Swarming along the evolutionary branches sheds light on genome rearrangement scenarios

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Résumé en anglais	A genome rearrangement scenario describes a series of chromosome fusion, fission, and translocation operations that suffice to rewrite one genome into another. Exact algorithmic methods for this important problem focus on providing one solution, while the set of distance-wise equivalent scenarios is very large. Moreover, no criteria for filtering for biologically plausible scenarios is currently proposed. We present an original metaheuristic method that uses Ant Colony Optimization to randomly explore the space of optimal and suboptimal rearrangement scenarios. It improves on the state of the art both by permitting large-scale enumeration of optimal scenarios, and by labeling each with metrics that can be used for post-processing filtering based on biological constraints.
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