

GRADUATE SEMINAR

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Model-based Variance Classification for Multiple Conditions Gene Expression

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Friday August 2nd

11:00

Math Lounge (CW307.20)

Abstract: Temporal gene expression data is one of the particular interests to researchers as it contains rich information in characterization of gene function and have been widely used in biomedical studies and cancer early detection. A dense temporal gene expression data in bacteria shows that the gene expression has various patterns under different biological conditions. In contrast to the rich literature on how to estimate the gene expression over the time under a given condition, few researchers consider identifying the different effects of multiple conditions on the gene expression profiles. In this talk, we will investigate the effects of multiple conditions to the gene expressions and then classify the conditions according to the obtained results on their effects to the gene profiles. We propose a non-linear regression model and log-normal distribution properties to characterize the variance function of genes under a given condition. Then, based on the parameter estimates, a chi-square test is proposed to test the equality of variance function for conditions. Furthermore, the Mahalanobis distance is used for the classification of conditions. The proposed methods are applied to the dataset of 21 genes in *P.aeruginosa* expressed in 24 biological conditions.