



A Memetic Algorithm for Phylogenetic Reconstruction with Maximum Parsimony

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Résumé en anglais	<p>The Maximum Parsimony problem aims at reconstructing a phylogenetic tree from DNA, RNA or protein sequences while minimizing the number of evolutionary changes. Much work has been devoted by the research community to solve this NP-complete problem and many algorithms and techniques have been devised in order to find high quality solutions with reasonable computational resources. In this paper we present a memetic algorithm (implemented in the software Hydra) which is based on an integration of an effective local search operator with a specific topological tree crossover operator. We report computational results of Hydra on a set of 12 benchmark instances from the literature and demonstrate its effectiveness with respect to one of the most powerful software (TNT). We also study the behavior of the algorithm with respect to some fundamental ingredients.</p>
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