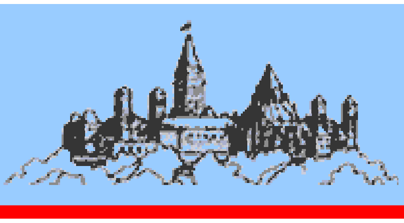
IEEE Ottawa Section



Genome rearrangements in evolution

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During evolution, the order of elements on chromosomes, and their partition among the chromosomes, is scrambled by the accumulation of rearrangement mutation events. The main kinds of genetic event are the inversion of a chromosomal segment of arbitrary length and the reciprocal translocation of segments of arbitrary length (prefix and/ or sufffix exchange) between two chromosomes. Given two related genomes, it is important to try to infer the evolutionary events that have intervened since their last common ancestor. We discuss the combinatorial optimization approach to this problem and its many generalizations, all based on the "breakpoint graph". There is also need for ways to statistically validate the results.

We explore idea that the null hypothesis for genome comparison is provided by two genomes, where the order of elements in one is an appropriately randomized permutation of the order in the other. I.e., are the characteristics of the evolutionary history of two related genomes as inferred from an algorithmic analysis different from the chance patterns obtained from two unrelated genomes? We illustrate these consideration using data from yeast, cereals, mammals and organelle genomes.

Nov 28, 2007
admission is free
13:30 – 15:00 pm
Mackenzie Building 4359
Carleton University

Light refreshment will be served

David Sankoff received his PhD in mathematics from McGill University under the direction of Donald Dawson, and has been a member of the Centre de recherches mathematiques in Montreal for many years. He currently 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. His research interest is comparative genomics, particularly probability models, statistics and algorithms for genome rearrangements.

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