Resource Summary Report

Generated by NIF on Apr 25, 2025

NanoSim

RRID:SCR_018243
Type: Tool

Proper Citation

NanoSim (RRID:SCR_018243)

Resource Information

URL: https://github.com/bcgsc/NanoSim

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Description: Software tool as Nanopore sequence read simulator based on statistical characterization. Oxford Nanopore Technology sequence simulator written in Python and R. Benefits development of scalable next generation sequencing technologies for long nanopore reads, including genome assembly, mutation detection, and metagenomic analysis software.

Resource Type: software resource, simulation software, software application

Defining Citation: DOI:10.1093/gigascience/gix010

Keywords: Nanopore sequence read, sequence simulator, Oxford Nanopore Technology, next generation sequencing, long nanopore read, genome assembly, mutation detection, bio.tools, bio.tools

Funding: NHGRI R01 HG007182;
Genome Canada ;
Genome British Columbia ;
British Columbia Cancer Foundation ;
University of British Columbia

Availability: Free, Available for download, Freely available

Resource Name: NanoSim

Resource ID: SCR_018243

Alternate IDs: biotools:trans-nanosim, biotools:nanosim

Alternate URLs: https://www.bcgsc.ca/resources/software/nanosim, https://bio.tools/nanosim, https://bio.tools/Trans-NanoSim

License: GNU GPL v3

Record Creation Time: 20220129T080339+0000

Record Last Update: 20250425T060305+0000

Ratings and Alerts

No rating or validation information has been found for NanoSim.

No alerts have been found for NanoSim.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Chen Z, et al. (2024) Advancing metagenome-assembled genome-based pathogen identification: unraveling the power of long-read assembly algorithms in Oxford Nanopore sequencing. Microbiology spectrum, 12(6), e0011724.

Prjibelski AD, et al. (2023) Accurate isoform discovery with IsoQuant using long reads. Nature biotechnology, 41(7), 915.

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

Shiraishi Y, et al. (2023) Precise characterization of somatic complex structural variations from tumor/control paired long-read sequencing data with nanomonsv. Nucleic acids research, 51(14), e74.

Mestre-Tomás J, et al. (2023) SQANTI-SIM: a simulator of controlled transcript novelty for lrRNA-seq benchmark. bioRxiv : the preprint server for biology.

Yang C, et al. (2023) Characterization and simulation of metagenomic nanopore sequencing data with Meta-NanoSim. GigaScience, 12.

Dong X, et al. (2022) Analysis of SARS-CoV-2 known and novel subgenomic mRNAs in cell culture, animal model, and clinical samples using LeTRS, a bioinformatic tool to identify unique sequence identifiers. GigaScience, 11.

Naarmann-de Vries IS, et al. (2022) Improved nanopore direct RNA sequencing of cardiac myocyte samples by selective mt-RNA depletion. Journal of molecular and cellular cardiology, 163, 175.

Tüns AI, et al. (2022) Detection and Validation of Circular DNA Fragments Using Nanopore Sequencing. Frontiers in genetics, 13, 867018.

Hu Y, et al. (2021) LIQA: long-read isoform quantification and analysis. Genome biology, 22(1), 182.

Fan J, et al. (2021) BugSeq: a highly accurate cloud platform for long-read metagenomic analyses. BMC bioinformatics, 22(1), 160.

Sutton JM, et al. (2021) Optimizing experimental design for genome sequencing and assembly with Oxford Nanopore Technologies. GigaByte (Hong Kong, China), 2021, gigabyte27.

Hafezqorani S, et al. (2020) Trans-NanoSim characterizes and simulates nanopore RNA-sequencing data. GigaScience, 9(6).

Pearman WS, et al. (2020) Testing the advantages and disadvantages of short- and long-read eukaryotic metagenomics using simulated reads. BMC bioinformatics, 21(1), 220.

Beaulaurier J, et al. (2020) Assembly-free single-molecule sequencing recovers complete virus genomes from natural microbial communities. Genome research, 30(3), 437.

Bethune K, et al. (2019) Long-fragment targeted capture for long-read sequencing of plastomes. Applications in plant sciences, 7(5), e1243.