

## Inferring gene regulatory networks from gene expression data by a dynamic Bayesian network-based model

### Abstract :

Enabled by recent advances in bioinformatics, the inference of gene regulatory networks (GRNs) from gene expression data has garnered much interest from researchers. This is due to the need of researchers to understand the dynamic behavior and uncover the vast information lay hidden within the networks. In this regard, dynamic Bayesian network (DBN) is extensively used to infer GRNs due to its ability to handle time-series microarray data and modeling feedback loops. However, the efficiency of DBN in inferring GRNs is often hampered by missing values in expression data, and excessive computation time due to the large search space whereby DBN treats all genes as potential regulators for a target gene. In this paper, we proposed a DBN-based model with missing values imputation to improve inference efficiency, and potential regulators detection which aims to lessen computation time by limiting potential regulators based on expression changes. The performance of the proposed model is assessed by using time-series expression data of yeast cell cycle. The experimental results showed reduced computation time and improved efficiency in detecting gene-gene relationships.