

Package: rnaseqGene (via r-universe)

October 4, 2026

Title RNA-seq workflow: gene-level exploratory analysis and differential expression

Version 1.36.0

Date 2026-04-13

Description Here we walk through an end-to-end gene-level RNA-seq differential expression workflow using Bioconductor packages. We will start from the FASTQ files, show how these were aligned to the reference genome, and prepare a count matrix which tallies the number of RNA-seq reads/fragments within each gene for each sample. We will perform exploratory data analysis (EDA) for quality assessment and to explore the relationship between samples, perform differential gene expression analysis, and visually explore the results.

Depends R (>= 3.3.0), BiocStyle, airway (>= 1.5.3), tximeta, magrittr, DESeq2, apeglm, vsn, dplyr, ggplot2, hexbin, pheatmap, RColorBrewer, PoiClaClu, glmpca, ggbeeswarm, genefilter, AnnotationDbi, org.Hs.eg.db, Gviz, sva, RUVSeq, fission

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews Workflow, GeneExpressionWorkflow, ImmunoOncologyWorkflow

Suggests knitr, rmarkdown

NeedsCompilation no

URL <https://github.com/thelovelab/rnaseqGene/>

Config/pak/sysreqs cmake make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

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RemoteUrl <https://github.com/bioc/rnaseqGene>

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