Abstract

The growth of bioinformatics and computational biology industry, multiple sequence alignment (MSA) applications have become an important emerging workload. In spite of the large amount of recent attention given to the MSA software design, there has been little quantitative understanding of the performance of such applications on modern microprocessors and systems. In this paper we try to analyze performance and characteristics of MSA software from
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the perspective of multicore machines. We use several popular MSA programs employing a wide variety of alignment approaches. The basic workload characteristics and the efficiencies of various multicore machines features are examined. In order to mapping parallelism in multicore machines we try to explore different parallel programming approaches using threads and MPI.
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- D. P. Tommaso, M. Orobitg, F. Guirado, F. Cores, T. Espinosa, C. Notredame,

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