

Resource Summary Report

Generated by [kravitz2](#) on Aug 2, 2026

[RAIphy](#)

RRID:SCR_004720

Type: Tool

Proper Citation

RAIphy (RRID:SCR_004720)

Resource Information

URL: <http://bioinfo.unl.edu/raiphy.php>

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Description: A semi-supervised metagenomic fragment classification software program that utilizes the genome signatures to characterize the DNA sequences and taxonomic classification is based on an information theoretic measure referred as Relative Abundance Index (RAI). A DNA sequence of unknown source is classified and taxonomically labeled based on the phylogenetic profiles of the previously sequenced genomes. The profiles are iteratively updated using the unknown DNA sequences and the classification results. After a few cycles, the metagenome is classified into operational taxonomic units.

Abbreviations: RAIphy

Resource Type: software resource

Defining Citation: [PMID:21281493](#)

Keywords: classification, metagenome, phylogenetic profile, genome, taxonomic classification, dna sequence, relative abundance index

Resource Name: RAIphy

Resource ID: SCR_004720

Alternate IDs: OMICS_01464

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260801T190244+0000

Ratings and Alerts

No rating or validation information has been found for RAlphy.

No alerts have been found for RAlphy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Benavides A, et al. (2018) CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. BMC genomics, 19(Suppl 8), 858.

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

Norling M, et al. (2016) MetLab: An In Silico Experimental Design, Simulation and Analysis Tool for Viral Metagenomics Studies. PloS one, 11(8), e0160334.