Resource Summary Report

Generated by RRID on Apr 8, 2025

BitSeq

RRID:SCR_009904
Type: Tool

Proper Citation

BitSeq (RRID:SCR_009904)

Resource Information

URL: http://code.google.com/p/bitseq/

Proper Citation: BitSeq (RRID:SCR_009904)

Description: A software application for inferring expression levels of individual transcripts from sequencing (RNA-Seq) data and estimating differential expression (DE) between conditions.

Abbreviations: BitSeq

Resource Type: software resource

Defining Citation: DOI:10.1093/bioinformatics/btv483, DOI:10.1093/bioinformatics/bts260

Keywords: bio.tools

Funding:

Resource Name: BitSeq

Resource ID: SCR_009904

Alternate IDs: OMICS_01269, biotools:bitseq

Alternate URLs: https://bio.tools/bitseq, https://sources.debian.org/src/bitseq/

Record Creation Time: 20220129T080255+0000

Record Last Update: 20250214T183137+0000

Ratings and Alerts

No rating or validation information has been found for BitSeq.

No alerts have been found for BitSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Abate A, et al. (2023) Microbiome single cell atlases generated with a commercial instrument. Research square.

Warner AD, et al. (2019) The C. elegans embryonic transcriptome with tissue, time, and alternative splicing resolution. Genome research, 29(6), 1036.

Baumgartner C, et al. (2018) An ERK-Dependent Feedback Mechanism Prevents Hematopoietic Stem Cell Exhaustion. Cell stem cell, 22(6), 879.

Papastamoulis P, et al. (2018) A Bayesian model selection approach for identifying differentially expressed transcripts from RNA sequencing data. Journal of the Royal Statistical Society. Series C, Applied statistics, 67(1), 3.

Williams CR, et al. (2017) Empirical assessment of analysis workflows for differential expression analysis of human samples using RNA-Seq. BMC bioinformatics, 18(1), 38.

Bronowski C, et al. (2017) Campylobacter jejuni transcriptome changes during loss of culturability in water. PloS one, 12(11), e0188936.

Gatto S, et al. (2017) ICF-specific DNMT3B dysfunction interferes with intragenic regulation of mRNA transcription and alternative splicing. Nucleic acids research, 45(10), 5739.

Rendeiro AF, et al. (2016) Chromatin accessibility maps of chronic lymphocytic leukaemia identify subtype-specific epigenome signatures and transcription regulatory networks. Nature communications, 7, 11938.

Ustianenko D, et al. (2016) TUT-DIS3L2 is a mammalian surveillance pathway for aberrant structured non-coding RNAs. The EMBO journal, 35(20), 2179.

?abaj PP, et al. (2016) Sensitivity, specificity, and reproducibility of RNA-Seq differential expression calls. Biology direct, 11(1), 66.

Sankar A, et al. (2016) Bayesian identification of bacterial strains from sequencing data. Microbial genomics, 2(8), e000075.

Topa H, et al. (2016) Analysis of differential splicing suggests different modes of short-term splicing regulation. Bioinformatics (Oxford, England), 32(12), i147.

Li J, et al. (2016) Single-cell transcriptomes reveal characteristic features of human pancreatic islet cell types. EMBO reports, 17(2), 178.

Liu X, et al. (2015) Improving RNA-Seq expression estimation by modeling isoform- and exon-specific read sequencing rate. BMC bioinformatics, 16, 332.

Gardiner LJ, et al. (2015) A genome-wide survey of DNA methylation in hexaploid wheat. Genome biology, 16, 273.

Kanitz A, et al. (2015) Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. Genome biology, 16(1), 150.

, et al. (2014) A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature biotechnology, 32(9), 903.