Resource Summary Report

Generated by NIF on Sep 11, 2026

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: simulation software, software application, software resource

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: British Columbia Cancer Foundation ;
Genome British Columbia ;
Genome Canada ;
NHGRI R01 HG007182;
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: 20260905T132833+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 21 mentions in open access literature.

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

Kazemi P, et al. (2026) AIEdit: Alignment-free genome assembly polisher trained on spaced seed match patterns. PLoS computational biology, 22(5), e1014245.

Lee J, et al. (2026) MIrROR release 02: Expanded and refined 16S-ITS-23S rRNA operon dataset. Scientific data, 13(1).

Cottingham H, et al. (2026) Nanopore sequencing enables highly accurate genotyping and identification of resistance determinants in key nosocomial pathogens. Microbial genomics, 12(3).

Peel N, et al. (2025) Real-time analysis and visualization of nanopore metagenomic samples with MARTi. Genome research, 35(11), 2488.

Chen X, et al. (2025) Species-resolved profiling of antibiotic resistance genes in complex metagenomes through long-read overlapping with Argo. Nature communications, 16(1), 1744.

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.

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

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

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.

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

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

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

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.

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

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.

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

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

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.