Abstract

Protein 3D structure alignment process has become the key focus of interest in structural bioinformatics. Yet, obtaining perfect alignment in a short execution time was not successful to this point. To overcome this problem, researchers tend to use parallel programming techniques to enhance the performance of the alignment process. In this article, we compare between two parallel programming paradigms for implementing a parallel version of the well-known pairwise alignment algorithm MatAlign. This parallel algorithm is implemented by using two common APIs for C++ parallel programming, which are OpenMP for multi-core CPUs and CUDA for multi-core GPUs. The results show that beside the significant improvement of the parallel implementation over the sequential one, it also shows that the multi-core GPU parallel programming model improves speedup over multi-core CPU programming model.


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Parallel Protein Structure Alignment: A Comparative Study of Two Parallel Programming Paradigms

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