

Resource Summary Report

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MLTreeMap

RRID:SCR_004792

Type: Tool

Proper Citation

MLTreeMap (RRID:SCR_004792)

Resource Information

URL: <http://mltreemap.org/>

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Description: Data analysis service that analyzes DNA sequences and determines their most likely phylogenetic origin. Its main use is in metagenomics projects, where DNA is isolated directly from natural environments and sequenced (the organisms from which the DNA originates are often entirely undescribed). It will search such sequences for suitable marker genes, and will use maximum likelihood analysis to place them in the "Tree of Life". This placement is more reliable than simply assessing the closest relative of a sequence using BLAST. More importantly, MLTreeMap decides not only who is the closest relative of your query sequence, but also how deep in the tree of life it probably branched off. Additionally, MLTreeMap searches the sequences for genes, which are coding for key enzymes of important functional pathways, such as RuBisCo, methane monooxygenase or nitrogenase. In case of a positive hit, MLTreeMap uses maximum likelihood analysis to place them in the respective "gene-family tree".

Abbreviations: MLTreeMap

Synonyms: Phylogenetic analysis of metagenomics sequence data

Resource Type: data analysis service, service resource, analysis service resource, production service resource

Defining Citation: [PMID:20687950](#)

Keywords: phylogeny, gene, fasta, dna sequence, nucleotide sequence, metagenomics, metagenome, bio.tools

Resource Name: MLTreeMap

Resource ID: SCR_004792

Alternate IDs: biotools:mltreemap, OMICS_01457

Alternate URLs: <https://bio.tools/mltreemap>

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260810T040358+0000

Ratings and Alerts

No rating or validation information has been found for MLTreeMap.

No alerts have been found for MLTreeMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

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

Bagnoud A, et al. (2016) Reconstructing a hydrogen-driven microbial metabolic network in Opalinus Clay rock. *Nature communications*, 7, 12770.

Sanli K, et al. (2015) Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. *Frontiers in microbiology*, 6, 1192.

Whiteson KL, et al. (2014) A genomic perspective on a new bacterial genus and species from the Alcaligenaceae family, *Basilea psittacipulmonis*. *BMC genomics*, 15, 169.