Rearrangement Scenarios Guided by Chromatin Structure

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Rearrangements of blocks of gene-coding DNA are responsible for diversity on many scales. They can trigger the advent of phenotypic changes, and are involved in devastating genomic disorders. There is a quarter century of theoretical and algorithmic work devoted to finding and sampling scenarios of rearrangements that could have transformed the gene order of one species into the gene order of another. Nonetheless there is still a lack of methodology for the inference of scenarios which conform to some extra biological constraints.

We have defined a framework for cost-constrained rearrangements and devised algorithms for finding optimal scenarios within this framework.

Our work is motivated by a couple of hypotheses. First, that the sequences undergoing rearrangement need to be in close spatial proximity in the nucleus to become joined. And second, that genome's spatial organization is somewhat conserved across evolutionary distances.

We use Hi-C data to infer the evolutionary scenarios maximizing the co-locality of the breakpoints. This enables us to study our hypotheses in detail and preliminary results concerning Drosophila species are in line with them.

Our framework is liberal and can be used with data concerning active/repressive epigenetic marks, intergenic lengths, repetitive elements or other biological information relevant to rearrangements.