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An Algebraic Theory for Genome Rearrangements

Genome rearrangements are evolutionary events where large, continuous pieces of the genome shuffle around, changing the order of genes in the genome of a species. Gene order data may be useful in estimating the evolutionary distance among genomes, and also in reconstructing the gene order of ancestral genomes.

In 2000, Meidanis and Dias proposed a framework for studying rearrangement problems, called *Algebraic Formalism*, based on permutation groups to model genomes and rearrangement operations. In its original formulation, it focuses on representing the order in which genes appear in chromosomes, and applies to circular chromosomes only.

Recently, Feijão and Meidanis introduced an extension of this formalism, called the *Adjacency Algebraic Theory*, where permutations represent the adjacencies between genes in a genome. This allowed the algebraic theory to model linear chromosomes and the use of the original algebraic distance formula in the general multichromosomal case, with both linear and circular chromosomes. It was also shown that there is a direct relationship between the original model (called *chromosomal*) and the adjacency model.

This resulting algebraic rearrangement distance is very similar, but not quite the same, to the Double-Cut-and-Join distance, a well known comprehensive model of genome rearrangements.

This talk is intended as an introduction to algebraic concepts used in genome rearrangement problems, where I will present the main ideas of the Algebraic Theory and some of its most recent developments.