Resource Summary Report

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BEERS

RRID:SCR_005090
Type: Tool

Proper Citation

BEERS (RRID:SCR_005090)

Resource Information

URL: http://cbil.upenn.edu/BEERS/

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Description: A simulation engine for generating RNA-Seq data that was designed to benchmark RNA-Seq alignment algorithms and also algorithms that aim to reconstruct different isoforms and alternate splicing from RNA-Seq data. By default BEERS simulates either mouse or human paired-end RNA-Seq data modeled on the illumina platform. It starts with a large number of gene models (approx 500K) taken from about ten different published annotation efforts, and then chooses a fixed number of these genes at random (30,000 by default). This avoids biasing for or against any particular set of annotations. BEERS then introduces substitutions, indels, alternate spice forms, sequencing errors, and intron signal. BEERS can also simulate strand specific reads. BEERS does not simulate quality scores. There are four configuration files required, these are available for human and mouse. BEERS can also be configured to use any set of gene models. Pre-built indexes for human refseq are given. Using these indexes will generate a much tamer set of transcripts. BEERS is written in perl.

Abbreviations: BEERS

Synonyms: Benchmarker for Evaluating the Effectiveness of RNA-Seq Software (BEERS), Benchmarker for Evaluating the Effectiveness of RNA-Seq Software

Resource Type: software resource

Defining Citation: PMID:21775302

Keywords: perl, rna-seq

Resource Name: BEERS

Resource ID: SCR_005090

Alternate IDs: OMICS_01364

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260801T190254+0000

Ratings and Alerts

No rating or validation information has been found for BEERS.

No alerts have been found for BEERS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Aicher JK, et al. (2025) MAJIQ-CLIN: A novel tool for the identification of Mendelian disease-causing variants from RNA-Seq data. medRxiv : the preprint server for health sciences.

Vaquero-Garcia J, et al. (2023) RNA splicing analysis using heterogeneous and large RNA-seq datasets. Nature communications, 14(1), 1230.

Chang CT, et al. (2023) Development of a Malaysian potentially inappropriate prescribing screening tool in older adults (MALPIP): a Delphi study. Journal of pharmaceutical policy and practice, 16(1), 122.

Mena S, et al. (2023) Implementation of interprofessional quality circles on deprescribing in Swiss nursing homes: an observational study. BMC geriatrics, 23(1), 620.

Sarantopoulou D, et al. (2021) Comparative evaluation of full-length isoform quantification from RNA-Seq. BMC bioinformatics, 22(1), 266.

Slaff B, et al. (2021) MOCCASIN: a method for correcting for known and unknown confounders in RNA splicing analysis. Nature communications, 12(1), 3353.

Yang A, et al. (2019) Scavenger: A pipeline for recovery of unaligned reads utilising similarity with aligned reads. F1000Research, 8, 1587.

Russell P, et al. (2019) A pilot cohort study of deprescribing for nursing home patients acutely admitted to hospital. Therapeutic advances in drug safety, 10, 2042098619854876.

Aguiar D, et al. (2018) Bayesian nonparametric discovery of isoforms and individual specific quantification. Nature communications, 9(1), 1681.

Sterne-Weiler T, et al. (2018) Efficient and Accurate Quantitative Profiling of Alternative Splicing Patterns of Any Complexity on a Laptop. Molecular cell, 72(1), 187.

Wallace E, et al. (2017) Impact of Potentially Inappropriate Prescribing on Adverse Drug Events, Health Related Quality of Life and Emergency Hospital Attendance in Older People Attending General Practice: A Prospective Cohort Study. The journals of gerontology. Series A, Biological sciences and medical sciences, 72(2), 271.

Medina I, et al. (2016) Highly sensitive and ultrafast read mapping for RNA-seq analysis. DNA research : an international journal for rapid publication of reports on genes and genomes, 23(2), 93.

Hayer KE, et al. (2015) Benchmark analysis of algorithms for determining and quantifying full-length mRNA splice forms from RNA-seq data. Bioinformatics (Oxford, England), 31(24), 3938.

Yang PJ, et al. (2015) Potentially Inappropriate Prescribing in Disabled Older Patients with Chronic Diseases: A Screening Tool of Older Persons' Potentially Inappropriate Prescriptions versus Beers 2012 Criteria. Medical principles and practice : international journal of the Kuwait University, Health Science Centre, 24(6), 565.

Davidson NM, et al. (2015) JAFFA: High sensitivity transcriptome-focused fusion gene detection. Genome medicine, 7(1), 43.

Chang Z, et al. (2014) The impacts of read length and transcriptome complexity for de novo assembly: a simulation study. PloS one, 9(4), e94825.

Toung JM, et al. (2014) Detection theory in identification of RNA-DNA sequence differences using RNA-sequencing. PloS one, 9(11), e112040.

Lahens NF, et al. (2014) IVT-seq reveals extreme bias in RNA sequencing. Genome biology, 15(6), R86.

Momin TG, et al. (2013) Use of potentially inappropriate medications in hospitalized elderly at a teaching hospital: a comparison between Beers 2003 and 2012 criteria. Indian journal of pharmacology, 45(6), 603.

Carrara M, et al. (2013) State-of-the-art fusion-finder algorithms sensitivity and specificity. BioMed research international, 2013, 340620.