Resource Summary Report

Generated by dkNET on Apr 22, 2025

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

Funding:

Resource Name: RAIphy

Resource ID: SCR_004720

Alternate IDs: OMICS_01464

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250420T014233+0000

Ratings and Alerts

No rating or validation information has been found for RAIphy.

No alerts have been found for RAIphy.

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 dkNET.

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.