Resource Summary Report

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ART

RRID:SCR_006538
Type: Tool

Proper Citation

ART (RRID:SCR_006538)

Resource Information

URL: http://www.niehs.nih.gov/research/resources/software/biostatistics/art/

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Description: A set of simulation tools to generate synthetic next-generation sequencing reads. ART simulates sequencing reads by mimicking real sequencing process with empirical error models or quality profiles summarized from large recalibrated sequencing data. ART can also simulate reads using user own read error model or quality profiles. ART supports simulation of single-end, paired-end/mate-pair reads of three major commercial next-generation sequencing platforms: Illumina""s Solexa, Roche""s 454 and Applied Biosystems"" SOLiD. ART can be used to test or benchmark a variety of method or tools for next-generation sequencing data analysis, including read alignment, de novo assembly, SNP and structure variation discovery. ART is implemented in C++ with optimized algorithms and is highly efficient in read simulation. ART outputs reads in the FASTQ format, and alignments in the ALN format. ART can also generate alignments in the SAM alignment or UCSC BED file format.

Abbreviations: ART

Synonyms: ART - Set of Simulation Tools

Resource Type: software resource

Defining Citation: PMID:22199392, DOI:10.1093/bioinformatics/btr708

Keywords: next-generation sequencing

Funding:

Availability: Free, Public

Resource Name: ART

Resource ID: SCR_006538

Alternate IDs: OMICS_00247

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

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250410T065441+0000

Ratings and Alerts

No rating or validation information has been found for ART.

No alerts have been found for ART.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Fuhrmann L, et al. (2024) V-pipe 3.0: a sustainable pipeline for within-sample viral genetic diversity estimation. GigaScience, 13.

Sotcheff S, et al. (2023) ViReMa: a virus recombination mapper of next-generation sequencing data characterizes diverse recombinant viral nucleic acids. GigaScience, 12.

An X, et al. (2022) BOA: A partitioned view of genome assembly. iScience, 25(11), 105273.

Dong R, et al. (2022) svaRetro and svaNUMT: modular packages for annotating retrotransposed transcripts and nuclear integration of mitochondrial DNA in genome sequencing data. GigaByte (Hong Kong, China), 2022, gigabyte70.

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

Almeida A, et al. (2018) Benchmarking taxonomic assignments based on 16S rRNA gene profiling of the microbiota from commonly sampled environments. GigaScience, 7(5).

Highnam G, et al. (2015) An analytical framework for optimizing variant discovery from personal genomes. Nature communications, 6, 6275.

Katta MA, et al. (2015) NGS-QCbox and Raspberry for Parallel, Automated and Rapid Quality Control Analysis of Large-Scale Next Generation Sequencing (Illumina) Data. PloS one, 10(10), e0139868.

Yi H, et al. (2013) Co-phylog: an assembly-free phylogenomic approach for closely related organisms. Nucleic acids research, 41(7), e75.