bioconductor.org/packages/release/bioc/html/DESeq2.html

Rule 3 Rule 7

DESeq2

Rule 8

platforms all | rank 26 / 1905 | posts 283 / 1 / 2 / 37 | in Bioc 7.5 years
build error | updated since release | dependencies 93

Rule 2

DOI: 10.18129/B9.bioc.DESeq2

Differential gene expression analysis based on the negative binomial distribution

Bioconductor version: Release (3.11) Rule 3

Estimate variance-mean dependence in count data from high-throughput sequencing assays and test for differential expression based on a model using the negative binomial distribution.

Rule 7

Author: Michael Love [aut, cre], Constantin Ahlmann-Eltze [ctb], Simon Anders [aut, ctb], Wolfgang Huber [aut, ctb]

Maintainer: Michael Love <michaelisaiahlove at gmail.com>

Rule 6

Citation (from within R, enter citation("DESeq2")):

Love MI, Huber W, Anders S (2014). "Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2." *Genome Biology*, **15**, 550. doi: 10.1186/s13059-014-0550-8.

Installation

To install this package, start R (version "4.0") and enter:

```
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")

BiocManager::install("DESeq2")
```

Rule 3

For older versions of R, please refer to the appropriate Bioconductor release.

Documentation

To view documentation for the version of this package installed in your system, start R and enter:

```
browseVignettes("DESeq2")
```

Rule 4

HTML	R Script	Analyzing RNA-seq data with DESeq2
PDF		Reference Manual
Text		NEWS

Rule 5

Details

biocViews	Bayesian, ChIPSeq, Clustering, DifferentialExpression, GeneExpression, ImmunoOncology, Normalization, PrincipalComponent, RNASeq, Regression, Sequencing, Software, Transcription
Version	1.28.1
In Bioconductor since	BioC 2.12 (R-3.0) (7.5 years)
License	LGPL (>= 3)
Depends	S4Vectors(>= 0.23.18), IRanges, GenomicRanges, SummarizedExperiment(>= 1.1.6)
Imports	BiocGenerics(>= 0.7.5), Biobase, BiocParallel, genefilter, methods, stats4, locfit, geneplotter, ggplot2, Rcpp (>= 0.11.0)
LinkingTo	Rcpp, RcppArmadillo
Suggests	testthat, knitr, rmarkdown, vsn, pheatmap, RColorBrewer, apeglm, ashr, tximport, tximeta, tximportData, readr, pbapply, airway, pasilla(>= 0.2.10)
SystemRequirements	
Enhances	
URL	https://github.com/mikelove/DESeq2
Depends On Me	DChIPRep, DEWSeq, DEXSeq, FourCSeq, metaseqR2, rgsepd, rnaseqDTU, rnaseqGene, TCC, XBSeq
Imports Me	anamiR, Anaquin, animalcules, anota2seq, BloodCancerMultiOmics2017, BRGenomics, CeTF, circRNAprofiler, consensusDE, coseq, countsimQC, DaMiRseq, debrowser, DEComplexDisease, DEFormats, DEGreport, deltaCaptureC, DEsubs, DiffBind, eegc, ERSSA, exomePeak2, GDCRNATools, GeneTonic, GenoGAM, HTSFilter, icetea, ideal, IHWpaper, ImpulseDE2, INSPEcT, IntEREst, isomiRs, JunctionSeq, kissDE, MLSeq, muscat, NBAMSeq, ORFik, OUTRIDER, PathoStat, pcaExplorer, phantasus, PowerExplorer, recountWorkflow, regionReport, ReportingTools, Rmmquant, RNASeqR, scBFA, singleCellTK, SNPhood, srnadiff, systemPipeR, TBSignatureProfiler, TimeSeriesExperiment, vidger
Suggests Me	apeglm, biobroom, BiocGenerics, BioCor, BiocSet, CAGEr, CAGEWorkflow, compcodeR, curatedAdipoChIP, curatedAdipoRNA, dearseq, derfinder, diffloop, dittoSeq, EnhancedVolcano, fishpond, fluentGenomics, gage, GenomicAlignments, GenomicRanges, Glimma, glmGamPoi, IHW, JctSeqData, miRmine, OPWeight, phyloseq, progeny, recount, RegParallel, RUVSeq, scran, Single.mTEC.Transcriptomes, subSeq, SummarizedBenchmark, TFEA.ChIP, ToPASeq, topconfects, tximeta, tximport, variancePartition, Wrench, zinbwave
Links To Me	
Build Report	

Rule 2 Rule 5 Rule 3/8 Rule 8 Rule 5

Package Archives

Follow Installation instructions to use this package in your R session.

Source Package	DESeq2_1.28.1.tar.gz
Windows Binary	DESeq2_1.28.1.zip (32- & 64-bit)
macOS 10.13 (High Sierra)	DESeq2_1.28.1.tgz
Source Repository	git clone https://git.bioconductor.org/packages/DESeq2
Source Repository (Developer Access)	git clone git@git.bioconductor.org:packages/DESeq2
Package Short Url	https://bioconductor.org/packages/DESeq2/
Package Downloads Report	Download Stats
Old Source Packages for BioC 3.11	Source Archive

Documentation »

Bioconductor

- Package vignettes and manuals.
- Workflows for learning and use.
- Course and conference material.
- Videos.
- Community resources and tutorials.

R / CRAN packages and documentation

Rule 4

Support »

Please read the posting guide. Post questions about Bioconductor to one of the following locations:

- Support site - for questions about Bioconductor packages
- Bioc-devel mailing list - for package developers

Rule 4