

Resource Summary Report

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Metapath

RRID:SCR_014621

Type: Tool

Proper Citation

Metapath (RRID:SCR_014621)

Resource Information

URL: <http://www.cbcb.umd.edu/software/metapath>

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Description: A statistical package for comparing metagenomic data-sets at the pathway level. It relies on a combination of metagenomic sequence data and prior metabolic pathway knowledge, which is pulled from KEGG.

Resource Type: data processing software, software resource, data analysis software, software application

Keywords: microbiome, statistics, metagenomics, pathway, sequence, comparison

Availability: Available for download

Resource Name: Metapath

Resource ID: SCR_014621

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260818T043504+0000

Ratings and Alerts

No rating or validation information has been found for Metapath.

No alerts have been found for Metapath.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Huang G, et al. (2026) MPHGNN: metapath-guided heterogeneous graph neural network for miRNA-drug resistance association prediction. *Briefings in bioinformatics*, 27(1).

He L, et al. (2026) Clinicopathologic Features of Genitourinary Malakoplakia and Analytical Utility of the MetaPath Assay. *Infection and drug resistance*, 19, 582917.

Xu X, et al. (2026) Metagenomic next-generation sequencing for pathology-suspected fungal infections at rare anatomical sites: a case series. *Future science OA*, 12(1), 2669032.

Li M, et al. (2025) Clinicopathological characteristics and diagnostic performance of metagenomic pathogen detection technology in mycobacterial infections among HIV patients. *Frontiers in cellular and infection microbiology*, 15, 1584189.

Li Y, et al. (2025) Integrating transcriptomic data with a novel drug efficacy prediction model for TCM active compound discovery. *Scientific reports*, 15(1), 7688.

Ma Z, et al. (2024) Z2F: Heterogeneous graph-based Android malware detection. *PloS one*, 19(3), e0300975.

Han S, et al. (2024) Standigm ASK???: knowledge graph and artificial intelligence platform applied to target discovery in idiopathic pulmonary fibrosis. *Briefings in bioinformatics*, 25(2).

Kolanczyk RC, et al. (2023) PFAS Biotransformation Pathways: A Species Comparison Study. *Toxics*, 11(1).

Milano M, et al. (2022) Challenges and Limitations of Biological Network Analysis. *Biotech (Basel (Switzerland))*, 11(3).

Zhao S, et al. (2021) Identification of Diagnostic Markers for Major Depressive Disorder Using Machine Learning Methods. *Frontiers in neuroscience*, 15, 645998.

Yazhini A, et al. (2021) Rewards of divergence in sequences, 3-D structures and dynamics of yeast and human spliceosome SF3b complexes. *Current research in structural biology*, 3, 133.

MohammadiPeyhani H, et al. (2021) NICEdrug.ch, a workflow for rational drug design and systems-level analysis of drug metabolism. *eLife*, 10.

Zeng X, et al. (2020) Comparative Pathway Integrator: A Framework of Meta-Analytic Integration of Multiple Transcriptomic Studies for Consensual and Differential Pathway Analysis. *Genes*, 11(6).

Pereira O, et al. (2019) Genomic ecology of Marine Group II, the most common marine planktonic Archaea across the surface ocean. *MicrobiologyOpen*, 8(9), e00852.

Hwang N, et al. (2017) Genes and Gut Bacteria Involved in Luminal Butyrate Reduction Caused by Diet and Loperamide. *Genes*, 8(12).

Zhang K, et al. (2016) Meta-analysis of gene expression and integrin-associated signaling pathways in papillary renal cell carcinoma subtypes. *Oncotarget*, 7(51), 84178.

Yepes S, et al. (2015) Regulatory network reconstruction reveals genes with prognostic value for chronic lymphocytic leukemia. *BMC genomics*, 16, 1002.

Liu B, et al. (2011) MetaPath: identifying differentially abundant metabolic pathways in metagenomic datasets. *BMC proceedings*, 5 Suppl 2(Suppl 2), S9.

Schwartz JM, et al. (2009) Local and global modes of drug action in biochemical networks. *BMC chemical biology*, 9, 4.