An introduction to the combinatorics of genome rearrangements

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Abstract

Abstract: The genome of a species can be thought of as a set of ordered sequences of genes, the ordering devices being the chromosomes, each gene having an orientation given by its location on the DNA double strand. One can model a configuration of genes as a signed permutation of the numbers 1 through n, where each number can be positive or negative. Different species often share similar genes that were inherited from common ancestors. However, these genes have been shuffled by mutations that modified the content of chromosomes, the order of genes within a particular chromosome, and/or the orientation of a gene. In the signed permutation model, one type of mutation corresponds to performing a sign-changing reversal of a consecutive subsequence of the permutation. Comparing two sets of similar genes appearing along a chromosome in two different species yields two signed permutations. The "reversal distance" between these two permutations is the minimum number of reversals required to convert one signed permutation into the other. The reversal distance provides a good estimate of the genetic distance between the two species. This talk will serve as an introduction to the field of genome rearrangements from a combinatorial point of view. During the talk we will also discuss some open problems.

Refreshments at 3:45