

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi.lab-sci-crunch.org) on Apr 11, 2025

## MetaSim

RRID:SCR\_011940

Type: Tool

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### Proper Citation

MetaSim (RRID:SCR\_011940)

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### 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

**Funding:**

**Resource Name:** MetaSim

**Resource ID:** SCR\_011940

**Alternate IDs:** OMICS\_01509

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20250410T070225+0000

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### Ratings and Alerts

No rating or validation information has been found for MetaSim.

No alerts have been found for MetaSim.

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### Data and Source Information

Source: [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 40 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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

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

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.

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

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.

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).

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.

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

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

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

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

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.