

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

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

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: 20260905T132717+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 12 mentions in open access literature.

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

Wang Y, et al. (2025) MNetClass: a control-free microbial network clustering framework for identifying central subcommunities across ecological niches. *mSystems*, 10(12), e0098925.

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.