345a Transcriptional Dynamics - a New Approach to Identification of Genetic Networks

Ian J. Laurenzi

A preeminent problem in functional genomics is the reconstruction of genetic networks from genome-scale RNA expression data. In many of the current approaches, groups of genes are related to each other via their expression timeseries, which correlate to the time courses of RNA abundance. However, RNA abundance can vary on account of both transcription and degradation, each of which are highly regulated processes. Therefore, we developed a new method of relating genes via the local clustering (and time-lag correlation analysis) of the time fluctuations of their Pol II transcription rates - calculated from RNA expression timeseries and mRNA degradation information. Applied to the yeast cell cycle dataset of Cho and coworkers (1998), this hybrid informatics/kinetics approach led to the identification of many novel relationships. Moreover, our technique lent support to many of the predictions of transcriptional cooperativity among genes from the analyses of expression timeseries.