BAYESIAN ANALYSIS OF MULTIFACTORIAL GENE EXPRESSION DESIGNS, AND IDENTIFICATION OF GENE PATHWAY SIGNATURES

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I will discuss a range of experiments designed to investigate gene expression patterns related to gene pathway deregulation in human disease genomics. The need for sensitive analysis of data generated from large-scale, multivariate factorial designs is exemplified by such experiments. Bayesian modelling and shrinkage tailored to such designs provides for routine evaluation of such data, automatic and coherent within-analysis "adjustments" for the very many simultaneous multiple comparisons related to gene-factor associations that may involve high-order interactions, and a range other critical issues including correlated residuals and systematic biases/errors due to treatement and protocol effects not anticipated. Some substantial results from analyses of data arising in some of our cardiovascular and cancer genomics projects will convey the key issues, ideas, and relevance of these statistics methods.