

BIOINFORMATICS SEMINAR

Time series expression data: From individual gene expression to genetic regulatory networks

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ABSTRACT:

Recent advances in DNA microarray technologies are enabling researchers to measure the expression levels of thousands of genes simultaneously. Time series expression data offers a particularly rich opportunity for understanding the dynamics of biological processes. Expression experiments and other high-throughput data sources hold the promise of revolutionizing molecular biology by providing a large-scale view of genetic regulatory networks. However, these high throughput sources are noisy and contain many missing data points. Time series expression data introduces additional complications, including sampling rate differences between experiments and variations in the timing of biological processes. Thus, principled computational methods are required in order to fully utilize these data sources.

In this talk I will present algorithms for two different levels of time series expression data analysis. For the individual gene level, I will present algorithms that permit the principled estimation of unobserved time-points, clustering, dataset alignment and the identification of differentially expressed genes. By using these algorithms on time series knockout data, we provide new insights to the role that two key cell cycle factors play in controlling cellular activity. For the network level, I will describe a new algorithm that efficiently combines complementary large-scale expression and protein-DNA binding data to discover co-regulated modules of genes. The discovered modules are used to build a regulatory network of transcription factors and modules, and can also be used to label transcription factors as activators or repressors and to identify several patterns of combinatorial regulation.

In order to discover dynamic regulatory networks, I will present an algorithm that combines the above methods to automatically infer such networks for specific biological processes. In particular, this algorithm accurately reconstructs key elements of the cell cycle sub-network in yeast.

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11:00 a.m. – 1:00 p.m.

(Talk starts at 11:30)

Building NE43, Room 941

*Refreshments at 11am in NE43-941
(LCS, 200 Tech Square, Cambridge, MA)*



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