Resource Summary Report

Generated by <u>RRID</u> on May 21, 2025

CoGAPS

RRID:SCR_001479 Type: Tool

Proper Citation

CoGAPS (RRID:SCR_001479)

Resource Information

URL: http://www.bioconductor.org/packages/release/bioc/html/CoGAPS.html

Proper Citation: CoGAPS (RRID:SCR_001479)

Description: Software that infers biological processes which are active in individual gene sets from corresponding microarray measurements. It achieves this inference by combining a MCMC matrix decomposition algorithm (GAPS) with a novel statistic inferring activity on gene sets.

Abbreviations: CoGAPS

Synonyms: Coordinated Gene Activity in Pattern Sets

Resource Type: software resource

Defining Citation: PMID:20810601

Keywords: gene expression, microarray

Funding:

Availability: GNU General Public License, v2

Resource Name: CoGAPS

Resource ID: SCR_001479

Alternate IDs: OMICS_01973

Record Creation Time: 20220129T080207+0000

Ratings and Alerts

No rating or validation information has been found for CoGAPS.

No alerts have been found for CoGAPS.

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 <u>RRID</u>.

Nelson ED, et al. (2024) An integrated single-nucleus and spatial transcriptomics atlas reveals the molecular landscape of the human hippocampus. bioRxiv : the preprint server for biology.

Bramel EE, et al. (2024) Intrinsic Gata4 expression sensitizes the aortic root to dilation in a Loeys-Dietz syndrome mouse model. Research square.

Bramel EE, et al. (2024) Intrinsic GATA4 expression sensitizes the aortic root to dilation in a Loeys-Dietz syndrome mouse model. Nature cardiovascular research, 3(12), 1468.

Kim SK, et al. (2024) Individual variation in the emergence of anterior-to-posterior neural fates from human pluripotent stem cells. Stem cell reports, 19(9), 1336.

Chenoweth JG, et al. (2024) Gene expression signatures in blood from a West African sepsis cohort define host response phenotypes. Nature communications, 15(1), 4606.

Weir K, et al. (2024) Identification of shared gene expression programs activated in multiple modes of torpor across vertebrate clades. Scientific reports, 14(1), 24360.

Herb BR, et al. (2023) Single-cell genomics reveals region-specific developmental trajectories underlying neuronal diversity in the human hypothalamus. Science advances, 9(45), eadf6251.

Yu B, et al. (2023) Molecular and cellular evolution of the amygdala across species analyzed by single-nucleus transcriptome profiling. Cell discovery, 9(1), 19.

Zhang S, et al. (2023) Informing virtual clinical trials of hepatocellular carcinoma with spatial multi-omics analysis of a human neoadjuvant immunotherapy clinical trial. bioRxiv : the

preprint server for biology.

Seo S, et al. (2023) iPSC-based modeling of helicase deficiency reveals impaired cell proliferation and increased apoptosis after NK cell lineage commitment. bioRxiv : the preprint server for biology.

Johnson JAI, et al. (2023) Digitize your Biology! Modeling multicellular systems through interpretable cell behavior. bioRxiv : the preprint server for biology.

Stein-O'Brien GL, et al. (2023) Transcriptional Signatures of Hippocampal Tau Pathology in Primary Age-Related Tauopathy and Alzheimer's Disease. medRxiv : the preprint server for health sciences.

Zhou X, et al. (2022) Deciphering the spatial-temporal transcriptional landscape of human hypothalamus development. Cell stem cell, 29(2), 328.

Sidiropoulos DN, et al. (2022) Integrated T cell cytometry metrics for immune-monitoring applications in immunotherapy clinical trials. JCI insight, 7(19).

Lê Cao KA, et al. (2021) Community-wide hackathons to identify central themes in single-cell multi-omics. Genome biology, 22(1), 220.

Davis-Marcisak EF, et al. (2021) Transfer learning between preclinical models and human tumors identifies a conserved NK cell activation signature in anti-CTLA-4 responsive tumors. Genome medicine, 13(1), 129.

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.

Morarach K, et al. (2021) Diversification of molecularly defined myenteric neuron classes revealed by single-cell RNA sequencing. Nature neuroscience, 24(1), 34.

Brodie-Kommit J, et al. (2021) Atoh7-independent specification of retinal ganglion cell identity. Science advances, 7(11).

Chen K, et al. (2021) A phenotypically supervised single-cell analysis protocol to study withincell-type heterogeneity of cultured mammalian cells. STAR protocols, 2(2), 100561.