



presents Guest Speaker:

Mathieu Blanchette

School of Computer Science, McGill University

*Ancestral genome reconstruction and its uses
toward annotating the human genome*

With the number of sequenced vertebrate genomes rapidly growing, the exciting prospect of being able to accurately infer ancestral genomes becomes within reach. In this presentation, I will discuss how ancestral DNA sequences can be inferred and how they can be then used to help addressing some key questions in genomics. Reconstructing ancestral sequences poses a number of algorithmic challenges. I will first describe some of our work on aligning orthologous sequence and inferring ancestral sequences, focusing on the accurate identification of insertions and deletions. Next, I will discuss how one can take advantage of the availability of inferred ancestral sequences to help at three important tasks: (i) identify non-coding sites under selection in the human genome; (ii) improve the detection of transcription factor binding sites; and (iii) determine the target gene(s) of long-range enhancers. Evolution has been conducting site-specific functionality assays for hundreds of millions of years. The ability to decipher the results of these experiments has and will continue to provide us with a wealth of information about our genome and the impact of mutations.

Introductory speaker (10 mins):

Thomas Hentrich, Gupta lab, SFU

Modelling a biomolecular flip-flop based on RNA interference

Thursday, January 20, 2010, 6:00 pm

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



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