Abstract

Bioinformatics is faced with accelerating increase of data set sizes originating from powerful high-throughput measuring devices. Extensive computational power is the basic requirement for solving problems in bioinformatics. One of the key solutions to time-efficient data processing is the proper implementation of computational intensive tasks using parallel technology. A large number of cores is combined into a single chip to improve the overall performance of the multi-core processors. This depicts the current trends in processor architecture. This paper proposes a new software-only speculative parallelization scheme for implementing RNA Secondary Structure Prediction algorithm in parallel. The scheme is developed after a systematic evaluation of the design options available. It is also shown to be efficient, robust and to outperform previously proposed schemes used for parallel implementation of RNA Secondary Structure Prediction.

References


SP-fold – Speculative Parallelization for Parallel Algorithm of RNA Secondary Structure Prediction on Multicore

Index Terms

- Computer Science
- Algorithms

Keywords

- RNA Secondary Structure Prediction
- Speculative Parallelization