

Resource Summary Report

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MetaSim

RRID:SCR_011940

Type: Tool

Proper Citation

MetaSim (RRID:SCR_011940)

Resource Information

URL: <http://ab.inf.uni-tuebingen.de/software/metasim/>

Proper Citation: MetaSim (RRID:SCR_011940)

Description: A Sequencing Simulator for Genomics and Metagenomics.

Abbreviations: MetaSim

Resource Type: software resource

Resource Name: MetaSim

Resource ID: SCR_011940

Alternate IDs: OMICS_01509

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260829T182408+0000

Ratings and Alerts

No rating or validation information has been found for MetaSim.

No alerts have been found for MetaSim.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

Yin H, et al. (2024) IPEV: identification of prokaryotic and eukaryotic virus-derived sequences in virome using deep learning. *GigaScience*, 13.

Rocha U, et al. (2024) Simulation of 69 microbial communities indicates sequencing depth and false positives are major drivers of bias in prokaryotic metagenome-assembled genome recovery. *PLoS computational biology*, 20(10), e1012530.

Liu CC, et al. (2022) MetaDecoder: a novel method for clustering metagenomic contigs. *Microbiome*, 10(1), 46.

Espindola AS, et al. (2021) Microbe Finder (MiFi??): Implementation of an Interactive Pathogen Detection Tool in Metagenomic Sequence Data. *Plants (Basel, Switzerland)*, 10(2).

Wu S, et al. (2021) DeePhage: distinguishing virulent and temperate phage-derived sequences in metavirome data with a deep learning approach. *GigaScience*, 10(9).

Allnutt TR, et al. (2021) Expanding the taxonomic range in the fecal metagenome. *BMC bioinformatics*, 22(1), 312.

Miossec MJ, et al. (2020) Evaluation of computational methods for human microbiome analysis using simulated data. *PeerJ*, 8, e9688.

Laso-Jadart R, et al. (2020) metaVaR: Introducing metavariant species models for reference-free metagenomic-based population genomics. *PloS one*, 15(12), e0244637.

Yang J, et al. (2020) An Improved Approach to Identify Bacterial Pathogens to Human in Environmental Metagenome. *Journal of microbiology and biotechnology*, 30(9), 1335.

Treiber ML, et al. (2020) Pre- and post-sequencing recommendations for functional annotation of human fecal metagenomes. *BMC bioinformatics*, 21(1), 74.

David L, et al. (2020) Targeted domain assembly for fast functional profiling of metagenomic datasets with S3A. *Bioinformatics (Oxford, England)*, 36(13), 3975.

Fang Z, et al. (2020) Identification of the conjugative and mobilizable plasmid fragments in the plasmidome using sequence signatures. *Microbial genomics*, 6(11).

Fang Z, et al. (2019) PPR-Meta: a tool for identifying phages and plasmids from metagenomic fragments using deep learning. *GigaScience*, 8(6).

Garretto A, et al. (2019) virMine: automated detection of viral sequences from complex metagenomic samples. *PeerJ*, 7, e6695.

Pereira-Flores E, et al. (2019) Fast and accurate average genome size and 16S rRNA gene average copy number computation in metagenomic data. *BMC bioinformatics*, 20(1), 453.

Ugarte A, et al. (2018) A multi-source domain annotation pipeline for quantitative metagenomic and metatranscriptomic functional profiling. *Microbiome*, 6(1), 149.

Yao Y, et al. (2018) An improved statistical model for taxonomic assignment of metagenomics. *BMC genetics*, 19(1), 98.

Wu J, et al. (2018) A fast and accurate enumeration-based algorithm for haplotyping a triploid individual. *Algorithms for molecular biology : AMB*, 13, 10.

Roosaare M, et al. (2018) PlasmidSeeker: identification of known plasmids from bacterial whole genome sequencing reads. *PeerJ*, 6, e4588.

Wang Y, et al. (2018) Identifying Group-Specific Sequences for Microbial Communities Using Long k-mer Sequence Signatures. *Frontiers in microbiology*, 9, 872.