



HAL
open science

KLAST: a new high-performance sequence similarity search tool

Erwan Drezen, Patrick Durand, Dominique Lavenier

► **To cite this version:**

Erwan Drezen, Patrick Durand, Dominique Lavenier. KLAST: a new high-performance sequence similarity search tool. Bio-IT World Conference, Apr 2014, Boston, United States. hal-01088629

HAL Id: hal-01088629

<https://hal.science/hal-01088629v1>

Submitted on 9 Dec 2014

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



KLAST

High-performance sequence similarity search tool

E. DREZEN – P. DURAND – D. LAVENIER
 Bio-IT – Boston – April 29th – 1st May 2014

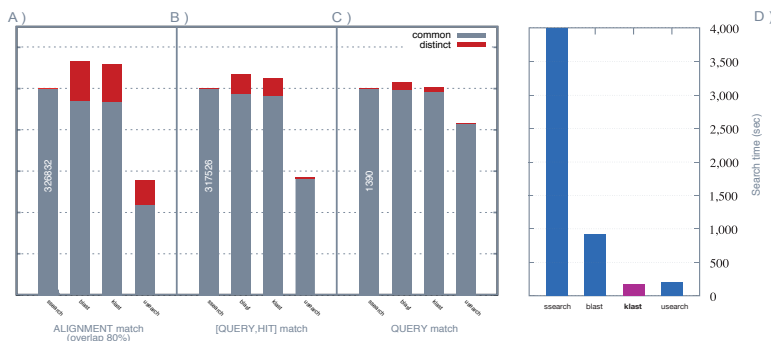
KLAST is a fast, accurate and NGS scalable bank-to-bank sequence similarity search tool providing significant accelerations of seeds-based heuristic comparison methods, such as the Blast suite of algorithms. Relying on unique software architecture, KLAST takes full advantage of recent multi-core personal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

Professional version of PLAST (BMC Bioinformatics, 2009)

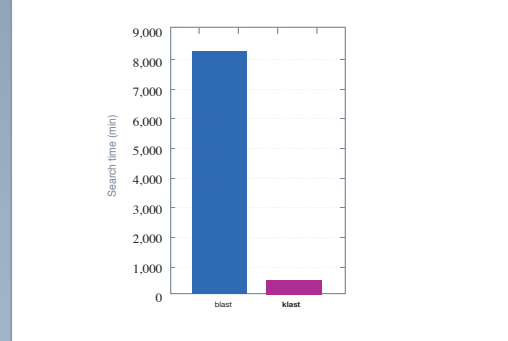
Optimized for bank-to-bank sequence comparisons

Provide high speed and high quality results

Tools benchmark



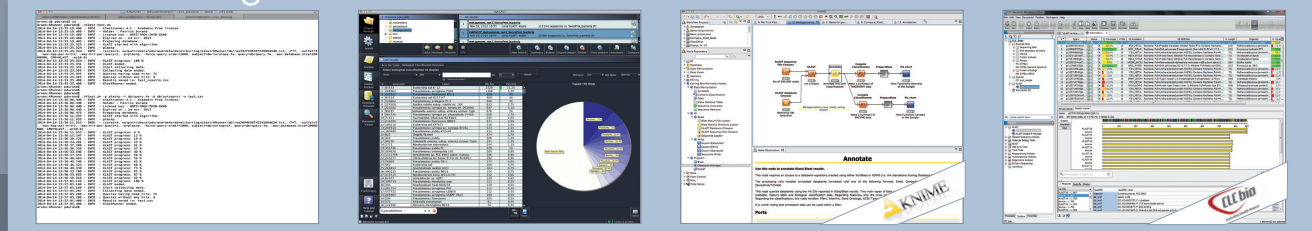
Tara Oceans benchmark



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 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). 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

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/d54ahr

KLAST integration



Command-line tool

Graphical platform

Workflow and data analytics platform

CLC Genomics workbench

KoriLog
 BIOINFORMATICS Solutions
 4 rue Gustave Eiffel
 56230 Questembert
 France
 Phone : + 33 960 368 038
www.korilog.com - klast@korilog.com



KLAST software development by



