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Towards speed up search of maximal unique matches in multicore architectutes

Abstract

Maximal Unique Matches are common substrings that are found between a reference and a query sequence. They are exact, unique and maximal; that is, they cannot be extended in left or right direction without incurring a mismatch. The computation of MUMs in large sequences is a heavy and repetitive task because the genomes are closely related, so there is a fair chance of parallelize and execute this search in multicore architectures. This research resembles a first novel approach to find MUMs in genomic sequences in parallel way. The reference genome is indexed by using a suffix tree in main memory and then the parallelized algorithm finds the MUMs against a query genome which is readed by several threads. This approach is based on MUMmer, a genome alignment tool, which is able to find Maximal Unique Matches (MUMs).

Keywords:

1.

References