



presents **Guest Speaker:**

Quaid Morris

Donnelly Centre, University of Toronto

*Predicting the targets of mRNA-binding proteins
(and a bit of GeneMANIA)*

RNA-binding domains are among the most common domains in eukaryotic genomes and RNA-binding proteins (RBPs) play critical roles in post-transcriptional regulation (PTR) of gene expression by regulating mRNA processing, mRNA translation, mRNA export and mRNA stability. Many RBPs bind in a sequence-specific manner however, their sequencing binding preferences alone are insufficient to uniquely identify their targets. As a first step towards building quantitative models of PTR, we are mapping out mRNA and RBP interactions using a combined biochemical and computational strategy. Our strategy is based on a microarray-based assay, called RNAcompete, that measures the binding affinity of a recombinant RBP for hundreds of thousands of short RNA sequences. These sequences are designed to comprehensively query the space of possible binding preferences. We use a new RNA motif finding algorithm, RNAcontext, to infer sequence and structural binding preferences of RBPs from both in vitro RNAcompete data, as well as, in vivo binding data from large-scale immunoprecipitation-based assays. Using these motif models to find RBP binding sites on mRNAs requires estimating mRNA secondary structure computationally. I will present some recent work that suggests that estimating this structure is easier than expected.

Introductory speaker (10 mins):

Ryan Morin, Marra lab, GSC, BCCA

Wednesday, November 10, 2010, 6:00 pm

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



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