

Resource Summary Report

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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>

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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

Availability: Free, Available for download, Freely available

Resource Name: CoGAPS

Resource ID: SCR_001479

Alternate IDs: OMICS_01973

License: GNU General Public License, v2

Record Creation Time: 20220129T080207+0000

Record Last Update: 20260829T182054+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 38 mentions in open access literature.

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

Lasse Opsahl EL, et al. (2026) Fibroblast STAT3 Activation Drives Organ-Specific Premetastatic Niche Formation. Cancer research, 86(1), 22.

Belanger K, et al. (2026) Cancer-Associated Fibroblasts Promote Epithelial-Mesenchymal Transition and Classical to Basal Subtype Shift in Pancreatic Cancer. Cancer research, 86(14), 3604.

Lyman MR, et al. (2025) Spatial proteomics and transcriptomics reveal early immune cell organization in pancreatic intraepithelial neoplasia. JCI insight, 10(15).

Johnson JAI, et al. (2025) Human interpretable grammar encodes multicellular systems biology models to democratize virtual cell laboratories. Cell, 188(17), 4711.

Noller K, et al. (2025) Integrative analysis of genomic and transcriptomic data informs precancer progression in the pancreas. bioRxiv : the preprint server for biology.

Bavais J, et al. (2025) SciGeneX: enhancing transcriptional analysis through gene module detection in single-cell and spatial transcriptomics data. NAR genomics and bioinformatics, 7(2), lqaf043.

Jiang L, et al. (2025) The Key Role of COA6 in Pancreatic Ductal Adenocarcinoma: Metabolic Reprogramming and Regulation of the Immune Microenvironment. Journal of cellular and molecular medicine, 29(13), e70685.

Stein-O'Brien GL, et al. (2025) Transcriptional signatures of hippocampal tau pathology in primary age-related tauopathy and Alzheimer's disease. Cell reports, 44(3), 115422.

Seo S, et al. (2025) Allelic bias contributes to heterogeneous phenotypes of NK cell deficiency. Cell reports, 44(8), 116102.

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.

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.

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.

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.

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.

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

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*.

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*.

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