method we present in here is especially suitable for inferring gene regulatory relationships from transcriptional complexities, in which regulators and their targets do not share similarities in their expression profiles.