Resource Summary Report

Generated by NIF on Apr 26, 2025

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

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: 20250426T060746+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 29 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Arnold M, et al. (2024) Individual bioenergetic capacity as a potential source of resilience to Alzheimer's disease. medRxiv: the preprint server for health sciences.

Sudalagunta PR, et al. (2024) The Functional Transcriptomic Landscape Informs Therapeutic Strategies in Multiple Myeloma. Cancer research.

Mostafa I, et al. (2024) A microbiota-directed complementary food intervention in 12-18-month-old Bangladeshi children improves linear growth. EBioMedicine, 104, 105166.

Rodriguez de Los Santos M, et al. (2024) Divergent landscapes of A-to-I editing in postmortem and living human brain. Nature communications, 15(1), 5366.

Jakobsen NA, et al. (2024) Selective advantage of mutant stem cells in human clonal hematopoiesis is associated with attenuated response to inflammation and aging. Cell stem cell, 31(8), 1127.

Andreu-Sánchez S, et al. (2024) Antibody signatures against viruses and microbiome reflect past and chronic exposures and associate with aging and inflammation. iScience, 27(6), 109981.

Willis AB, et al. (2024) Serum protein and imaging biomarkers after intermittent steroid treatment in muscular dystrophy. medRxiv: the preprint server for health sciences.

de Los Santos MR, et al. (2024) Divergent landscapes of A-to-I editing in postmortem and living human brain. medRxiv: the preprint server for health sciences.

Chien JF, et al. (2024) Cell-type-specific effects of age and sex on human cortical neurons. Neuron, 112(15), 2524.

Bhati M, et al. (2023) Structural variants and short tandem repeats impact gene expression and splicing in bovine testis tissue. Genetics, 225(3).

Xu A, et al. (2023) Transcriptomes of aging brain, heart, muscle, and spleen from female and male African turquoise killifish. Scientific data, 10(1), 695.

Nguyen JH, et al. (2023) Developmental pyrethroid exposure disrupts molecular pathways for circadian rhythms and MAP kinase in mouse brain. bioRxiv: the preprint server for biology.

Bowles KR, et al. (2023) Development of MAPT S305 mutation models exhibiting elevated 4R tau expression, resulting in altered neuronal and astrocytic function. bioRxiv: the preprint server for biology.

Lütge M, et al. (2023) Conserved stromal-immune cell circuits secure B cell homeostasis and function. Nature immunology, 24(7), 1149.

van Oostrum M, et al. (2023) The proteomic landscape of synaptic diversity across brain regions and cell types. Cell, 186(24), 5411.

Workman MJ, et al. (2023) Large-scale differentiation of iPSC-derived motor neurons from ALS and control subjects. Neuron, 111(8), 1191.

Sparks R, et al. (2022) Influenza vaccination and single cell multiomics reveal sex dimorphic immune imprints of prior mild COVID-19. medRxiv: the preprint server for health sciences.

Wang S, et al. (2022) Amino acids, microbiota-related metabolites, and the risk of incident diabetes among normoglycemic Chinese adults: Findings from the 4C study. Cell reports. Medicine, 3(9), 100727.

Lütge A, et al. (2021) CellMixS: quantifying and visualizing batch effects in single-cell RNA-seq data. Life science alliance, 4(6).

Beckmann ND, et al. (2021) Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature communications, 12(1), 4854.