

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

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: 20260728T043444+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 16 mentions in open access literature.

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

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.

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.

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.