Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

FABIA

RRID:SCR_012002
Type: Tool

Proper Citation

FABIA (RRID:SCR_012002)

Resource Information

URL: http://www.bioinf.jku.at/software/fabia/fabia.html

Proper Citation: FABIA (RRID:SCR_012002)

Description: A model-based technique for biclustering that is clustering rows and columns simultaneously.

Abbreviations: FABIA

Synonyms: Factor Analysis for Bicluster Acquisition

Resource Type: software resource

Defining Citation: PMID:20418340

Keywords: bio.tools

Funding:

Availability: Free

Resource Name: FABIA

Resource ID: SCR_012002

Alternate IDs: OMICS_01797, biotools:fabia

Alternate URLs: https://bio.tools/fabia

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250410T070226+0000

Ratings and Alerts

No rating or validation information has been found for FABIA.

No alerts have been found for FABIA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Xu X, et al. (2024) Biclustering of Log Data: Insights from a Computer-Based Complex Problem Solving Assessment. Journal of Intelligence, 12(1).

Köhler N, et al. (2022) Kupffer cells are protective in alcoholic steatosis. Biochimica et biophysica acta. Molecular basis of disease, 1868(6), 166398.

Yazdanparast A, et al. (2022) Bi-EB: Empirical Bayesian Biclustering for Multi-Omics Data Integration Pattern Identification among Species. Genes, 13(11).

Nicholls K, et al. (2021) Comparison of sparse biclustering algorithms for gene expression datasets. Briefings in bioinformatics, 22(6).

Rahaman MA, et al. (2020) N-BiC: A Method for Multi-Component and Symptom Biclustering of Structural MRI Data: Application to Schizophrenia. IEEE transactions on bio-medical engineering, 67(1), 110.

Röttjers L, et al. (2020) manta: a Clustering Algorithm for Weighted Ecological Networks. mSystems, 5(1).

Grau M, et al. (2019) Dissection of gene expression datasets into clinically relevant interaction signatures via high-dimensional correlation maximization. Nature communications, 10(1), 5417.

Quan Y, et al. (2019) Integrated Analysis of DNA Methylation and Biochemical/Metabolic Parameter During the Long-Term Isolation Environment. Frontiers in physiology, 10, 917.

Gu Q, et al. (2018) Bi-clustering of metabolic data using matrix factorization tools. Methods (San Diego, Calif.), 151, 12.

Bentham RB, et al. (2017) MCbiclust: a novel algorithm to discover large-scale functionally related gene sets from massive transcriptomics data collections. Nucleic acids research, 45(15), 8712.

Chen HC, et al. (2013) Identification of bicluster regions in a binary matrix and its applications. PloS one, 8(8), e71680.