



Improvement of Fitch function for Maximum Parsimony in Phylogenetic Reconstruction with Intel AVX2 assembler instructions

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Résumé en anglais 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 Computer Science community to solve this NP-complete problem and many techniques have been used or designed in order to decrease the computation time necessary to obtain an acceptable solution. In this paper we report an improvement of the evaluation of the Fitch function for Maximum Parsimony using AVX2 assembler instruction of Intel (TM) processors

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