

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, data processing software, software application, data analytics software, software resource

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: 20260810T040749+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 62 mentions in open access literature.

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

Ahn C, et al. (2026) Multi-omic responses to acute exercise in abdominal subcutaneous adipose tissue of sedentary adults: findings from MoTrPAC. bioRxiv : the preprint server for biology.

Wang N, et al. (2026) Molecular characterization of humanized APOE mouse models reveals source and genotype dependent differences. Molecular neurodegeneration, 21(1).

Charney AW, et al. (2026) A transcriptional program associated with neurotransmission in the living human brain. Molecular psychiatry, 31(5), 2727.

Robbins JM, et al. (2026) Blood Biochemical Responses to Acute Exercise: Findings from the Molecular Transducers of Physical Activity Consortium (MoTrPAC). bioRxiv : the preprint server for biology.

Krockenberger L, et al. (2026) FastGxC: Fast and powerful context-specific eQTL mapping in bulk and single-cell data. Cell genomics, 6(6), 101250.

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

Witonsky D, et al. (2026) Genomic profiling of active vitamin D colonic responses in African- and European-Americans identifies an ancestry-related regulatory variant of POLB. PLoS genetics, 22(1), e1011983.

Bandesh K, et al. (2026) Deep single-cell decoding of human pancreatic islets reveals T2D β -cell gene expression defects. The EMBO journal, 45(11), 3978.

Nagaraja S, et al. (2026) Epigenetic memory of colitis promotes tumour growth. *Nature*, 652(8110), 774.

Wang X, et al. (2026) A dish-to-biobank framework links β -cell nutrient-stress programs to genetic and dietary risk for Type 2 Diabetes. *bioRxiv : the preprint server for biology*.

Li Z, et al. (2026) Gemcitabine plus Nivolumab with Carboplatin or Oxaliplatin in Cisplatin-Ineligible Patients with Metastatic Urothelial Carcinoma: A Randomized Phase II Trial. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(14), 2911.

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

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

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).

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.

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. *bioRxiv : the preprint server for biology*.

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

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.