## McMASTER UNIVERSITY

### GRADUATE PROGRAM IN STATISTICS

# STATISTICS SEMINAR

- **Speaker:** Dr. Angelo Canty, Department of Developmental Biology, Hospital for Sick Children, Toronto, and Department of Mathematics and Statistics, McMaster University
- **Title:** *"Finding Differentially Expressed Genes from Affymetrix Microarray Data"*
- **Day:** Tuesday March 1, 2005
- **Time:** 2:30 3:30 PM
- **Place:** HH/102

(Note change from regular time and location)

#### SUMMARY

In this talk I will describe the Affymetrix microarray platform for finding gene expression of large numbers of genes. These arrays are commonly used to look for genes that are differentially expressed between two populations. One of the most popular ways to find such genes is the Significance Analysis of Microarrays (SAM) methodology introduced by Tusher et al. (2001) which I shall describe. I will talk about some of the issues that arise in such an analysis. I will also describe a mouse model in which we wish to study locus interactions in susceptibility to Type 1 Diabetes and how the basic SAM methods can be extended to such situations.

### REEFERENCES

- 1. Storey & Tibshirani (2003a) "SAM Thresholding and False Discovery Rates for Detecting Differential Gene Expression in DNA Microarrays," in *The Analysis of Gene Expression Data: Methods and Software*, (Parmigiani, Garrett, Irizarry & Zeger, editors) New York: Springer.
- 2. Storey & Tibshirani (2003b) "Statistical Significance for Genome-Wide Studies," *Proceedings of the National Academy of Sciences*, *USA* **100**, pp. 9440-9445.
- Tusher, Tibshirani & Chu (2001) "Significance Analysis of Microarrays Applied to Transcriptional Responses to Ionizing Radiation," *Proceedings of the National Academy of Sciences, USA* 98, pp. 5116--5121.



**ABOUT THE SPEAKER.** Dr. **Angelo J. Canty** is an Assistant Professor of Statistics in the Department of Mathematics and Statistics at McMaster University. During the 2004-2005 academic year, he is on a leave sponsored by the CIHR Institute of Genetics working on the analysis of genetic microarray data at the Toronto Hospital for Sick

Children. His other main area of interest is in computational and Monte Carlo methods for statistical inference. Canty did his undergraduate training in statistics and computer science at University College, Cork, Ireland. His graduate work was done at the University of Toronto under the supervision of Professor Nancy Reid. During post-doctoral work in Oxford, UK and Lausanne, Switzerland, Canty worked with Anthony Davison and David Hinkley and produced the boot library of functions for resampling methods in S-Plus and R. Before coming to McMaster, Canty was an Assistant Professor at Concordia University, Montreal. (Picture by Cheryl McGill, 2001).

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