Resource Summary Report

Generated by NIF on Apr 26, 2025

PBSIM

RRID:SCR_002512
Type: Tool

Proper Citation

PBSIM (RRID:SCR_002512)

Resource Information

URL: http://code.google.com/p/pbsim/

Proper Citation: PBSIM (RRID:SCR_002512)

Description: Software that simulates PacBio reads by using either a model-based or sampling-based simulation.

Synonyms: PacBio reads simulator

Resource Type: simulation software, software resource, software application

Defining Citation: PMID:23129296, DOI:10.1093/bioinformatics/bts649

Keywords: pacbio simulation, model-based simulation, sampling-based simulation

Funding:

Availability: Open source, Available for download

Resource Name: PBSIM

Resource ID: SCR_002512

Alternate IDs: OMICS_00253

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

License: GNU GPL v2

License URLs: http://www.gnu.org/licenses/old-licenses/gpl-2.0.html

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250426T055552+0000

Ratings and Alerts

No rating or validation information has been found for PBSIM.

No alerts have been found for PBSIM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Yu W, et al. (2024) Comprehensive assessment of 11 de novo HiFi assemblers on complex eukaryotic genomes and metagenomes. Genome research, 34(2), 326.

Zong P, et al. (2024) TSTA: thread and SIMD-based trapezoidal pairwise/multiple sequence-alignment method. GigaByte (Hong Kong, China), 2024, gigabyte141.

Xie M, et al. (2022) gcaPDA: a haplotype-resolved diploid assembler. BMC bioinformatics, 23(1), 68.

Fijarczyk A, et al. (2020) The Genome Sequence of the Jean-Talon Strain, an Archeological Beer Yeast from Québec, Reveals Traces of Adaptation to Specific Brewing Conditions. G3 (Bethesda, Md.), 10(9), 3087.

Fukasawa Y, et al. (2020) LongQC: A Quality Control Tool for Third Generation Sequencing Long Read Data. G3 (Bethesda, Md.), 10(4), 1193.

Kosugi S, et al. (2019) Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. Genome biology, 20(1), 117.

Liu B, et al. (2019) deSALT: fast and accurate long transcriptomic read alignment with de Bruijn graph-based index. Genome biology, 20(1), 274.

Križanovic K, et al. (2018) Evaluation of tools for long read RNA-seq splice-aware alignment. Bioinformatics (Oxford, England), 34(5), 748.

Zhao X, et al. (2017) A recurrence-based approach for validating structural variation using

long-read sequencing technology. GigaScience, 6(8), 1.

Afshar PT, et al. (2017) COSINE: non-seeding method for mapping long noisy sequences. Nucleic acids research, 45(14), e132.

Gao S, et al. (2016) OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. Genome biology, 17, 102.