

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: 20260815T182158+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 [dkNET](#) .

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.

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

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.

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. *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.

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*.