

GRADUATE SEMINAR

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Quantile Regression Approach for Analyzing Gene Expression Data

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Abstract: Temporal gene expression data contains ample information to characterize gene function and is now widely used in bio-medical research. A dense temporal gene expression usually shows various patterns in expression levels under different biological conditions. Existing literature models the gene trajectory using the mean function. Moreover, temporal gene expression curves generally show strong degree of heterogeneity between multiple conditions. As a result, rate of change of gene expressions may be different in non-central locations and a mean model can not explore the non-central location of the distribution.

In this presentation, we will briefly discuss the linear quantile mixed model to analyze gene expression data. Using simulation study, we will try to demonstrate the statistical performance of proposed test statistic to test the equality of two different gene expressions based on estimated quantile regression parameters. Furthermore, this proposed method is applied to analyze a data set of 18 genes in *P. aeruginosa*, expressed in 24 biological conditions.