PLEASE NOTE UNUSUAL TIME AND PLACE

Seminar Notice

Statistical Laboratory
Iowa State University

DATE AND TIME: Tuesday, March 7, 2006, 4:10 p.m.

PLACE: 1126 Sweeney

SPEAKER: Guanghua Xiao
Division of Biostatistics
University of Minnesota

TITLE: Improved detection of differentially expressed genes through incorporation of gene locations

ABSTRACT

In determining differential expression in c-DNA microarray experiments, the expression level of an individual gene is usually assumed to be independent of the expression level of other genes, but many recent studies have shown that a gene's expression level tends to be similar to that of its neighbors on a chromosome, and differentially expressed genes are likely to form clusters of similar transcriptional activity along the chromosome. When modeled as a one-dimensional spatial series, the expression levels of genes on the same chromosome frequently are spatially correlated, indicating spatial patterns in transcription. Based on these spatial correlations, we can obtain more adequate estimates of gene expression by utilizing the information about gene location. Using the autocorrelation function, we demonstrated the existence of spatial correlations of transcriptional activity in the Escherichia coli chromosome across more than 50 experimental conditions. Based on this finding, we proposed a hierarchical Bayesian model that borrows information from neighboring genes to improve the estimation of the transcription level of a given gene and hence the detection of differentially expressed genes. Both, simulation studies and the analysis of experimental data showed that the proposed method outperforms the SAM t statistic, which is widely used in detecting differentially expressed genes.

COFFEE: 3:45 p.m., 104 Snedecor Hall

Seminar schedules and abstracts are available via WWW: http://www.stat.iastate.edu/