

Resource Summary Report

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

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

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: 20260729T044405+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 15 mentions in open access literature.

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

Chi W, et al. (2025) Comparative genomic analysis of 255 *Oenococcus oeni* isolates from China: unveiling strain diversity and genotype-phenotype associations of acid resistance. *Microbiology spectrum*, 13(6), e0326524.

Du W, et al. (2025) Inferring *Staphylococcus aureus* host species and cross-species transmission from a genome-based model. *BMC genomics*, 26(1), 149.

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

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).

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.

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

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

Watts SC, et al. (2021) Genomic Diversity and Antimicrobial Resistance of *Haemophilus* Colonizing the Airways of Young Children with Cystic Fibrosis. *mSystems*, 6(4), 101128msystems0017821.

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.