A Study of Parallel Algorithms for Multiple Sequence Alignment

Mohammed Wajid Al-Neama

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A Study of Parallel Algorithms for Multiple Sequence Alignment Mohammed Wajid Al-Neama The exponential growth of available biological data has caused bioinformatics to be rapidly moving towards a data-intensive, computational science. As a result, the computational power needed by bioinformatics applications is growing exponentially as well. Traditional approaches to sequence analysis techniques are expensive in terms of time and memory. This leads to the use of HPC which is a widely used method to improve performance. The emergence of accelerator technologies such as multi-core architecture has made it possible to achieve an excellent improvement in execution time for many bioinformatics applications, compared to current general-purpose platforms. Therefore, using multi-cores to solve sequence analysis problems is a promising and challenging research field because large-scale computational bioinformatics problems can benefit greatly from this kind of processing power. Providing a comparison between the parallel methods available for MSA. Guiding biologists to the most convenient tool to align multiple sequences. Designing and implementing a new parallel and effective method to align multiple sequences using both multi-cores and cluster systems.

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