Resource Summary Report

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RNASeqReadSimulator

RRID:SCR_000270
Type: Tool

Proper Citation

RNASeqReadSimulator (RRID:SCR_000270)

Resource Information

URL: https://github.com/davidliwei/RNASeqReadSimulator

Proper Citation: RNASeqReadSimulator (RRID:SCR_000270)

Description: A software tool to generate simulated single-end or paired-end RNA-Seq reads. # It allows users to randomly assign expression levels of transcripts and generate simulated single-end or paired-end RNA-Seq reads. # It is able to generate RNA-Seq reads that have a specified positional bias profile. # It is able to simulate random read errors from sequencing platforms. # The simulator consists of a few simple Python scripts. All scripts are command line driven, allowing users to invoke and design more functions.

Abbreviations: RNASeqReadSimulator

Resource Type: software resource

Keywords: rna-seq, command line

Funding:

Availability: Free, Public

Resource Name: RNASeqReadSimulator

Resource ID: SCR_000270

Alternate IDs: OMICS_01964

Record Creation Time: 20220129T080200+0000

Record Last Update: 20250410T064536+0000

Ratings and Alerts

No rating or validation information has been found for RNASeqReadSimulator.

No alerts have been found for RNASeqReadSimulator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Peng G, et al. (2016) A novel codon-based de Bruijn graph algorithm for gene construction from unassembled transcriptomes. Genome biology, 17(1), 232.