Resource Summary Report

Generated by NIF on Apr 27, 2025

Fsm-lite

RRID:SCR_016115
Type: Tool

Proper Citation

Fsm-lite (RRID:SCR_016115)

Resource Information

URL: https://github.com/nvalimak/fsm-lite

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Description: Software application as a single-core implementation of frequency-based substring mining. It can be used in bioinformatics to extract substrings that discriminate two (or more) datasets inside high-throughput sequencing data.

Synonyms: fsm, Frequency-based String Mining, Frequency-based String Mining (lite)

Resource Type: data analysis software, software application, software resource, data processing software

Keywords: protein, dna, rna, sequence, analysis, core, implementation, frequency, based, substring, mining, extract, discriminate, dataset, sequencing, high throughput

Funding:

Availability: Free, Available for download

Resource Name: Fsm-lite

Resource ID: SCR_016115

Alternate IDs: OMICS_28406

Alternate URLs: https://sources.debian.org/src/fsm-lite/

License: GNU General Public License v3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20250426T060525+0000

Ratings and Alerts

No rating or validation information has been found for Fsm-lite.

No alerts have been found for Fsm-lite.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Tam YL, et al. (2024) GWarrange: a pre- and post- genome-wide association studies pipeline for detecting phenotype-associated genome rearrangement events. Microbial genomics, 10(7).

Zhou H, et al. (2024) Simple and accurate genomic classification model for distinguishing between human and pig Staphylococcus aureus. Communications biology, 7(1), 1171.

Chen J, et al. (2024) Genome-based model for differentiating between infection and carriage Staphylococcus aureus. Microbiology spectrum, 12(10), e0049324.

Yang S, et al. (2024) Disease-Associated Streptococcus pneumoniae Genetic Variation. Emerging infectious diseases, 30(1), 39.

Carrara A, et al. (2024) Association of pathogenic determinants of Fusobacterium necrophorum with bacteremia, and Lemierre's syndrome. Scientific reports, 14(1), 19804.

Tiwari SK, et al. (2023) Genome-wide association reveals host-specific genomic traits in Escherichia coli. BMC biology, 21(1), 76.

De Silva PM, et al. (2023) Escherichia coli killing by epidemiologically successful sublineages of Shigella sonnei is mediated by colicins. EBioMedicine, 97, 104822.

Eriksson L, et al. (2023) Genetic variants linked to the phenotypic outcome of invasive disease and carriage of Neisseria meningitidis. Microbial genomics, 9(10).

Weber RE, et al. (2021) Genome-Wide Association Studies for the Detection of Genetic

Variants Associated With Daptomycin and Ceftaroline Resistance in Staphylococcus aureus. Frontiers in microbiology, 12, 639660.

Su M, et al. (2020) Genomic analysis of variability in Delta-toxin levels between Staphylococcus aureus strains. PeerJ, 8, e8717.

Chewapreecha C, et al. (2019) Genetic variation associated with infection and the environment in the accidental pathogen Burkholderia pseudomallei. Communications biology, 2, 428.

Jaillard M, et al. (2018) A fast and agnostic method for bacterial genome-wide association studies: Bridging the gap between k-mers and genetic events. PLoS genetics, 14(11), e1007758.