

Package: recountWorkflow (via r-universe)

October 4, 2026

Title recount workflow: accessing over 70,000 human RNA-seq samples with Bioconductor

Version 1.36.0

Date 2024-05-21

Description The recount2 resource is composed of over 70,000 uniformly processed human RNA-seq samples spanning TCGA and SRA, including GTEx. The processed data can be accessed via the recount2 website and the recount Bioconductor package. This workflow explains in detail how to use the recount package and how to integrate it with other Bioconductor packages for several analyses that can be carried out with the recount2 resource. In particular, we describe how the coverage count matrices were computed in recount2 as well as different ways of obtaining public metadata, which can facilitate downstream analyses. Step-by-step directions show how to do a gene level differential expression analysis, visualize base-level genome coverage data, and perform an analyses at multiple feature levels. This workflow thus provides further information to understand the data in recount2 and a compendium of R code to use the data.

Depends R (>= 3.6.0)

License Artistic-2.0

Encoding UTF-8

biocViews Workflow, ResourceQueryingWorkflow

VignetteBuilder knitr

Imports recount, GenomicRanges, limma, edgeR, DESeq2, pheatmap, regionReport, clusterProfiler, org.Hs.eg.db, gplots, derfinder, GenomicState, bumphunter, derfinderPlot

Suggests BiocStyle, BiocWorkflowTools, knitr, magick, sessioninfo, rmarkdown

NeedsCompilation no

Workflow true

URL <https://github.com/LieberInstitute/recountWorkflow>

BugReports <https://support.bioconductor.org/t/recountWorkflow/>

RoxygenNote 7.2.3

Config/pak/sysreqs

libcairo2-dev cmake libfontconfig1-dev libfreetype6-dev libglpk-dev make libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

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

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