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.

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 dataset 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).

Application on comparative bacterial genomics KLAST and BLAST benchmark comparison of 8,245 sequences (translated 454 reads) from Tara Oceans metagenomic data against 15 million proteins from Uniprot. Both algorithms ran on 8 Intel Xeon cores. KLAST achieved sequence comparisons 18x times faster than BLAST, while covering up to 96% of the results produced by BLAST. Benchmark data courtesy of Thomas Vannier and Jean-Marc Aury research team (Genoscope/CEA). More on this study is available at tinyurl.com/d54ahrb

More benchmarks are available at koriscale.inria.fr