

22. Guide structure calculation: a critical step for the accuracy of progressive multiple sequence alignment algorithms

Laure Vescovo Jean-Christophe Aude, Geraldine Polailon

Email: laure.vescovo@supelec.fr

Affiliation: Supelec

Country: France

We test selected clustering and phylogenetic reconstruction methods, implemented in ClustalW, to compare their efficiency with the benchmark database Balibase. The evaluation of their performance gives statistically significant results. They provide guidelines for the improvement of progressive algorithms.

MOTIVATION: Despite the importance of the guide structure calculation in progressive multiple sequence alignment algorithms, its influence on alignments accuracy was under studied. In this article, we test selected clustering and phylogenetic reconstruction methods, implemented in ClustalW, to compare their efficiency with the benchmark database Balibase.

RESULTS : The evaluation of their performance gives statistically significant results. Three methods outperform the Neighbor-Joining, which is the algorithm implemented in ClustalW. Moreover, the best method appears to depend on tested reference set. These results provide guidelines for the improvement of progressive algorithms