Genome Rearrangements: from Biological Problems to Combinatorial Algorithms (and back)

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Abstract

Recent large-scale sequencing projects fueled the comparative genomics studies and revealed that some classical biological theories may be incomplete or even incorrect. I describe three controversial and hotly debated topics: *Whole Genome Duplications*, *Random Breakage Model of Chromosome Evolution*, and *Mammalian Phylogenomics*, and three related challenging combinatorial problems: *Genome Halving Problem*, *Breakpoint Re-Use Problem*, and *Ancestral Genomes Reconstruction Problem*. I have recently addressed these problems within a new *"Multi-Break Rearrangements"* framework that simplified their analysis and led to efficient algorithmic solutions. I have further applied the developed algorithms to sequenced mammalian genomes to study the aforementioned biological problems.