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# A Quasi-Likelihood Method to Detect Differential Expression in RNA-Seq Data

Séminaire de statistique

**Conférencier: Angelo J. Canty**

Department of Mathematics and Statistics  
McMaster University, Hamilton

**Date, heure et endroit**

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## Résumé

Sequencing of mRNA is the current gold standard for measuring gene expression across an entire transcriptome. RNA-Seq has many advantages over previous array-based methods. Since the resulting data are counts of reads mapped to a transcript, most current methods are based on the assumption that the data follow a Poisson or negative binomial distribution. In this talk I will introduce a new method, QuasiDE, developed by my student Chu-Shu Gu to analyze RNA-Seq data without any explicit distributional assumptions. The method is based on quasi-likelihood and utilizes an empirically estimated variance function. I will show simulation results showing that this new method (QuasiDE) compares favourably to existing popular methods for analysis of RNA-Seq data. In the second part of this talk I will discuss the analysis of RNA-Seq data that has been transformed to the reads per kilobase of transcript per million mapped reads (RPKM) scale. I will show simulation evidence that RPKM data still needs further normalization and some of the methods originally developed for gene expression microarray data perform best. I will show, by simulation, that the QuasiDE method described earlier performs well for this type of data also. Finally I will present analyses of a real dataset that motivated some of this work. That dataset comes from a cross-species time-course experiment in which orthologs of two related species are compared for different expression patterns over time. I will compare the results of the analysis of this dataset for both RPKM and raw count data using QuasiDE and two competing statistical methods. This talk represents work with my recently graduated student Chu-Shu Gu.

**Ting-Huei Chen & Louis-Paul Rivest**  
Responsables du séminaire de statistique



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