

UNIVERSITY OF SYDNEY

SCHOOL OF MATHEMATICS AND STATISTICS

Statistics Seminar

Friday, 11 April 2008, 2.00pm Carslaw 375

Towards a method for resolving the dependence structure amongst gene expression.

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Abstract

Understanding gene expression networks is one of the key aims of microarray experiments however many commonly used data analysis techniques work on the assumption of independence among all genes. Specifically, it can be difficult to get a complete picture using correlation-based tools such as Expression Angler (http://www.bar.utoronto.ca/), which uses a gene as input to return a list of genes with correlation coefficients above a user-defined threshold. Results from a gene used as input can in turn be used as input and there is no rigourous procedure for choosing the threshold. This means that this type of analysis can be subjective, and a more objective treatment is needed. Random Matrix Theory (RMT) was developed throughout the 1950s and 1960s to study and explain the spectra of complex nuclei, and has since been used to explain other complex systems as varied as disordered mesoscopic systems, financial systems and traffic networks. In the context of microarray data, there is promise that RMT will be able to unravel the genes that are dependent on each other and the genes that are effectively independent of each other under certain experimental conditions by examining the properties of the eigenvalues of a gene-gene correlation matrix. This talk will commence with a brief introduction to some important RMT results, followed by a summary of possible output of RMT as applied to microarray data.

Selected references:

Luo et al. (2006), Application of random matrix theory to microarray data for discovering functional gene modules, Phys. Rev. E 73

Luo et al. (2007), Constructing gene co-expression networks and predicting functions of unknown genes by random matrix theory, BMC Bioinformatics 8

Guhr et al. (1997), Random matrix theory in quantum physics: common concepts, arXiv:cond-mat/9707301

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