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Genome rearrangements: when intuition fails

Genome rearrangements are genomic "earthquakes" that change the chromosomal architectures. The minimum number of rearrangements between two genomes (called "genomic distance") represents a rather accurate measure for the evolutionary distance between them and is often used as such in comparative genomics studies.

In this talk I shall describe an unexpected phenomenon in genome rearrangements analysis that the weighted genomic distance designed to bound the proportion of transpositions (that are complex rearrangements rarely happening in reality) in rearrangement scenarios between two genomes does not actually achieve this goal.