

Extraction of Gene Regulatory Network (GRN) From Genome-Wide Expression Data

The extraction of Gene Regulatory Network (GRN) for genome-wide microarray data is still at an early stage. In this project Bayesian belief networks (BBN), a graph based representation of joint probability distributions that capture the conditional dependencies between genes are applied to *Saccharomyces cerevisiae* cell cycle data. The extracted GRN is found to be valid when compared with genome pathway databases such as KEGG and SGD.

The GRN was extracted using the Taboo order algorithm from temporal expression data for 104 genes previously identified as cell cycle regulated using wet lab methods. Missing values were estimated using the EM algorithm. The extracted GRN shows strong similarity with the actual classification of the phases of yeast cell cycle. The architecture of individual phases was largely preserved even when all cell cycle phases were extracted simultaneously. This GRN provides a richer model for analysing gene expression patterns, which captures the interaction among various genes in terms of probabilities and conditional dependencies.

This results of this proof of concept study demonstrate that the BBN approach is well suited to modelling DNA microarray data, which is characterised by a high degree of measurement noise and variability. These results, and BBN's strengths in stochastic modelling and incorporation of prior knowledge, indicate potential for determining previously unknown or incomplete GRNs.

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