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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