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Analysis for Temporal Gene Expressions under Multiple Biological Conditions

Friday, Feb 24, 2:00 P.M. – 3:00 P.M. SPHIS Room 103

Temporal gene expression data are of particular interest to researchers as it contains rich information in characterization of gene function and have been widely used in biomedical studies and cancer early detection. However, the current temporal gene expressions usually have few measuring time series levels, extracting information and identifying efficient treatment effects without loss temporal information are still in problem. A dense temporal gene expression data in bacteria shows that the gene expression has various patterns under different biological conditions. Instead of analysis of gene expression levels, we consider the relative change-rates of gene in the observation period in this talk. We propose a non-linear regression model to characterize the relative change-rates of genes, in which individual expression trajectory is modeled as longitudinal data with changeable variance and covariance structure. Then, based on the parameter estimates, a chi-square test is proposed to test the equality of gene expressions. Furthermore, the Mahalanobis distance is used for the classification of genes. The proposed methods are applied to the dataset of 32 genes in *P. aeruginosa* expressed in 39 biological conditions. The simulation studies show that our methods perform well for analysis of temporal gene expressions.