Reverse-Engineering Genetic Regulatory Interactions from Transcriptomic Data with Dynamic Bayesian Networks

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Abstract

Gene regulatory networks are collections of genes that interact, whether directly or indirectly, with each other and with other substances in the cell. Such interactions regulate the rate and degree to which genes are transcribed into mRNA and proteins. Even though these systems are typically difficult to elucidate due to the large number of genes and the limited number of biological replicates available, by measuring gene expression over time, it is possible to estimate the structure of a regulatory network involved in a particular cell process.

A valuable tool for inferring interaction networks from temporal microarray expression data is the Dynamic Bayesian Network (DBN). A DBN is a directed graphical model of stochastic processes that can incorporate hidden variables as driving factors (e.g., genes not included on a microarray or transcription factors). Our current work uses an iterative empirical hierarchical Bayesian estimation procedure in tandem with Kalman estimators to estimate the posterior distributions of network parameters. Significant network edges are chosen based on a z-score calculated from the posterior distribution of the interaction matrix. In the early stages of this work we have demonstrated that our method has the potential to identify gene networks comparable to existing methods within a reasonable amount of computational time.