Resource Summary Report

Generated by NIF on Apr 26, 2025

SimSeq

RRID:SCR_006947
Type: Tool

Proper Citation

SimSeq (RRID:SCR_006947)

Resource Information

URL: https://github.com/jstjohn/SimSeq

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Description: An illumina paired-end and mate-pair short read simulator. This project attempts to model as many of the quirks that exist in Illumina data as possible. Some of these quirks include the potential for chimeric reads, and non-biotinylated fragment pull down in mate-pair libraries .

Abbreviations: SimSeq

Resource Type: simulation software, software resource, software application

Keywords: bio.tools

Funding:

Availability: Free

Resource Name: SimSeq

Resource ID: SCR_006947

Alternate IDs: biotools:simseq, OMICS_00258

Alternate URLs: https://bio.tools/simseq

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250426T055909+0000

Ratings and Alerts

No rating or validation information has been found for SimSeq.

No alerts have been found for SimSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Tonkin-Hill G, et al. (2023) Robust analysis of prokaryotic pangenome gene gain and loss rates with Panstripe. Genome research, 33(1), 129.

Buratin A, et al. (2023) Systematic benchmarking of statistical methods to assess differential expression of circular RNAs. Briefings in bioinformatics, 24(1).

Fleming JF, et al. (2023) nRCFV: a new, dataset-size-independent metric to quantify compositional heterogeneity in nucleotide and amino acid datasets. BMC bioinformatics, 24(1), 145.

Venturini C, et al. (2022) Haplotype assignment of longitudinal viral deep sequencing data using covariation of variant frequencies. Virus evolution, 8(2), veac093.

Carruthers T, et al. (2022) The Implications of Incongruence between Gene Tree and Species Tree Topologies for Divergence Time Estimation. Systematic biology, 71(5), 1124.

Knyazev S, et al. (2021) Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. Nucleic acids research, 49(17), e102.

Sekizuka T, et al. (2020) A Genome Epidemiological Study of SARS-CoV-2 Introduction into Japan. mSphere, 5(6).

Lammers F, et al. (2019) Retrophylogenomics in rorquals indicate large ancestral population sizes and a rapid radiation. Mobile DNA, 10, 5.

Lewitus E, et al. (2019) A non-parametric analytic framework for within-host viral phylogenies and a test for HIV-1 founder multiplicity. Virus evolution, 5(2), vez044.

Assefa AT, et al. (2018) Differential gene expression analysis tools exhibit substandard performance for long non-coding RNA-sequencing data. Genome biology, 19(1), 96.

Nakada-Tsukui K, et al. (2018) AIG1 affects in vitro and in vivo virulence in clinical isolates of Entamoeba histolytica. PLoS pathogens, 14(3), e1006882.

Eisfeldt J, et al. (2018) AMYCNE: Confident copy number assessment using whole genome sequencing data. PloS one, 13(3), e0189710.

Baaijens JA, et al. (2017) De novo assembly of viral quasispecies using overlap graphs. Genome research, 27(5), 835.

Imamura D, et al. (2017) Comparative genome analysis of VSP-II and SNPs reveals heterogenic variation in contemporary strains of Vibrio cholerae O1 isolated from cholera patients in Kolkata, India. PLoS neglected tropical diseases, 11(2), e0005386.

Klopfstein S, et al. (2017) More on the Best Evolutionary Rate for Phylogenetic Analysis. Systematic biology, 66(5), 769.

Zojer M, et al. (2017) Variant profiling of evolving prokaryotic populations. PeerJ, 5, e2997.

Sikdar S, et al. (2017) EAMA: Empirically adjusted meta-analysis for large-scale simultaneous hypothesis testing in genomic experiments. PloS one, 12(10), e0187287.

Briskine RV, et al. (2017) Positional bias in variant calls against draft reference assemblies. BMC genomics, 18(1), 263.

Tripathi R, et al. (2017) Unraveling long non-coding RNAs through analysis of high-throughput RNA-sequencing data. Non-coding RNA research, 2(2), 111.

Ni S, et al. (2016) Improvement in detection of minor alleles in next generation sequencing by base quality recalibration. BMC genomics, 17, 139.