

Resource Summary Report

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PVCA

RRID:SCR_001356

Type: Tool

Proper Citation

PVCA (RRID:SCR_001356)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/pvca.html>

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Description: Software package that contains the function to assess the batch sources by fitting all sources as random effects including two-way interaction terms in the Mixed Model (depends on lme4 package) to selected principal components, which were obtained from the original data correlation matrix. This package accompanies the book Batch Effects and Noise in Microarray Experiments, chapter 12.

Abbreviations: PVCA

Synonyms: Principal Variance Component Analysis

Resource Type: software resource

Keywords: microarray

Availability: Free, Available for download, Freely available

Resource Name: PVCA

Resource ID: SCR_001356

Alternate IDs: OMICS_01983

License: GNU Lesser General Public License, v2 or newer

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260725T190501+0000

Ratings and Alerts

No rating or validation information has been found for PVCA.

No alerts have been found for PVCA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Engel A, et al. (2025) A spatio-temporal brain miRNA expression atlas identifies sex-independent age-related microglial driven miR-155-5p increase. bioRxiv : the preprint server for biology.

Cutler S, et al. (2025) Novel proteomic characterization of multiple myeloma bone marrow interstitial fluid links prognosis to coagulation pathways. Clinical proteomics, 22(1), 40.

Engel A, et al. (2025) A spatio-temporal brain miRNA expression atlas identifies sex-independent age-related microglial driven miR-155-5p increase. Nature communications, 16(1), 4588.

Zuccoli E, et al. (2025) Reproducibility of PD patient-specific midbrain organoid data for in vitro disease modeling. iScience, 28(10), 113541.

Wu Y, et al. (2025) BEEEx Is an Open-Source Tool That Evaluates Batch Effects in Medical Images to Enable Multicenter Studies. Cancer research, 85(2), 218.

Wang H, et al. (2024) An entanglement association polymer electrolyte for Li-metal batteries. Nature communications, 15(1), 2500.

Desponds E, et al. (2024) Immuno-Transcriptomic Profiling of Blood and Tumor Tissue Identifies Gene Signatures Associated with Immunotherapy Response in Metastatic Bladder Cancer. Cancers, 16(2).

Littleton SH, et al. (2024) Variant-to-function analysis of the childhood obesity chr12q13 locus implicates rs7132908 as a causal variant within the 3' UTR of FAIM2. Cell genomics, 4(5), 100556.

Zheng Y, et al. (2024) Multi-omics data integration using ratio-based quantitative profiling with Quartet reference materials. Nature biotechnology, 42(7), 1133.

Karakaslar EO, et al. (2023) Transcriptional activation of Jun and Fos members of the AP-1 complex is a conserved signature of immune aging that contributes to inflammaging. Aging cell, 22(4), e13792.

Webb KA, et al. (2022) Genomic diversity and antimicrobial resistance of *Prevotella* species isolated from chronic lung disease airways. *Microbial genomics*, 8(2).

Lambole CR, et al. (2021) Ryanodine receptor leak triggers fiber Ca^{2+} redistribution to preserve force and elevate basal metabolism in skeletal muscle. *Science advances*, 7(44), eabi7166.

Leylek R, et al. (2020) Chromatin Landscape Underpinning Human Dendritic Cell Heterogeneity. *Cell reports*, 32(12), 108180.

Varma S, et al. (2020) Blind estimation and correction of microarray batch effect. *PloS one*, 15(4), e0231446.

Pringle S, et al. (2019) Salivary Gland Stem Cells Age Prematurely in Primary Sjögren's Syndrome. *Arthritis & rheumatology (Hoboken, N.J.)*, 71(1), 133.

Williamson LM, et al. (2019) Genomic characterization of a well-differentiated grade 3 pancreatic neuroendocrine tumor. *Cold Spring Harbor molecular case studies*, 5(3).

Ewbank R, et al. (2019) Building resilience to El Niño-related drought: experiences in early warning and early action from Nicaragua and Ethiopia. *Disasters*, 43 Suppl 3(Suppl 3), S345.

Le Sciellour M, et al. (2019) Effect of chronic and acute heat challenges on fecal microbiota composition, production, and thermoregulation traits in growing pigs^{1,2}. *Journal of animal science*, 97(9), 3845.

Stinkens R, et al. (2018) The effects of angiotensin receptor neprilysin inhibition by sacubitril/valsartan on adipose tissue transcriptome and protein expression in obese hypertensive patients. *Scientific reports*, 8(1), 3933.

Rojas-Peña ML, et al. (2018) Individualized Transcriptional Resolution of Complicated Malaria in a Colombian Study. *Journal of personalized medicine*, 8(3).