Statistics Seminar

Friday, April 9   12:00 pm - 1:00 pm

Ancestral gene order reconstruction after whole genome doubling, massive gene loss and extensive genome rearrangement

David Sankoff, University of Ottawa

Abstract: The RACCROCHE pipeline reconstructs ancestral gene orders and chromosomal contents of the ancestral genomes at all internal vertices of a phylogenetic tree. The strategy is to accumulate a very large number of generalized adjacencies, phylogenetically justified for each ancestor, in order to produce long ancestral contigs through maximum weight matching. It constructs chromosomes by counting the frequencies of ancestral contig co-occurrence on the extant genomes, clustering these for each ancestor and ordering them. We describe how to closely simulate the evolutionary process giving rise to the gene content and order of a set of extant genomes, using the example of six distantly related monocots, and to assess to what extant RACCROCHE can recover the artificial ancestral genome at the root of the phylogenetic tree relating the simulated genomes.

Bio: Dr. David Sankoff holds the Canada Research Chair in Mathematical Genomics in the Mathematics and Statistics Department at the University of Ottawa, and is cross-appointed to the Biology Department and the School of Information Technology and Engineering. Previously he was at the University of Montreal., where he introduced dynamic programming for sequence alignment, RNA structure, multiple alignment and the small phylogeny problem under parsimony. He also initiated the formal analysis of genome rearrangements. His main research interest is comparative genomics, particularly of flowering plants, the polyploidy-fractionation cycle and models for ancestral genome reconstruction.