

Combinatorial problems in genomics

Organizer(s):

Anne Bergeron (Université du Québec à Montréal)

Description:

The links between combinatorics and genomics are deeply rooted in the fact that the instructions for the construction of a living organism are coded sequentially in DNA molecules. Concepts such as permutations, words, patterns, or formal grammars, have been extensively used to model evolution and function of genomic sequences. On a higher level, the various parts constructed from the elementary instructions, mainly proteins and RNAs, have complex interactions that are captured by networks and graphs. In this minisymposium, we will explore some of the challenging combinatorial problems that arise from genomics.

Titles and Speakers:

- *Genome rearrangements: the two parsimonies*
Eric Tannier (Université Claude Bernard, Lyon)
- *Towards more accurate RNA structure prediction*
Anne Condon (University of British Columbia)
- *Application of combinatorial optimization to prediction of domain-domain interactions*
Teresa Przytycka (NCBI/NLM/NIH)
- *Handling duplications in genome rearrangements models*
Cedric Chauve (Simon Fraser University)
- *Counting the number of breakpoints between genomes containing duplicates*
Guillaume Fertin (Université de Nantes)