Resource Summary Report

Generated by NIF on Apr 28, 2025

RSVSim

RRID:SCR_001777
Type: Tool

Proper Citation

RSVSim (RRID:SCR_001777)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/RSVSim.html

Proper Citation: RSVSim (RRID:SCR_001777)

Description: A software package for the simulation of deletions, insertions, inversions, tandem duplications and translocations of various sizes in any genome available as FASTA-file or data package in R. SV breakpoints can be placed uniformly accross the whole genome, with a bias towards repeat regions and regions of high homology (for hg19) or at user-supplied coordinates.

Synonyms: RSVSim: an R/Bioconductor package for the simulation of structural variations

Resource Type: software resource

Defining Citation: PMID:23620362

Keywords: unix/linux, mac os x, windows, r, sequencing, structural variation

Funding:

Availability: GNU Lesser General Public License, v3

Resource Name: RSVSim

Resource ID: SCR_001777

Alternate IDs: OMICS_03822

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014039+0000

Ratings and Alerts

No rating or validation information has been found for RSVSim.

No alerts have been found for RSVSim.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Jung YH, et al. (2023) Characterization of a strain-specific CD-1 reference genome reveals potential inter- and intra-strain functional variability. BMC genomics, 24(1), 437.

Xu J, et al. (2023) A comprehensive analysis of copy number variations in diverse apple populations. BMC genomics, 24(1), 256.

Wei L, et al. (2021) SimFFPE and FilterFFPE: improving structural variant calling in FFPE samples. GigaScience, 10(9).

Wolujewicz P, et al. (2021) Genome-wide investigation identifies a rare copy-number variant burden associated with human spina bifida. Genetics in medicine : official journal of the American College of Medical Genetics, 23(7), 1211.

Smolander J, et al. (2021) Evaluation of tools for identifying large copy number variations from ultra-low-coverage whole-genome sequencing data. BMC genomics, 22(1), 357.

Lisiecka A, et al. (2021) Linearization of genome sequence graphs revisited. iScience, 24(7), 102755.

Wang TY, et al. (2020) ScanITD: Detecting internal tandem duplication with robust variant allele frequency estimation. GigaScience, 9(8).

Tham CY, et al. (2020) NanoVar: accurate characterization of patients' genomic structural variants using low-depth nanopore sequencing. Genome biology, 21(1), 56.

Zhou A, et al. (2019) Evaluating nanopore sequencing data processing pipelines for structural variation identification. Genome biology, 20(1), 237.

Chen L, et al. (2017) Detection and validation of structural variations in bovine whole-genome sequence data. Genetics, selection, evolution : GSE, 49(1), 13.

Alhakami H, et al. (2017) A comparative evaluation of genome assembly reconciliation tools. Genome biology, 18(1), 93.

Stuart T, et al. (2016) Population scale mapping of transposable element diversity reveals links to gene regulation and epigenomic variation. eLife, 5.

Camiolo S, et al. (2016) Altools: a user friendly NGS data analyser. Biology direct, 11(1), 8.

Lim JQ, et al. (2015) BatAlign: an incremental method for accurate alignment of sequencing reads. Nucleic acids research, 43(16), e107.