New Models and Algorithms for Genome Comparison

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Abstract

The comparison of genomes with the same gene content relies on our ability to compare permutations, either by measuring how much they differ, or by measuring how much they are alike. With the notable exception of the breakpoint distance, which is based on the concept of conserved adjacencies, measures of distance do not generalize easily to sets of more than two permutations.

In this presentation, we introduce a basic unifying notion, conserved intervals, as a powerful generalization of adjacencies, and as a key feature of genome rearrangement theories like sorting by reversals or transpositions. We also show that sets of conserved intervals have elegant nesting and chaining properties that allow the development of compact graphic representations, and linear time algorithms to manipulate them.