

Resource Summary Report

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FR-HIT

RRID:SCR_002181

Type: Tool

Proper Citation

FR-HIT (RRID:SCR_002181)

Resource Information

URL: <http://code.google.com/p/frhit/>

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Description: An efficient fragment recruitment software program for next generation sequences against microbial reference genomes. It produces similar sensitivity of BLASTN, but runs at a 100 times higher speed. The algorithm adopts a seeding heuristic strategy with overlapping k-mer hashing to locate candidate matching blocks on the reference sequences, and then apply an effective filtering within the candidate blocks to filter out blocks that do not meet the minimum criteria for containing an alignment with specified parameters. For each candidate block that passed the filter, the best matching sub-regions between a candidate block and a read are determined, and used subsequently by the banded Smith-Waterman algorithm to carry out the actual alignment efficiently, which will finally verify if this can be a valid recruitment hit.

Abbreviations: FR-HIT

Synonyms: FR-HIT: Metagenome Fragment Recruitment at High Identity with Tolerance, Metagenome Fragment Recruitment at High Identity with Tolerance, Fragment Recruitment at High Identity with Tolerance

Resource Type: software resource

Keywords: metagenomics, bioinformatics, sequence analysis, next-generation sequencing

Availability: Free, Freely available

Resource Name: FR-HIT

Resource ID: SCR_002181

Alternate IDs: OMICS_01850

License: MIT License

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260801T190208+0000

Ratings and Alerts

No rating or validation information has been found for FR-HIT.

No alerts have been found for FR-HIT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Nelkner J, et al. (2023) Abundance, classification and genetic potential of Thaumarchaeota in metagenomes of European agricultural soils: a meta-analysis. Environmental microbiome, 18(1), 26.

Tabacchioni S, et al. (2021) Identification of Beneficial Microbial Consortia and Bioactive Compounds with Potential as Plant Biostimulants for a Sustainable Agriculture. Microorganisms, 9(2).

Maus I, et al. (2020) The Role of Petrimonas mucosa ING2-E5AT in Mesophilic Biogas Reactor Systems as Deduced from Multiomics Analyses. Microorganisms, 8(12).

Dhakan DB, et al. (2019) The unique composition of Indian gut microbiome, gene catalogue, and associated fecal metabolome deciphered using multi-omics approaches. GigaScience, 8(3).

Maus I, et al. (2017) Genomics and prevalence of bacterial and archaeal isolates from biogas-producing microbiomes. Biotechnology for biofuels, 10, 264.

Jungbluth SP, et al. (2017) Genomic comparisons of a bacterial lineage that inhabits both marine and terrestrial deep subsurface systems. PeerJ, 5, e3134.

F??ssel J, et al. (2017) Adaptability as the key to success for the ubiquitous marine nitrite oxidizer Nitrococcus. Science advances, 3(11), e1700807.

Maus I, et al. (2016) Unraveling the microbiome of a thermophilic biogas plant by metagenome and metatranscriptome analysis complemented by characterization of bacterial and archaeal isolates. Biotechnology for biofuels, 9, 171.

Li RW, et al. (2014) Metagenomic insights into the RDX-degrading potential of the ovine rumen microbiome. PloS one, 9(11), e110505.

Li RW, et al. (2012) Perturbation dynamics of the rumen microbiota in response to exogenous butyrate. PloS one, 7(1), e29392.

Li RW, et al. (2011) Metagenome plasticity of the bovine abomasal microbiota in immune animals in response to *Ostertagia ostertagi* infection. PloS one, 6(9), e24417.