Resource Summary Report

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mrFAST

RRID:SCR_005487
Type: Tool

Proper Citation

mrFAST (RRID:SCR_005487)

Resource Information

URL: http://mrfast.sourceforge.net/

Proper Citation: mrFAST (RRID:SCR_005487)

Description: Software designed to map short reads generated with the Illumina platform to reference genome assemblies; in a fast and memory-efficient mannerl. Currently Supported Features: * Output in SAM format * Indels up to 8 bp (4 bp deletions and 4 bp insertions) * Paired-end mapping ** Discordant option to generate mapping file ready for VariationHunter to detect structural variants. * One end anchored (OEA) map locations for novel sequence insertion detection with NovelSeq * Matepair library mapping (long inserts with RF orientation). Planned Features: * Multithreading

Abbreviations: mrFAST

Synonyms: mrFAST - Micro Read Fast Alignment Search Tool, Micro Read Fast Alignment Search Tool

Resource Type: software resource

Defining Citation: PMID:19718026

Keywords: next-generation sequencing, bio.tools

Resource Name: mrFAST

Resource ID: SCR_005487

Alternate IDs: biotools:mrfast, OMICS_00671

Alternate URLs: https://bio.tools/mrfast

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260725T190604+0000

Ratings and Alerts

No rating or validation information has been found for mrFAST.

No alerts have been found for mrFAST.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

L??pez JO, et al. (2024) Improved LINE-1 Detection through Pattern Matching by Increasing Probe Length. Biology, 13(4).

Nuttle X, et al. (2024) Parallelized engineering of mutational models using piggyBac transposon delivery of CRISPR libraries. Cell reports methods, 4(1), 100672.

Aversano R, et al. (2024) Distinct structural variants and repeat landscape shape the genomes of the ancient grapes Aglianico and Falanghina. BMC plant biology, 24(1), 88.

Warren WC, et al. (2018) Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. Nature ecology & evolution, 2(4), 669.

Kim JS, et al. (2018) GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. BMC genomics, 19(Suppl 2), 89.

Zhernakova DV, et al. (2018) Analytical "bake-off" of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. PloS one, 13(7), e0200423.

Serres-Armero A, et al. (2017) Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. BMC genomics, 18(1), 977.

Hintzsche JD, et al. (2016) A Survey of Computational Tools to Analyze and Interpret Whole Exome Sequencing Data. International journal of genomics, 2016, 7983236.

Drozdova PB, et al. (2016) Genome Sequencing and Comparative Analysis of Saccharomyces cerevisiae Strains of the Peterhof Genetic Collection. PloS one, 11(5), e0154722.

Rubin BE, et al. (2016) Comparative genomics reveals convergent rates of evolution in ant-plant mutualisms. Nature communications, 7, 12679.

Dobrynin P, et al. (2015) Genomic legacy of the African cheetah, Acinonyx jubatus. Genome biology, 16, 277.

Zhuang J, et al. (2014) TEMP: a computational method for analyzing transposable element polymorphism in populations. Nucleic acids research, 42(11), 6826.

Keane TM, et al. (2014) Identification of structural variation in mouse genomes. Frontiers in genetics, 5, 192.

Miyake K, et al. (2013) Comparison of Genomic and Epigenomic Expression in Monozygotic Twins Discordant for Rett Syndrome. PloS one, 8(6), e66729.

Itsara A, et al. (2012) Resolving the breakpoints of the 17q21.31 microdeletion syndrome with next-generation sequencing. American journal of human genetics, 90(4), 599.

Kidd JM, et al. (2010) A human genome structural variation sequencing resource reveals insights into mutational mechanisms. Cell, 143(5), 837.