Genome Rearrangement Analysis

Genome rearrangements are large-scale mutations that permute blocks of DNA within and between chromosomes. Central problems are the computation of (i) the rearrangement distance which reflects the number of mutations have occurred in the disjoint evolutionary history of two genomes and (ii) rearrangement scenarios which detail the kind and order of these mutations. In this talk, I will review key contributions of the field from the past two decades and showcase derived methods with particular practical benefit for biological data analysis.

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Everyone is welcome!