LAST
RRID:SCR_006119
Type: Tool

Proper Citation
LAST (RRID:SCR_006119)

Resource Information
URL: http://last.cbrc.jp/
Proper Citation: LAST (RRID:SCR_006119)

Description: A tool for aligning sequences, similar to BLAST 2 sequences that colour-codes the alignments by reliability. Another useful feature of LAST is that it can compare huge (vertebrate-genome-sized) datasets. Unfortunately, this only applies to the downloadable version of LAST, not the web service. The web service can just about handle bacterial genomes, but it will take a few minutes and the output will be large. LAST can: * Handle big sequence data, e.g: ** Compare two vertebrate genomes ** Align billions of DNA reads to a genome * Indicate the reliability of each aligned column. * Use sequence quality data properly. * Compare DNA to proteins, with frameshifts. * Compare PSSMs to sequences * Calculate the likelihood of chance similarities between random sequences. LAST cannot (yet): * Do spliced alignment The main way of analyzing biological sequences is by comparing and aligning them to each other. It remains difficult, however, to compare modern multi-billionbase DNA data sets. The difficulty is caused by the nonuniform (oligo)nucleotide composition of these sequences, rather than their size per se. To solve this problem, we modified the standard seed-and-extend approach (e.g., BLAST) to use adaptive seeds. Adaptive seeds are matches that are chosen based on their rareness, instead of using fixed-length matches. This method guarantees that the number of matches, and thus the running time, increases linearly, instead of quadratically, with sequence length. LAST, our open source implementation of adaptive seeds, enables fast and sensitive comparison of large sequences with arbitrarily nonuniform composition.

Resource Type: Resource, data analysis service, data processing software, production service resource, analysis service resource, software application, service resource, software resource
References: PMID:21209072, PMID:20144198, PMID:20110255

Keywords: sequence alignment, align, vertebrate, genome, sequence, alignment

Parent Organization: National Institute of Advanced Industrial Science and Technology

Funding Agency: INTEuropean Union Systems Institute, Japanese Ministry of Education Culture Sports Science and Technology MEXT, National Genome Research Network

Related resources: RecountDB

Availability: Free, Public, Acknowledgement requested

Website Status: Last checked up

Abbreviations: LAST

Resource Name: LAST

Resource ID: SCR_006119

Alternate IDs: nlx_151594, OMICS_00584

Ratings and Alerts

No rating or validation information has been found for LAST.

No alerts have been found for LAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 193 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


Grau ET, et al. (2020) Survey of mitochondrial sequences integrated into the bovine nuclear

Rimbara E, et al. (2020) Complete Genome Sequence of Helicobacter suis Strain SNTW101c, Originally Isolated from a Patient with Nodular Gastritis. Microbiology resource announcements, 9(1).


Keum HL, et al. (2020) Structures of the Skin Microbiome and Mycobiome Depending on Skin Sensitivity. Microorganisms, 8(7).


Luo E, et al. (2020) Double-stranded DNA virioplankton dynamics and reproductive strategies in the oligotrophic open ocean water column. The ISME journal.


Chen Y, et al. (2020) Temporal transcriptional patterns of cyanophage genes suggest synchronized infection of cyanobacteria in the oceans. Microbiome, 8(1), 68.


and Physical Mapping of the Painted Turtle and Slider Turtle Genomes. Genes, 11(8).
