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Cédric Midoux

► To cite this version:

Cédric Midoux. Easy16S : a user-friendly Shiny web-service for exploration and visualization of microbiome data.. Journées NEM, INRAE, Apr 2024, Paris, France. hal-04549290

HAL Id: hal-04549290

<https://hal.inrae.fr/hal-04549290>

Submitted on 17 Apr 2024

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Easy16S : a user-friendly Shiny web-service for exploration and visualization of microbiome data.

Journées Nutrition et Ecosystèmes Microbiens 2024

Cédric Midoux 

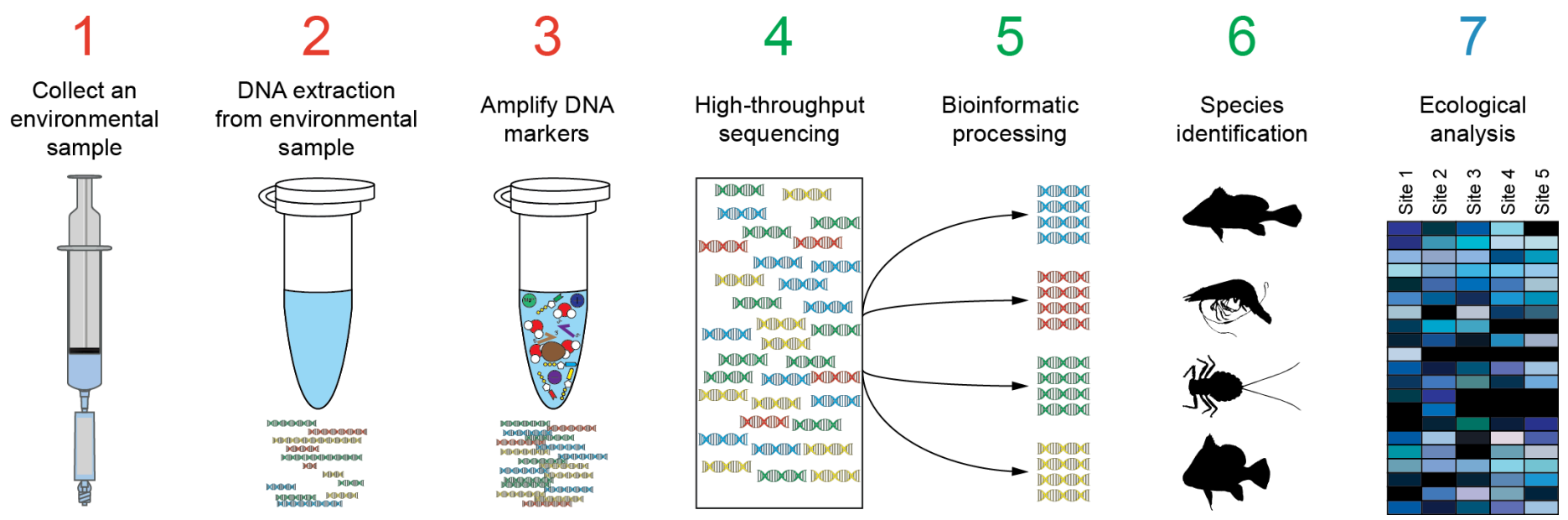
PROSE & MaIAGE

April 16, 2024



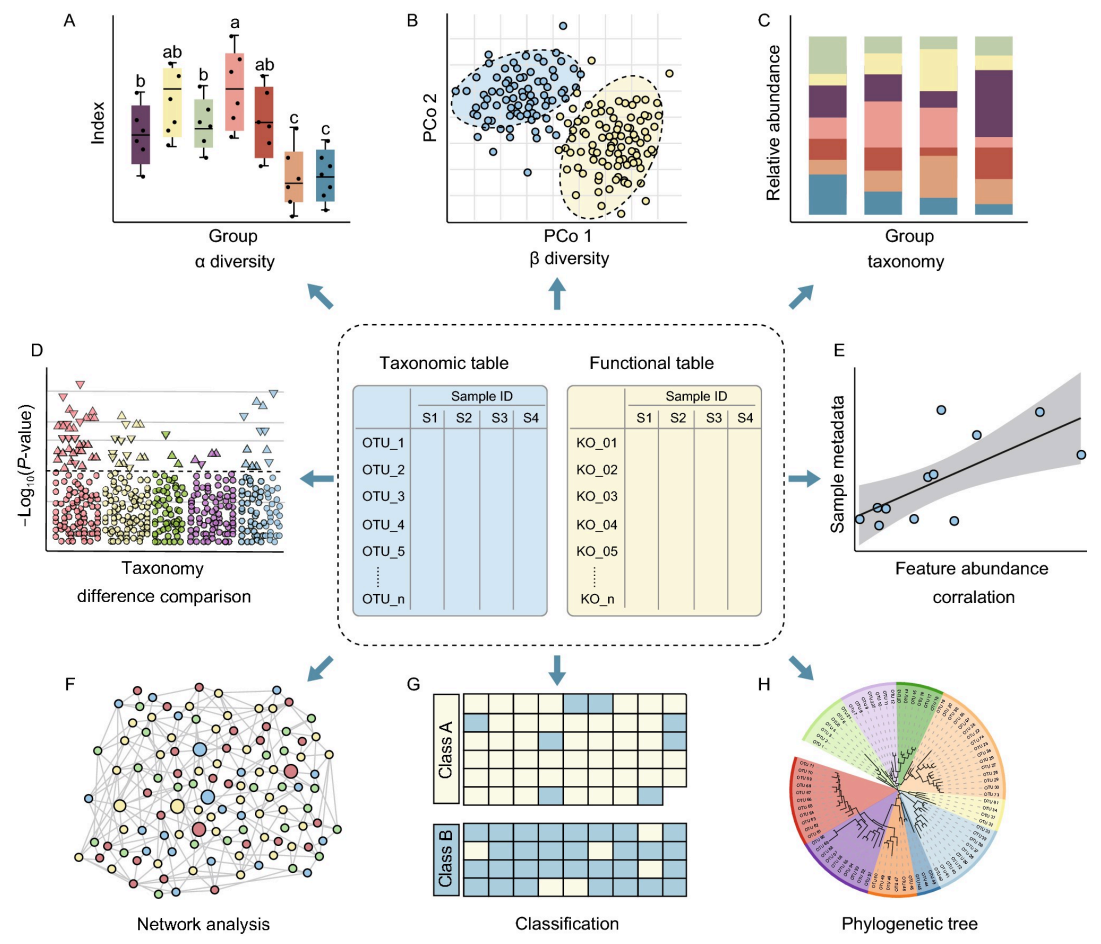
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Metabarcoding workflow



Alvaro (2017)

Exploration and visualisation?



Perform Complex Analyses?

- Depends on huge data, specific formats
- Requires computational resources
- Need to install tools locally
- Training and acquiring expertise in analyses
- Need time to carry out analyses
- Integrate data and metadata
- Tools lack interactivity

We generally use Rscripts but it can be long, complex and requires specific knowledge ...

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Statement of need

Easy16S is designed to facilitate the exploration, visualization, and analysis of microbiome data !

- User-friendly interactive web application
- Convenient functions and default settings
- To explore, visualize, and analyze metabarcoding data
- Hosted on an online instance

- Built with R and based on the phyloseq package
- Integrated with the FROGS sequence processing suite



Live Demo

Upload data

Demo | **Input data** | RData / RDS

Select a demo dataset

food

Cancel OK

Demo | Input data | **RData / RDS**

RDS with a phyloseq object or a RData where `data` is a phyloseq object : *

Browse... phyloseq.RDS

Cancel OK

Demo | **Input data** | RData / RDS

Abundance BIOM file come from FROGS, Qiime or another metagenomic tool.*

Browse... abundance.biom Standard BIOM

Metadata table

Browse... data.csv

Delimiter: Gussed if empty

Column types: Gussed if empty

Add sample names as metadata

Phylogenetic tree

Browse... tree.nwk

Representative FASTA sequences

Browse... seq.fasta

Cancel OK

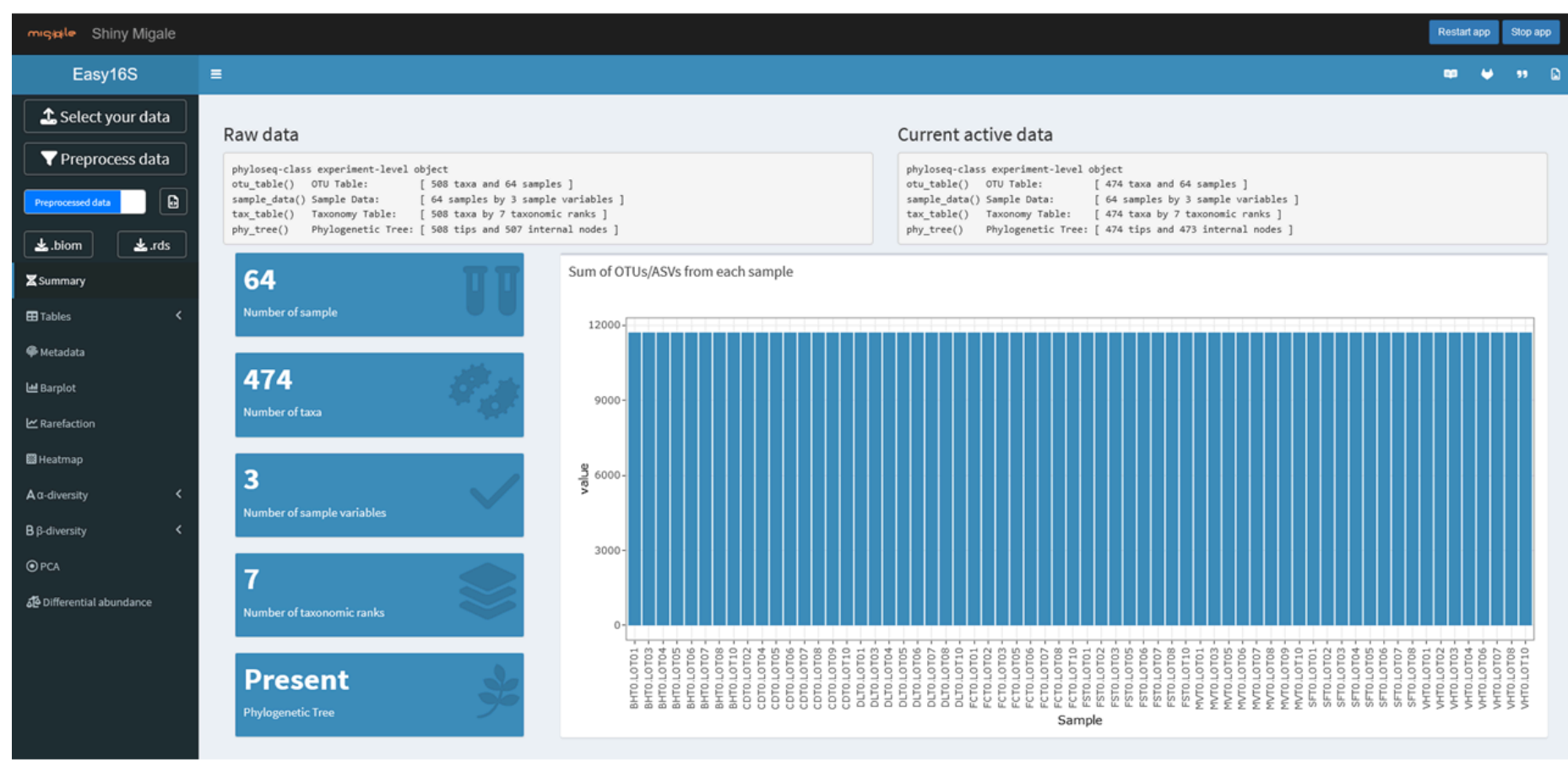
Transform data

Transformations are applied iteratively, starting from raw data.

Transformation module_1	Upper to :
Samples sums ▾	10000 ▾
Transformation module_2	To keep :
EnvType ▾	DesLardons, MerguezVolaille, BoeufHac ▾
Transformation module_3	Rank to agglomerate over :
Agglomerate taxa ▾	<input type="radio"/> Kingdom <input type="radio"/> Phylum <input type="radio"/> Class
	<input type="radio"/> Order <input type="radio"/> Family <input type="radio"/> Genus
	<input checked="" type="radio"/> Species
Transformation module_4	Depth
Rarefaction ▾	<input checked="" type="radio"/> min(sample_sums(physeq))



Summary





Tables

Shiny Migale Restart app Stop app

Easy16S CSV Copy Excel Search:

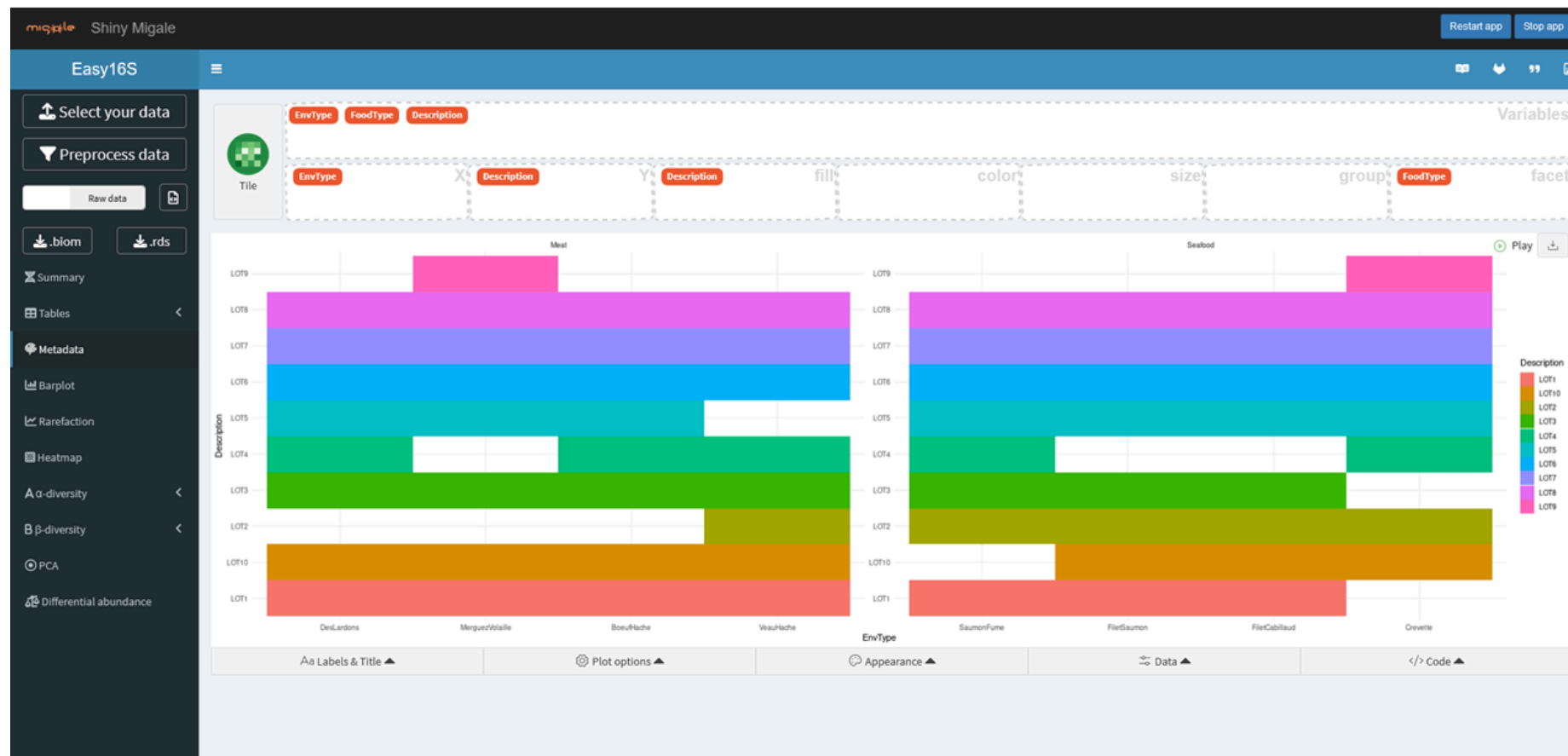
DLT0.LOT08 DLT0.LOT05 DLT0.LOT03 DLT0.LOT07 DLT0.LOT06 DLT0.LOT01 DLT0.LOT04 DLT0.LOT10 MVT0.LOT05 MVT0.LOT01 MVT0.LOT06 MVT0.LOT07 MVT0.LOT03 MVT0.LOT09 MVT

All All All All All All All All All All All All All All All

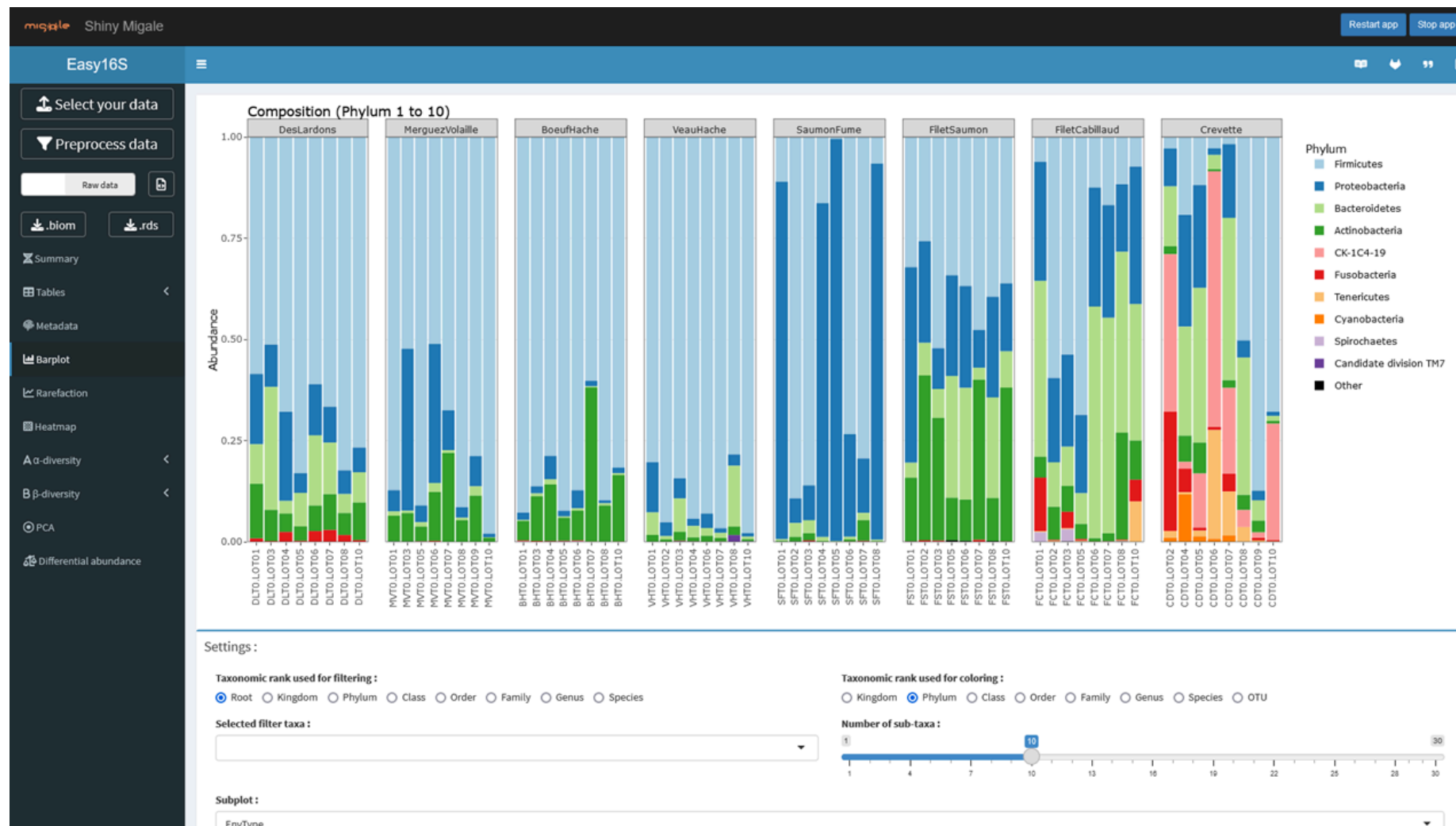
otu_00520	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_00555	4	0	8	3	15	4	2	0	12	17	25	31	11	40
otu_00568	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_00566	0	3	0	0	0	0	0	0	0	0	0	0	0	0
otu_00569	12	3	26	16	38	0	4	0	10	15	40	35	11	119
otu_00545	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_00527	0	0	0	0	0	0	0	0	0	0	0	8	0	0
otu_00521	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_00526	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01626	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01827	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01630	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01798	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01825	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01826	0	0	0	0	0	0	0	0	0	0	0	0	0	0
otu_01824	0	0	0	0	0	0	0	0	0	0	0	8	99	0

Showing 1 to 17 of 508 entries

Metadata



Barplot



Beta diversity



Differential abundance

Shiny Migale Restart app Stop app

Easy16S

Select your data

Preprocess data

Raw data

.biom .rds

Summary

Tables

Metadata

Barplot

Rarefaction

Heatmap

α -diversity

β -diversity

PCA

Differential abundance

Settings :

Experimental design : FoodType Contrast left : Meat Contrast right : Seafood Title : Volcano plot

Compute!

Volcano plot

You compare Seafood and Meat of the binary variable FoodType. A positive log2FoldChange means more abundant in Seafood than in Meat.

Table of OTUs/ASVs with significant effect (padj <= 0.05)

Abundance of DA OTU/ASV according to FoodType

[1] "Click on any OTU on volcano plot"

Differential abundance

Shiny Migale Restart app Stop app

Easy16S

Settings:

Experimental design: FoodType Contrast left: Meat Contrast right: Seafood Title: Volcano plot

Compute!

Volcano plot

You compare Seafood and Meat of the binary variable FoodType.
A positive log2FoldChange means more abundant in Seafood than in Meat.

Abundance of otu_01101 according to FoodType

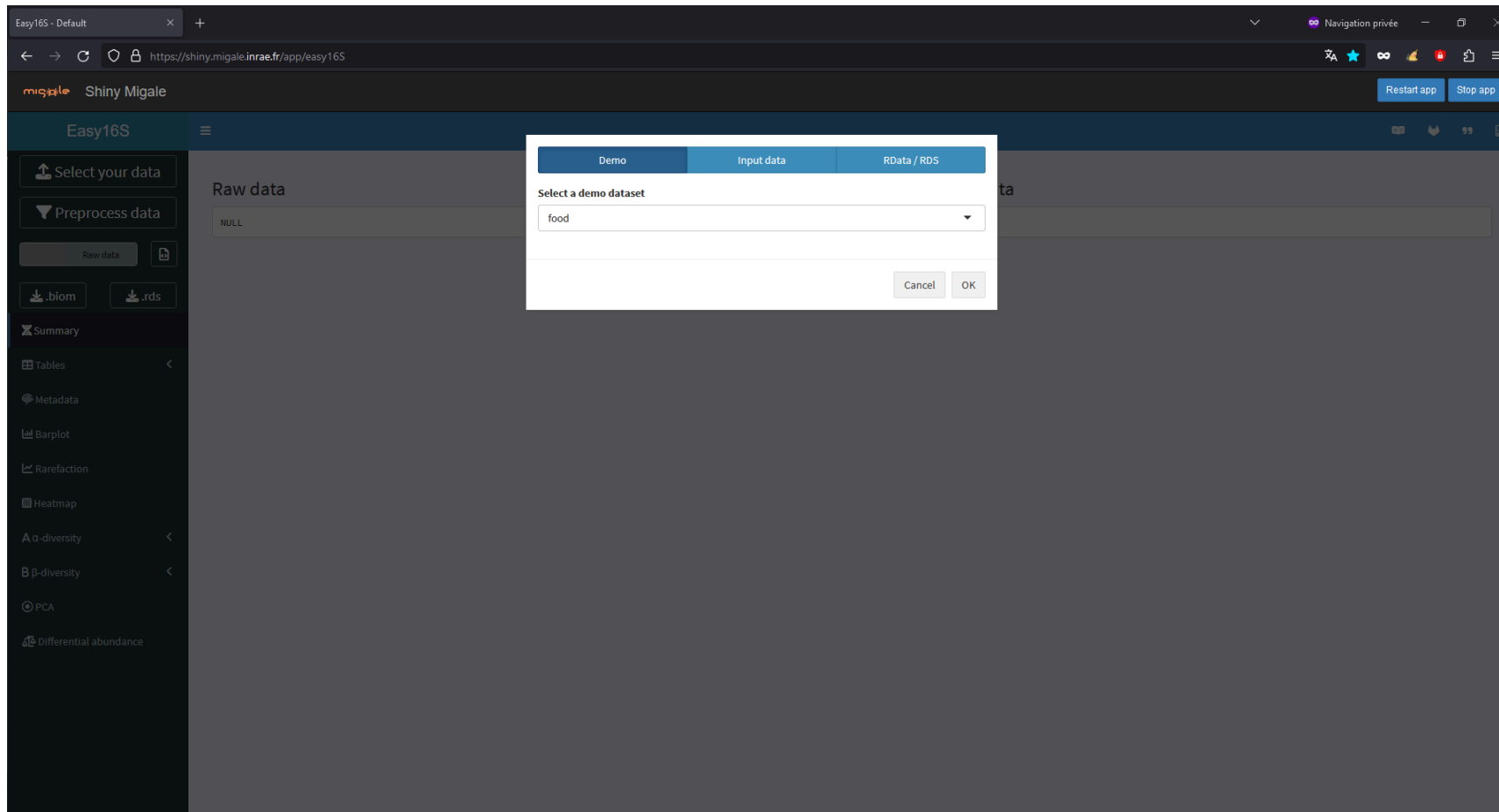
OTU	Kingdom	Phylum	Class	Order
1 otu_01101	Bacteria	Proteobacteria	Gammaproteobacteria	Vibrionales
	Family	Genus	Species	
1	Vibrionaceae	Photobacterium	Phosphoreum	

Table of OTUs/ASVs with significant effect (padj <= 0.05)



Take Home Messages

Online instance



The screenshot shows a web browser window displaying the Easy16S online instance. The browser address bar shows the URL <https://shiny.migale.inrae.fr/app/easy16S>. The application interface includes a sidebar with navigation options: Select your data, Preprocess data, Raw data, Download .biom, Download .rds, Summary, Tables, Metadata, Barplot, Rarefaction, Heatmap, Alpha diversity, Beta diversity, PCA, and Differential abundance. The main content area displays 'Raw data' with a 'NULL' value. A modal dialog box is open, titled 'Select a demo dataset', with a dropdown menu showing 'food' and 'Cancel' and 'OK' buttons.

<https://shiny.migale.inrae.fr/app/easy16S>


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Documentation

easy16S 0.0.0.9000 [Get started](#) [Reference](#) [Changelog](#)

easy16S



Easy16S is designed to facilitate the exploration, visualization, and analysis of microbiome data.

The goal of easy16S is to provide a user-friendly interactive web-application with convenient functions and default settings to explore, visualize and analyze metabarcoding data.

It builds upon the [phyloseq](#) package and its extensions and is tightly integrated with the [FROGS](#) sequence processing suite.

Easy16S can be accessed directly via an online instance: <https://shiny.migale.inrae.fr/app/easy16S>.

Installation

You can install the development version of easy16S like so:

```
# install.packages("remotes")
remotes::install_gitlab(
  repo = "migale/easy16S@main",
  host = "forgemia.inra.fr"
)
```

Run the Shiny Application

To run the Shiny application, execute the following code in your R environment:

```
easy16S::run_app()
easy16S::run_app(physeq = phyloseq.extended::food) # directly load your data
```

Links

[Report a bug](#)

License

[Full license](#)
AGPL (>= 3)

Community

[Code of conduct](#)

Citation

[Citing easy16S](#)

Developers

Cédric Midoux
Maintainer, author

[More about authors...](#)

Dev status

lifecycle: experimental
 JOSS Submitted
 archived swin:1:dir:5d122436bf50a8cac09857ef266170585a3fddc9
 hal-04304559

GitLab (issues and contributions)

Explorer Connexion

Rechercher ou aller à... migale / Easy16S

Projet

- Easy16S
- Gestion
- Programmation
- Code
- Compilation
- Déploiement
- Opération
- Surveillance
- Analyse

Easy16S ☆ Ajouter aux favoris 1

130 validations 6 branches 7 étiquettes

Server : <https://shiny.migale.inrae.fr/app/easy16S> | Doc : <https://easy16s.migale.inrae.fr/>

add logo
Cedric Midoux rédigé il y a 5 jours

main easy16s Historique Rechercher un fichier Code

[README](#) [GNU AGPLV3](#) [CHANGELOG](#)

Nom	Dernière validation	Dernière mise à jour
JOSS	bibtex curation + JOSS badge	il y a 6 jours
R	domaine https://easy16s.migale.inrae.fr	il y a 3 semaines
dev	add logo	il y a 5 jours
inst	add logo	il y a 5 jours
man	add logo	il y a 5 jours
renv	renv::init()	il y a 4 mois
tests	mod_pca	il y a 4 mois
vignettes	Filter based on sample sums	il y a un mois
.Rbuildignore	"get started" vignette	il y a un mois
.Rprofile	renv::init()	il y a 4 mois
dockerignore	nittah:use nittah cil	il y a 2 mois

<https://forgemia.inra.fr/migale/easy16s>

NEM research network 2024

Publication



Easy16S: a user-friendly Shiny web-service for exploration and visualization of microbiome data.

Cédric Midoux^{1,2,3}, Olivier Rué^{2,3}, Olivier Chapleur¹, Ariane Bize¹, Valentin Loux^{2,3}, and Mahendra Mariadassou^{2,3}

¹ Université Paris-Saclay, INRAE, PROSE, 92761, Antony, France; ² Université Paris-Saclay, INRAE, MaIAGE, 78350, Jouy-en-Josas, France; ³ Université Paris-Saclay, INRAE, BioInOmicS, MIGALE, bioinformatics facility, 78350, Jouy-en-Josas, France

DOI: 10.xxxxxx/draft

- Software
- Review
 - Repository
 - Archive

Editor:

Submitted: 27 March 2024
Published: unpublished

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Summary

The analysis of microbiome data has become a major asset for investigating microbial diversity and dynamics, in diverse fields, like health (Chapleur et al., 2013), environmental studies (Karimi et al., 2020), food-processing (Chailou et al., 2014), or environmental biotechnologies (Poirier et al., 2016). Due to sequencing advances, microbiome studies now require exploration, analysis and interpretation of large and high-dimensional datasets. Metabarcoding approaches, in particular, are based on a two-step process. First, a bioinformatics pipeline processes raw amplicon sequencing reads into Operational Taxonomic Unit (OTU) or Amplicon Sequence Variant (ASV), generating counts and taxonomic affiliations for each of them. Second, these tables are enriched with sample metadata to investigate relevant biological questions using statistical analyses. The affordability of amplicon sequencing has led to its widespread use in microbial ecology. Therefore, there is a growing demand for user-friendly interactive tools, enabling researchers to analyze their data autonomously, alleviating the dependence on bioinformaticians, biostatisticians or the need to acquire skills in R programming.

Regarding the bioinformatics part, many solutions are available to produce count tables from reads (Hajmizadeh et al., 2022), relying either on command-line tools provided through a Galaxy interface (ie. QIIME (Caporaso et al., 2010), FRIGS (Escudé et al., 2017)), or on R pipelines (ie. DADA2 (Callahan et al., 2016)). For the second step, several packages dedicated to the analysis and visualization of microbiomes are available, such as phyloseq (Paul J. McMurdie & Holmes, 2013), microbome (Lahti & Shetty, 2012-2019), metacoder (Foster et al., 2011) and many others. Their use can however sometimes be complex. There are relatively few tools available for rapid, interactive analysis of microbiome data (shiny-phyloseq (P. J. McMurdie & Holmes, 2014) is no longer supported; antimacules (Zhao et al., 2021) requires local installation; shanan (Volant et al., 2020) is integrated into a global workflow and cannot be decoupled from the bioinformatics components).

Statement of need

Here, we introduce Easy16S, an R-package and an interactive Shiny application (Chang et al., 2021), aiming to facilitate exploratory microbiome data analysis, data visualization, and statistical analysis. This tool is specifically designed for biologists eager to swiftly explore their data and generate figures interactively. It is easy-to-use and especially focused on the mapping of covariates of interest to microbiome structure.

This application is built upon phyloseq-class objects powered by (Paul J. McMurdie & Holmes, 2013). These objects integrate a matrix of OTU/ASV abundances per sample, a data.frame of

Midoux et al. (2024). Easy16S: a user-friendly Shiny web-service for exploration and visualization of microbiome data. *Journal of Open Source Software*, 0(0), 0564. <https://doi.org/10.xxxxxx/draft>.



Take Home Messages

- Online instance:
 - shiny.migale.inrae.fr/app/easy16S
- Documentation:
 - easy16s.migale.inrae.fr
- GitLab (issues and contributions) :
 - forgemia.inra.fr/migale/easy16s
- Publication: JOSS Submitted



Bibliography

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- Liu, Yong-Xin, Yuan Qin, Tong Chen, Meiping Lu, Xubo Qian, Xiaoxuan Guo, and Yang Bai. 2020. “A Practical Guide to Amplicon and Metagenomic Analysis of Microbiome Data.” *Protein & Cell* 12 (5): 315–30. <https://doi.org/10.1007/s13238-020-00724-8>.