

{affiliationExplorer} a Shiny webapp to resolve taxonomy conflicts

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Abstract (300 words)

Metabarcoding studies in microbial ecology generate taxonomic abundance profiles, with each taxon usually represented by an ASV (*Amplicon Sequence Variant*). Some taxa may be associated with several, sometimes conflicting, taxonomic affiliations. These ambiguities (or multi-affiliations) [1], may be frequent when analysing short sequences and/or when reference databases are incomplete. This complicates ecological interpretation and decreases the reproducibility of results. According to the origin of the samples (*e.g.* food, fecal, biowaste, etc.) or the conflict source (spelling typo in the reference databases), manual curation can sometimes resolve these ambiguities. Likewise, some inconsistencies can be easily corrected programmatically if a manual curation was performed on a similar dataset and needs to be reapplied. The {affiliationExplorer} R-package provides a user interface dedicated to exploring and resolving these conflicts, and can easily be inserting in BIOM (*Biological Observation Matrix*) data analysis workflows.

Developed in Shiny with the {golem} framework, this package offers a user-friendly interface for ① loading a BIOM file, a multi-affiliation file, and, optionally, one or more expert-verified sequence–taxonomy dictionaries (in FASTA format), ② visualising and ordering multi-affiliated taxa by abundance, ③ automatically resolving conflicts using the provided dictionaries for curated ASV references, ④ performing expert manual curation by selecting the most relevant affiliation among those proposed or specifying it manually, and ⑤ exporting a corrected BIOM file and a sequence–taxonomy dictionary to log the performed curations and for potential reuse in subsequent curation sessions. The produced BIOM file follows the standards of biom-format.org and is fully compatible with standard metabarcoding workflows. The exported FASTA files can be reused as is in the interface.

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Affiliation explorer

Upload Biom File

Browse... FROGS_Aff

Upload complete

Optional: upload Fasta File

Browse... No file select

Upload Multihits TSV File

Browse... Galaxy25-IT

Upload complete

Download data

Affiliation selection

Affiliation edition

Select OTU

Cluster_19

Update OTU

Skip OTU

Cluster_19 - 4 conflicting affiliations, ambiguity at rank Family

Select new affiliation by clicking on a row (double click on a cell to edit its content).

Click "Update OTU" to update affiliation (with selected row) or "Skip OTU" to move to the next one.

Show 10 entries

Search:

	Kingdom	Phylum	Class	Order	Family	Genus	Species	Blast ID	%id	%cov
1	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	unknown species	EU452525.1.1399	99.525	100
2	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	unknown genus	unknown species	EU453301.1.1393	99.525	100
3	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides acidifaciens JCM 10556	BAIW01000188.173.1680	99.525	100
4	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidaceae	Bacteroides	Bacteroides acidifaciens	AB510606.1.1490	99.525	100

Showing 1 to 4 of 4 entries

Previous 1 Next

Show sequence

Current affiliation:

Bacteria / Bacteroidetes / Bacteroidia / Bacteroidales / Multi-affiliation / Multi-affiliation / Multi-affiliation

to be replaced with:

Bacteria / Bacteroidetes / Bacteroidia / Bacteroidales / Bacteroidaceae / Bacteroides / Bacteroides acidifaciens

Figure 1: Interface of the {affiliationExplorer} webapp

Keywords (10) : Biostatistics - R Package - Shiny - Taxonomy - Metabarcoding

Bibliography

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