Resource Summary Report

Generated by NIF on May 15, 2025

MetaPhyler

RRID:SCR_004848
Type: Tool

Proper Citation

MetaPhyler (RRID:SCR_004848)

Resource Information

URL: http://metaphyler.cbcb.umd.edu/

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Description: A taxonomic classifier for metagenomic shotgun reads, which uses phylogenetic marker genes as a taxonomic reference. The classifier, based on BLAST, uses different thresholds (automatically learned from the reference database) for each combination of taxonomic rank, reference gene, and sequence length. The reference database includes marker genes from all complete genomes, several draft genomes and the NCBI nr protein database.

Synonyms: MetaPhyler - Estimating Bacterial Composition from Metagenomic Sequences

Resource Type: software resource

Defining Citation: PMID:21989143

Keywords: metagenome, classification, sequence, taxonomy, genome, microbiome, bio.tools

Funding:

Availability: Acknowledgement requested, Available for download

Resource Name: MetaPhyler

Resource ID: SCR_004848

Alternate IDs: OMICS_01455, biotools:metaphyler

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

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250420T014240+0000

Ratings and Alerts

No rating or validation information has been found for MetaPhyler.

No alerts have been found for MetaPhyler.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Koslicki D, et al. (2024) YACHT: an ANI-based statistical test to detect microbial presence/absence in a metagenomic sample. Bioinformatics (Oxford, England), 40(2).

Elmassry MM, et al. (2021) Predicting drug-metagenome interactions: Variation in the microbial ?-glucuronidase level in the human gut metagenomes. PloS one, 16(1), e0244876.

Alvarenga DO, et al. (2017) A Metagenomic Approach to Cyanobacterial Genomics. Frontiers in microbiology, 8, 809.

Moller AG, et al. (2017) Determining virus-host interactions and glycerol metabolism profiles in geographically diverse solar salterns with metagenomics. PeerJ, 5, e2844.

Gerth M, et al. (2017) Short reads from honey bee (Apis sp.) sequencing projects reflect microbial associate diversity. PeerJ, 5, e3529.

Kim M, et al. (2016) MetaCRAM: an integrated pipeline for metagenomic taxonomy identification and compression. BMC bioinformatics, 17, 94.

Lindgreen S, et al. (2016) An evaluation of the accuracy and speed of metagenome analysis tools. Scientific reports, 6, 19233.

Peabody MA, et al. (2015) Evaluation of shotgun metagenomics sequence classification methods using in silico and in vitro simulated communities. BMC bioinformatics, 16, 363.

Johnson SS, et al. (2015) Insights from the metagenome of an acid salt lake: the role of biology in an extreme depositional environment. PloS one, 10(4), e0122869.

Maynard SM, et al. (2013) A knowledge based approach to matching human neurodegenerative disease and animal models. Frontiers in neuroinformatics, 7, 7.