

STATISTICS COLLOQUIUM

THURSDAY, May 08, 2008

TALK: 4:00 PM — SCIENCE CENTER RM. 705

RECEPTION: 5:15 PM — SCIENCE CENTER, 7TH FLOOR

“Bayesian Meta-analysis for Identification of Cell Cycle-regulated Genes”

Xiaodan Fan
Statistics Department
Harvard University

ABSTRACT

The effort of identifying cell cycle-regulated genes based on genome-wide microarray time series data has continued for a decade. However the lack of rigorous modeling of periodic expression and the lack of comprehensive model for integrating information across genes and experiments continue to impair accurate identification of periodically expressed genes and hence of various downstream analyses. We introduced a Bayesian model-based approach to integrate multiple microarray data sets from three recent cell cycle studies on fission yeast. A matrix model was used for data integration. MCMC method was used to draw samples from the joint posterior distribution of all parameters. New Metropolis-Hastings algorithm was developed for fast mixing on the matrix model. The integrated analysis combined with various statistical tests suggested that about 40% of the genes are significantly periodically expressed, far beyond the reported percentage 10-15% in the current literature. While increasing number of data sets accumulate in microarray databases, the power and potential of model-based Bayesian meta-analysis is appealing. This talk is based on Chapter 2 of my dissertation.