Resource Summary Report

Generated by NIF on Apr 29, 2025

DeconRNASeq

RRID:SCR_006713
Type: Tool

Proper Citation

DeconRNASeq (RRID:SCR_006713)

Resource Information

URL: http://www.bioconductor.org/packages/2.12/bioc/html/DeconRNASeq.html

Proper Citation: DeconRNASeq (RRID:SCR_006713)

Description: An R package for deconvolution of heterogeneous tissues based on mRNA-Seq data. It modeled expression levels from heterogeneous cell populations in mRNA-Seq as the weighted average of expression from different constituting cell types and predicted cell type proportions of single expression profiles.

Abbreviations: DeconRNASeq

Resource Type: software resource

Funding:

Resource Name: DeconRNASeq

Resource ID: SCR_006713

Alternate IDs: OMICS_01230

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250420T014343+0000

Ratings and Alerts

No rating or validation information has been found for DeconRNASeq.

No alerts have been found for DeconRNASeq.

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.

Sémon M, et al. (2025) Comparative transcriptomics in serial organs uncovers early and pan-organ developmental changes associated with organ-specific morphological adaptation. Nature communications, 16(1), 768.

Cao D, et al. (2025) Time-series single-cell transcriptomic profiling of luteal-phase endometrium uncovers dynamic characteristics and its dysregulation in recurrent implantation failures. Nature communications, 16(1), 137.

Wang L, et al. (2024) Single-cell transcriptomic-informed deconvolution of bulk data identifies immune checkpoint blockade resistance in urothelial cancer. iScience, 27(6), 109928.

Larsen JH, et al. (2024) Benchmarking transcriptome deconvolution methods for estimating tissue- and cell-type-specific extracellular vesicle abundances. Journal of extracellular vesicles, 13(9), e12511.

Ahn C, et al. (2024) An optimized pipeline for high-throughput bulk RNA-Seq deconvolution illustrates the impact of obesity and weight loss on cell composition of human adipose tissue. bioRxiv : the preprint server for biology.

Wang C, et al. (2024) Deconvolution from bulk gene expression by leveraging sample-wise and gene-wise similarities and single-cell RNA-Seq data. BMC genomics, 25(1), 875.

Armero AS, et al. (2024) Co-analysis of methylation platforms for signatures of biological aging in the domestic dog reveals previously unexplored confounding factors. Aging, 16(13), 10724.

Hurtado M, et al. (2024) Transcriptomics profiling of the non-small cell lung cancer microenvironment across disease stages reveals dual immune cell-type behaviors. Frontiers in immunology, 15, 1394965.

Revkov E, et al. (2023) PUREE: accurate pan-cancer tumor purity estimation from gene expression data. Communications biology, 6(1), 394.

Tran TH, et al. (2022) Whole-transcriptome analysis in acute lymphoblastic leukemia: a

report from the DFCI ALL Consortium Protocol 16-001. Blood advances, 6(4), 1329.

Sutton GJ, et al. (2022) Comprehensive evaluation of deconvolution methods for human brain gene expression. Nature communications, 13(1), 1358.

Schmidt AF, et al. (2022) Fetal maturation revealed by amniotic fluid cell-free transcriptome in rhesus macaques. JCI insight, 7(18).

Barone DG, et al. (2022) Prevention of the foreign body response to implantable medical devices by inflammasome inhibition. Proceedings of the National Academy of Sciences of the United States of America, 119(12), e2115857119.

Rostovskaya M, et al. (2022) Amniogenesis occurs in two independent waves in primates. Cell stem cell, 29(5), 744.

Betto RM, et al. (2021) Metabolic control of DNA methylation in naive pluripotent cells. Nature genetics, 53(2), 215.

Elosua-Bayes M, et al. (2021) SPOTlight: seeded NMF regression to deconvolute spatial transcriptomics spots with single-cell transcriptomes. Nucleic acids research, 49(9), e50.

Özgümü? T, et al. (2021) Reduced expression of OXPHOS and DNA damage genes is linked to protection from microvascular complications in long-term type 1 diabetes: the PROLONG study. Scientific reports, 11(1), 20735.

Lackner A, et al. (2021) Cooperative genetic networks drive embryonic stem cell transition from naïve to formative pluripotency. The EMBO journal, 40(8), e105776.

Stirparo GG, et al. (2021) OCT4 induces embryonic pluripotency via STAT3 signaling and metabolic mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 118(3).

Xu F, et al. (2020) Genome-wide transcriptome architecture in a mouse model of Gulf War Illness. Brain, behavior, and immunity, 89, 209.