

THE CHINESE UNIVERSITY OF HONG KONG

Department of Statistics

will present a seminar entitled

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

by

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on

Tuesday, 4 March 2008
2:00pm – 3:00pm

in

Lady Shaw Building C5
The Chinese University of Hong Kong

Abstract:

The effort of identifying cell cycle-regulated genes from genome-wide microarray time-course data has continued for a decade in particular following the study of yeast cell cycle-regulated expression by Spellman et al. (1998) and Cho et al. (1998). However, the lack of rigorous genome-wide modeling of periodic expression in the presence of microarray noise as well as the loss of synchronization continues to impair an accurate identification of cell cycle-regulated genes, hence affecting various downstream analyses. In this work, we introduced a Bayesian model-based approach to integrate multiple microarray data sets from three recent cell cycle studies on the fission yeast. New Monte Carlo Markov Chain algorithm was designed to draw samples from the joint posterior distribution of all parameters. The posterior distributions of several quantities of interest, such as the strength of the periodicity, uncertainty of the estimated phases, and BIC values, are examined. The integrated analysis combined with various statistical tests and visual inspections suggests that about 40% or even more of the genes are significantly periodically expressed, far beyond the reported 10-15% in the current literature. It calls for a reconsideration of the definition of cell cycle-regulated genes and their detections. While data sets in microarray databases accumulate rapidly, the power and potential of a model-based Bayesian meta-analysis are appealing.

All are Welcome