KLAST: a new high-performance sequence similarity search tool
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KLAST is a fast, accurate and NGS scalable bank-to-bank sequence similarity search tool providing significant accelerations of seeds-based heuristic comparison methods, such as the Blast suite of algorithms. Relying on unique software architecture, KLAST takes full advantage of recent multi-core personal computers without requiring any additional hardware devices.

Professional version of PLAST (BMC Bioinformatics, 2009)
Optimized for bank-to-bank sequence comparisons
Provide high speed and high quality results

Tools benchmark

Tara Oceans benchmark

The SSEARCH, BLAST, USEARCH software are considered
Comparison of 2,329 protein sequences from bacterium A.hospitalis against the SwissProt databank
The reference is given by SSEARCH since it implements the rigorous Smith and Waterman algorithm and generates optimal alignments. Alignments are evaluated on a moderate-size datasset due to the long execution time of SSEARCH. The diagrams synthesize the numbers of alignments found by the different softwares (A, B), the number of queries matching the reference databank (C) and the search time (D).

The gray section identifies similar alignments, i.e. alignments having an overlap greater than 80%. The red section reports other alignments. As it can be seen, the total number of alignments can exceed the number of alignments found by SSEARCH. This is mainly due to the fragmentation of long alignments (including large gaps) into shorter ones by KLAST, BLAST and USEARCH.

More benchmarks are available at koriscale.inria.fr

KLAST integration

Command-line tool
Graphical platform
Workflow and data analytics platform
CLC Genomics workbench

KLAST software development by

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