LAST

RRID:SCR_006119
Type: Tool

Proper Citation

LAST (RRID:SCR_006119)

Resource Information

URL: http://last.cbrc.jp/

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.

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**Resource Type:** Resource, data analysis service, data processing software, production service resource, analysis service resource, software application, service resource, software resource

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

**Resource ID:** SCR_006119

**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

**Alternate IDs:** nlx_151594, OMICS_00584

**Abbreviations:** LAST

**Mentions Count:** 145

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**Ratings and Alerts**

No rating or validation information has been found for LAST.

No alerts have been found for LAST.

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**Data and Source Information**

**Source:** [SciCrunch Registry](https://www.sci.crunch.org)

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**Usage and Citation Metrics**

We found 145 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](https://www.sci.crunch.org).


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).


