Resource Summary Report

Generated by NIF on Apr 17, 2025

Mugsy

RRID:SCR_001414
Type: Tool

Proper Citation

Mugsy (RRID:SCR_001414)

Resource Information

URL: http://mugsy.sourceforge.net/

Proper Citation: Mugsy (RRID:SCR_001414)

Description: Software resource for multiple whole genome alignment. It uses Nucmer, a custom graph-based segmentation procedure, for pairwise alignment, and the Seqan:TCoffee's multiple alignment strategy.

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

Defining Citation: PMID:21148543, DOI:10.1093/bioinformatics/btq665

Keywords: software, genome, genome alignment, segmentation, pairwise alignment, sequence analysis software

Funding:

Availability: Available for download

Resource Name: Mugsy

Resource ID: SCR_001414

Alternate IDs: OMICS_03606

Old URLs: https://sources.debian.org/src/mugsy/

Record Creation Time: 20220129T080207+0000

Record Last Update: 20250417T065043+0000

Ratings and Alerts

No rating or validation information has been found for Mugsy.

No alerts have been found for Mugsy.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 69 mentions in open access literature.

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

Steensen K, et al. (2024) Tailless and filamentous prophages are predominant in marine Vibrio. The ISME journal, 18(1).

Papudeshi B, et al. (2023) Host Association and Spatial Proximity Shape but Do Not Constrain Population Structure in the Mutualistic Symbiont Xenorhabdus bovienii. mBio, 14(3), e0043423.

Shallom SJ, et al. (2023) Evolution of Mycobacterium abscessus in the human lung: Cumulative mutations and genomic rearrangement of porin genes in patient isolates. Virulence, 14(1), 2215602.

Shi ZJ, et al. (2023) Maast: genotyping thousands of microbial strains efficiently. Genome biology, 24(1), 186.

Xu T, et al. (2023) A Global Survey of Hypervirulent Aeromonas hydrophila (vAh) Identified vAh Strains in the Lower Mekong River Basin and Diverse Opportunistic Pathogens from Farmed Fish and Other Environmental Sources. Microbiology spectrum, 11(2), e0370522.

Drewes JL, et al. (2022) Human Colon Cancer-Derived Clostridioides difficile Strains Drive Colonic Tumorigenesis in Mice. Cancer discovery, 12(8), 1873.

Gundappa MK, et al. (2022) Genome-Wide Reconstruction of Rediploidization Following Autopolyploidization across One Hundred Million Years of Salmonid Evolution. Molecular biology and evolution, 39(1).

Hénault M, et al. (2022) Hybridization drives mitochondrial DNA degeneration and metabolic shift in a species with biparental mitochondrial inheritance. Genome research, 32(11-12), 2043.

Allué-Guardia A, et al. (2022) Pathogenomes and variations in Shiga toxin production among geographically distinct clones of Escherichia coli O113:H21. Microbial genomics, 8(4).

Barros CP, et al. (2022) A new haplotype-resolved turkey genome to enable turkey genetics and genomics research. GigaScience, 12.

Udaondo Z, et al. (2022) Insertion sequences and other mobile elements associated with antibiotic resistance genes in Enterococcus isolates from an inpatient with prolonged bacteraemia. Microbial genomics, 8(8).

Wade KJ, et al. (2022) Phylodynamics of a regional SARS-CoV-2 rapid spreading event in Colorado in late 2020. PloS one, 17(10), e0274050.

Dienstbier A, et al. (2021) Comparative Omics Analysis of Historic and Recent Isolates of Bordetella pertussis and Effects of Genome Rearrangements on Evolution. Emerging infectious diseases, 27(1), 57.

Uengwetwanit T, et al. (2021) A chromosome-level assembly of the black tiger shrimp (Penaeus monodon) genome facilitates the identification of growth-associated genes. Molecular ecology resources, 21(5), 1620.

Bendixsen DP, et al. (2021) Genomic Evidence of an Ancient East Asian Divergence Event in Wild Saccharomyces cerevisiae. Genome biology and evolution, 13(2).

Queen J, et al. (2021) Comparative Analysis of Colon Cancer-Derived Fusobacterium nucleatum Subspecies: Inflammation and Colon Tumorigenesis in Murine Models. mBio, 13(1), e0299121.

Islam MT, et al. (2021) Population Analysis of Vibrio cholerae in Aquatic Reservoirs Reveals a Novel Sister Species (Vibrio paracholerae sp. nov.) with a History of Association with Humans. Applied and environmental microbiology, 87(17), e0042221.

Lin M, et al. (2021) Comparative Analysis of Genome of Ehrlichia sp. HF, a Model Bacterium to Study Fatal Human Ehrlichiosis. BMC genomics, 22(1), 11.

Lovchik JA, et al. (2021) Identification of an Attenuated Substrain of Francisella tularensis SCHU S4 by Phenotypic and Genotypic Analyses. Pathogens (Basel, Switzerland), 10(6).

Hénault M, et al. (2020) The effect of hybridization on transposable element accumulation in an undomesticated fungal species. eLife, 9.