Resource Summary Report

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DWGSIM

RRID:SCR_002342
Type: Tool

Proper Citation

DWGSIM (RRID:SCR_002342)

Resource Information

URL: https://github.com/nh13/DWGSIM

Proper Citation: DWGSIM (RRID:SCR_002342)

Description: Whole Genome Simulator for Next-Generation Sequencing.

Abbreviations: DWGSIM

Resource Type: software resource

Keywords: next-generation sequencing, whole genome simulation

Funding:

Availability: GNU General Public License, v2

Resource Name: DWGSIM

Resource ID: SCR_002342

Alternate IDs: OMICS_00249

Alternate URLs: https://sources.debian.org/src/dwgsim/

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250410T064857+0000

Ratings and Alerts

No rating or validation information has been found for DWGSIM.

No alerts have been found for DWGSIM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 51 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Bahk K, et al. (2024) SigAlign: an alignment algorithm guided by explicit similarity criteria. Nucleic acids research, 52(15), 8717.

Hu T, et al. (2024) Comparison of the DNBSEQ platform and Illumina HiSeq 2000 for bacterial genome assembly. Scientific reports, 14(1), 1292.

Chen J, et al. (2024) CropGS-Hub: a comprehensive database of genotype and phenotype resources for genomic prediction in major crops. Nucleic acids research, 52(D1), D1519.

Yang H, et al. (2024) Kssdtree: an interactive Python package for phylogenetic analysis based on sketching technique. Bioinformatics (Oxford, England), 40(10).

Diener C, et al. (2024) Metagenomic estimation of dietary intake from human stool. bioRxiv : the preprint server for biology.

Wang S, et al. (2023) SpecHLA enables full-resolution HLA typing from sequencing data. Cell reports methods, 3(9), 100589.

Villalba de la Peña M, et al. (2023) Chromatin structure influences rate and spectrum of spontaneous mutations in Neurospora crassa. Genome research, 33(4), 599.

Weiner S, et al. (2023) CNAsim: improved simulation of single-cell copy number profiles and DNA-seq data from tumors. Bioinformatics (Oxford, England), 39(7).

Ajaykumar A, et al. (2022) Integrative Comparison of Burrows-Wheeler Transform-Based Mapping Algorithm with de Bruijn Graph for Identification of Lung/Liver Cancer-Specific Gene. Journal of microbiology and biotechnology, 32(2), 149.

Hayden HS, et al. (2022) Genome Capture Sequencing Selectively Enriches Bacterial DNA and Enables Genome-Wide Measurement of Intrastrain Genetic Diversity in Human Infections. mBio, 13(5), e0142422.

Wang Y, et al. (2021) 2-kupl: mapping-free variant detection from DNA-seq data of matched samples. BMC bioinformatics, 22(1), 304.

Kolodziej MC, et al. (2021) A membrane-bound ankyrin repeat protein confers race-specific leaf rust disease resistance in wheat. Nature communications, 12(1), 956.

Hawari MA, et al. (2021) SomatoSim: precision simulation of somatic single nucleotide variants. BMC bioinformatics, 22(1), 109.

B?inda K, et al. (2021) Simplitigs as an efficient and scalable representation of de Bruijn graphs. Genome biology, 22(1), 96.

Xu P, et al. (2021) ClipSV: improving structural variation detection by read extension, spliced alignment and tree-based decision rules. NAR genomics and bioinformatics, 3(1), lqab003.

Liang KC, et al. (2021) MetaVelvet-DL: a MetaVelvet deep learning extension for de novo metagenome assembly. BMC bioinformatics, 22(Suppl 6), 427.

He C, et al. (2020) Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. NAR genomics and bioinformatics, 2(3), lqaa075.

Bush SJ, et al. (2020) Evaluation of methods for detecting human reads in microbial sequencing datasets. Microbial genomics, 6(7).

Durrant MG, et al. (2020) A Bioinformatic Analysis of Integrative Mobile Genetic Elements Highlights Their Role in Bacterial Adaptation. Cell host & microbe, 27(1), 140.

, et al. (2020) Selected abstracts of "Bioinformatics: from Algorithms to Applications 2020" conference. BMC bioinformatics, 21(Suppl 20), 567.