The ruin of gene network analysis by multifunctionality

A major goal of biology is to identify the functional relationships and interactions among genes and apply this knowledge to make predictive models. In bioinformatics, it is now routine to use various types of gene network and gene function information to interpret high-throughput experiments. Examples include "GO enrichment", network-motivated clustering or gene function prediction methods (e.g. "guilt by association") and candidate gene prioritization methods. I will describe how a phenomenon we call "gene multifunctionality" distorts such analyses. Genes having high multifunctionality are the source of serious biases or artifacts that can distract attention from more interesting signals, cause misleading results in algorithm evaluations, and generally make meaningfully applying known information on gene function extremely difficult. I will argue that this problem is ignored at our peril, and suggest some possible remedies and strategies for making progress.

Introductory speaker (10 mins):

**Rebecca Worsley Hunt**, Wasserman lab, CMMT, UBC

*Genome nucleotide composition and sequence length affect over-representation predictions of transcription factor binding sites in ChIP-based experiments*

**Thursday, November 17, 2011, 6:00 pm**

Gordon and Leslie Diamond Family Theatre,
BC Cancer Research Centre,
675 West 10th Avenue