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***Modeling Gene Regulatory Pathways***

***Abstract:***

Although many genomes have been sequenced and many genes within them have been identified, it is the specific control or regulation of the expression of these genes as proteins that determine whether the cell functions properly or not. Uncovering this regulatory pathway remains a challenge both experimentally and computationally. We present our previous work combining prior knowledge with dynamic Bayesian networks (DBNs) to learn gene regulatory pathways from time series microarray data. Following earlier work, due to the high cost of running microarray experiments, we were interested in developing an experimental design for time series data generation. Specifically, we were interested in determining properties of time series data that make them more suitable for DBN modeling. We present our theoretical results on the ability of DBNs without hidden variables to learn microarray time series data. The analysis reveals, among other lessons, that under a reasonable set of assumptions a fixed budget is better spent on many short time series rather than on a few long time series.

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**Tuesday, April 19<sup>th</sup>, 2005**  
**4:00 p.m.**

Genetics/Biotechnology Center Auditorium  
425 Henry Mall