

1077-92-1751

Kam Dahlquist (kdahlquist@lmu.edu), Department of Biology, 1 LMU Drive, Los Angeles, CA 90045, and **Ben G Fitzpatrick*** (bfitzpatrick@lmu.edu), Department of Mathematics, 1 LMU Drive, Los Angeles, CA 90045. *Modeling and Estimation in Gene Regulatory Networks.*

Saccharomyces cerevisiae respond to cold shock by altering gene expression, which is controlled by the binding of transcription factors to regulatory sequences. In this talk, we discuss the modeling of the effect of cold shock on a network of transcription factors and their subsequent influence on gene expression. DNA microarrays were used to collect data over time as the yeast cells respond to cold shock. Spatial and intensity biases are present in microarray data, requiring Loess normalization and median absolute deviation scaling on the microarray data. The microarray data is then used to calibrate a differential equation model for transcription factor regulation. The model includes activation and repression relationships (which must be inferred from the data) in a complex network of interactions. We provide numerical results using microarray data from the literature as well as from our lab. (Received September 20, 2011)