Resource Summary Report

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ReCount - A multi-experiment resource of analysis-ready RNA-seq gene count datasets

RRID:SCR_001774
Type: Tool

Proper Citation

ReCount - A multi-experiment resource of analysis-ready RNA-seq gene count datasets (RRID:SCR_001774)

Resource Information

URL: http://bowtie-bio.sourceforge.net/recount/

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Description: RNA-seq gene count datasets built using the raw data from 18 different studies. The raw sequencing data (.fastq files) were processed with Myrna to obtain tables of counts for each gene. For ease of statistical analysis, they combined each count table with sample phenotype data to form an R object of class ExpressionSet. The count tables, ExpressionSets, and phenotype tables are ready to use and freely available. By taking care of several preprocessing steps and combining many datasets into one easily-accessible website, we make finding and analyzing RNA-seq data considerably more straightforward.

Abbreviations: ReCount

Resource Type: data set, data or information resource

Defining Citation: PMID:22087737

Keywords: rna-seq, gene count, gene, phenotype, r

Funding: NIGMS T32GM074906

Resource Name: ReCount - A multi-experiment resource of analysis-ready RNA-seq gene count datasets

Resource ID: SCR_001774

Alternate IDs: OMICS_01953

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250411T054655+0000

Ratings and Alerts

No rating or validation information has been found for ReCount - A multi-experiment resource of analysis-ready RNA-seq gene count datasets.

No alerts have been found for ReCount - A multi-experiment resource of analysis-ready RNA-seq gene count datasets.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Volpe R, et al. (2024) Restaurant outlet density and the healthfulness of food purchases: evidence from FoodAPS. Frontiers in nutrition, 11, 1369240.

Bernal V, et al. (2022) GeneNetTools: tests for Gaussian graphical models with shrinkage. Bioinformatics (Oxford, England), 38(22), 5049.

Wang Y, et al. (2022) Addressing the mean-correlation relationship in co-expression analysis. PLoS computational biology, 18(3), e1009954.

Bernal V, et al. (2021) The 'un-shrunk' partial correlation in Gaussian graphical models. BMC bioinformatics, 22(1), 424.

Schulz L, et al. (2021) Direct long-read RNA sequencing identifies a subset of questionable exitrons likely arising from reverse transcription artifacts. Genome biology, 22(1), 190.

Baik B, et al. (2020) Benchmarking RNA-seq differential expression analysis methods using spike-in and simulation data. PloS one, 15(4), e0232271.

Shahjaman M, et al. (2020) Robust identification of differentially expressed genes from RNA-seq data. Genomics, 112(2), 2000.

Park K, et al. (2019) BALLI: Bartlett-adjusted likelihood-based linear model approach for identifying differentially expressed genes with RNA-seq data. BMC genomics, 20(1), 540.

Lin B, et al. (2019) Stability of methods for differential expression analysis of RNA-seq data. BMC genomics, 20(1), 35.

Wang Z, et al. (2019) A Method Based on Differential Entropy-Like Function for Detecting Differentially Expressed Genes Across Multiple Conditions in RNA-Seq Studies. Entropy (Basel, Switzerland), 21(3).

Zhao S, et al. (2018) Silhouette Scores for Arbitrary Defined Groups in Gene Expression Data and Insights into Differential Expression Results. Biological procedures online, 20, 5.

Križanovic K, et al. (2018) Evaluation of tools for long read RNA-seq splice-aware alignment. Bioinformatics (Oxford, England), 34(5), 748.

Gao Z, et al. (2018) DREAMSeq: An Improved Method for Analyzing Differentially Expressed Genes in RNA-seq Data. Frontiers in genetics, 9, 588.

Van den Berge K, et al. (2017) stageR: a general stage-wise method for controlling the gene-level false discovery rate in differential expression and differential transcript usage. Genome biology, 18(1), 151.

Li D, et al. (2017) Bon-EV: an improved multiple testing procedure for controlling false discovery rates. BMC bioinformatics, 18(1), 1.

Low JZB, et al. (2017) CORNAS: coverage-dependent RNA-Seq analysis of gene expression data without biological replicates. BMC bioinformatics, 18(Suppl 16), 575.

Karthik D, et al. (2016) Elucidating tissue specific genes using the Benford distribution. BMC genomics, 17, 595.

Nguyen T, et al. (2016) RNA-Seq Count Data Modelling by Grey Relational Analysis and Nonparametric Gaussian Process. PloS one, 11(10), e0164766.

Yang W, et al. (2016) ABSSeq: a new RNA-Seq analysis method based on modelling absolute expression differences. BMC genomics, 17, 541.

Yoon S, et al. (2016) Improving Gene-Set Enrichment Analysis of RNA-Seq Data with Small Replicates. PloS one, 11(11), e0165919.