

A parallel computing algorithm for 16S rRNA probe design

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accepted 14 March 2006. Available online 2 May 2006.

Abstract

With the continuing rapid increase in the number of available 16S ribosomal RNA (rRNA) sequences, it is a significant computational challenge to efficiently design 16S rRNA targeted probes. In our previous work, we designed a fast software tool called ProkProbePicker (PPP) that takes $O(\log N)$ time for a worst-case scenario search. Despite this improvement, it can still take many hours for PPP to extract probes for all the clusters in a phylogenetic tree. Herein, a parallelized version of PPP is described. When run on 80 processors, this version of PPP took only 67 min to extract probes, while some 87 h were needed by the sequential version of PPP. The speedup increased linearly with the increase of CPU numbers, which revealed the outstanding scalability of the parallelized version of PPP.