Resource Summary Report

Generated by RRID on Apr 28, 2025

PEMA

RRID:SCR_017676
Type: Tool

Proper Citation

PEMA (RRID:SCR_017676)

Resource Information

URL: https://github.com/hariszaf/pema

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Description: Software as flexible pipeline for environmental DNA metabarcoding analysis of 16S/18S rRNA, ITS and COI marker genes. Performs reads' pre-processing, clustering to (M)OTUs and taxonomy assignment for 16S rRNA and COI marker gene data. Allows users to explore alternative algorithms for specific steps of pipeline without need of complete re-execution.

Synonyms: Pipeline for Environmental DNA Metabarcoding Analysis

Resource Type: data processing software, software resource, data analysis software, software toolkit, software application

Defining Citation: DOI:10.1101/709113

Keywords: Environmental, DNA, metabarcoding, analysis, ASVs, OTUs, 16S rRNA, COI, ITS, marker, gene, clustering, taxonomy, bio.tools

Funding:

Availability: Free, Freely available

Resource Name: PEMA

Resource ID: SCR_017676

Alternate IDs: biotools:PEMA

Alternate URLs:
https://docs.google.com/presentation/d/1lVH23DPa2NDNBhVvOTRoip8mraw8zfw8VQwbK4vkB1U/edit
https://bio.tools/PEMA

License: GNU GPL v3

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Ratings and Alerts

No rating or validation information has been found for PEMA .

No alerts have been found for PEMA .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Zafeiropoulos H, et al. (2020) PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes. GigaScience, 9(3).