

Resource Summary Report

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variancePartition

RRID:SCR_019204

Type: Tool

Proper Citation

variancePartition (RRID:SCR_019204)

Resource Information

URL: <https://bioconductor.org/packages/variancePartition/>

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Description: Software R package to quantify and interpret divers of variation in multilevel gene expression experiments. Provides statistical and visualization framework for studying drivers of variation in RNA-seq datasets in many types of high throughput genomic assays including RNA-seq gene-, exon- and isoform-level quantification, splicing efficiency, protein quantification, metabolite quantification, metagenomic assays, methylation arrays and epigenomic sequencing assays.

Resource Type: data analysis software, software application, software resource, data processing software, data analytics software

Defining Citation: [PMID:27884101](#)

Keywords: Repeated measures, variation in gene expression, RNA-seq datasets, high throughput genomic assays, splicing efficiency, protein quantification, metabolite quantification, metagenomic assays, methylation arrays, epigenomic sequencing assays, bio.tools

Funding: NHLBI U01 HL107388;
Icahn School of Medicine at Mount Sinai

Availability: Free, Available for download, Freely available

Resource Name: variancePartition

Resource ID: SCR_019204

Alternate IDs: biotools:variancepartition

Alternate URLs: <https://bio.tools/variancepartition>

License: GPL

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260801T042847+0000

Ratings and Alerts

No rating or validation information has been found for variancePartition.

No alerts have been found for variancePartition.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 52 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Liharska LE, et al. (2026) A study of gene expression in the living human brain. Molecular psychiatry, 31(1), 137.

Costa EK, et al. (2025) Multi-tissue transcriptomic aging atlas reveals predictive aging biomarkers in the killifish. bioRxiv : the preprint server for biology.

Amouzgar M, et al. (2025) A deep single cell mass cytometry approach to capture canonical and noncanonical cell cycle states. bioRxiv : the preprint server for biology.

Tamvaka N, et al. (2025) Characterizing the expression profile of 3R tau pathology in Pick's disease. Science advances, 11(18), eadt6105.

Thorpe AC, et al. (2025) National-scale biogeography and function of river and stream bacterial biofilm communities. Nature communications, 16(1), 10571.

Dinasarapu AR, et al. (2025) Modeling rare genetic disease with gene-edited induced pluripotent stem cells: relevance of the starting stock line. Stem cells translational medicine, 14(12).

Temba GS, et al. (2025) Immune and metabolic effects of African heritage diets versus Western diets in men: a randomized controlled trial. Nature medicine, 31(5), 1698.

Hoffman GE, et al. (2025) Fast, flexible analysis of differences in cellular composition with crumblr. Research square.

Hoffman GE, et al. (2025) Fast, flexible analysis of differences in cellular composition with crumblr. bioRxiv : the preprint server for biology.

Tkach VV, et al. (2025) Combined neocortical protein and morphological profiling of reactive microglia across Alzheimer's and Creutzfeldt-Jakob disease. *Acta neuropathologica communications*, 13(1), 244.

Boving I, et al. (2025) The Unstable Relationship Between Drought Status and Leaf Water Content Complicates the Remote Sensing of Tree Drought Stress. *Global change biology*, 31(4), e70188.

Sommer F, et al. (2025) Life-long microbiome rejuvenation improves intestinal barrier function and inflammaging in mice. *Microbiome*, 13(1), 91.

Wang Z, et al. (2025) Cross-platform clinical proteomics using the Charit?? open standard for plasma proteomics (OSPP). *Nature communications*, 16(1), 11377.

Shi Z, et al. (2025) Single-nucleus multi-omics identifies shared and distinct pathways in Pick's and Alzheimer's disease. *Science advances*, 11(46), eads7973.

Aastha A, et al. (2025) Systematic evaluation of analytical methods for CSF proteomics. *Research square*.

Mokhtari A, et al. (2025) Using multiomic integration to improve blood biomarkers of major depressive disorder: a case-control study. *EBioMedicine*, 113, 105569.

Tian W, et al. (2025) Genetic transcriptional regulation profiling of cartilage reveals pathogenesis of osteoarthritis. *EBioMedicine*, 117, 105821.

Isacson S, et al. (2025) Small RNA in sperm-Paternal contributions to human embryo development. *Nature communications*, 16(1), 6571.

Benoit-Pilven C, et al. (2025) Early establishment and life course stability of sex biases in the human brain transcriptome. *Cell genomics*, 5(7), 100890.

Amouzgar M, et al. (2025) A deep single cell mass cytometry approach to capture canonical and noncanonical cell cycle states. *Nature communications*, 16(1), 8821.