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Seminar series:
BCCA Trainee Seminar Presentation

Location:
BC Cancer Research Centre
Gordon & Leslie Diamond Family Theatre
675 West 10th Avenue, Vancouver

Date:
9:00AM, Thursday, June 14, 2007

Title:
Novel bioinformatics methods for the identification of coexpressed, differentially expressed, and differentially coexpressed genes with application to cancer.

Abstract:
The human genome contains tens of thousands of gene loci. The highly complex temporal and spatial expression of these genes makes possible all the biological processes of life. Altered gene expression by mutation or deregulation is a fundamental factor in many human diseases including cancer. As a result, large-scale expression profiling has become an important tool for the identification of genes and pathways involved in cancer. Two common methods for the analysis of expression data are coexpression (or clustering) and differential expression. Clustering attempts to identify pairs or groups of genes whose expression is correlated over a series of conditions or time points. This information allows us to infer functional associations between genes, identify groups of related genes that are important in specific cancers and define new molecular subtypes of cancer. Differential expression attempts to identify genes with significantly increased or decreased transcript levels between two patient or tissue subsets (e.g. normal versus tumour). Such comparisons allow the identification of genes for use as diagnostic or prognostic biomarkers and potential drug targets. A major challenge of expression profiling studies is the high level of noise inherent to the technologies and complexity of the system. Thus, in any expression profiling experiment, dozens or hundreds of genes are typically identified, many of which are expected to be false-positives and only a small fraction useful as biomarkers or therapeutic targets. A common criticism of expression profiling studies is a lack of agreement between studies. This seminar will present four bioinformatics strategies developed to overcome this challenge: (1) A multi-platform integration approach to identify high-confidence coexpressed genes; (2) A novel subspace clustering algorithm designed to isolate subsets of very large datasets for which genes are strongly coexpressed; (3) A new method for differential coexpression analysis designed to predict deregulated genes in prostate cancer; (4) A meta-analysis method for identifying consistently multi-study differentially expressed genes for use as a diagnostic panel in thyroid cancer.