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

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Rencontres R 2024

Cédric Midoux
PROSE & MaIAGE

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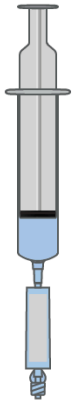
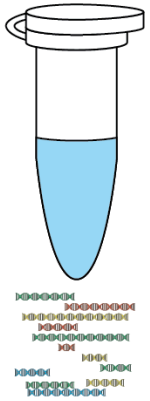
Metabarcoding (16S) workflow

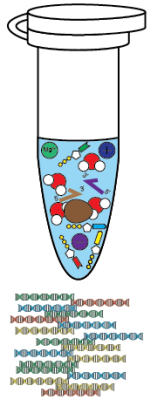
1 Collect an environmental sample



2 DNA extraction from environmental sample

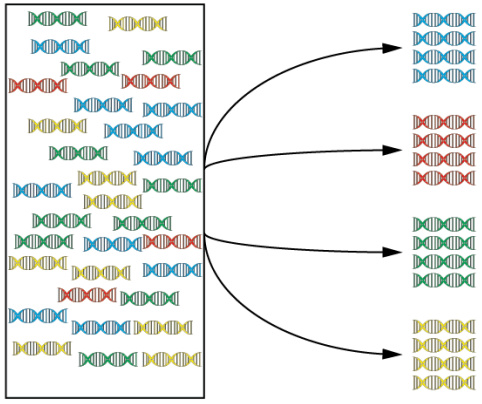


3 Amplify DNA markers



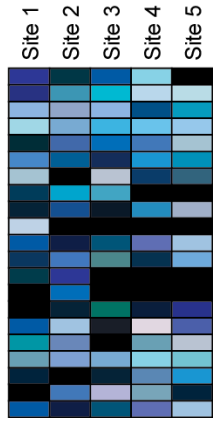
4 High-throughput sequencing

5 Bioinformatic processing



6 Species identification

7 Ecological analysis

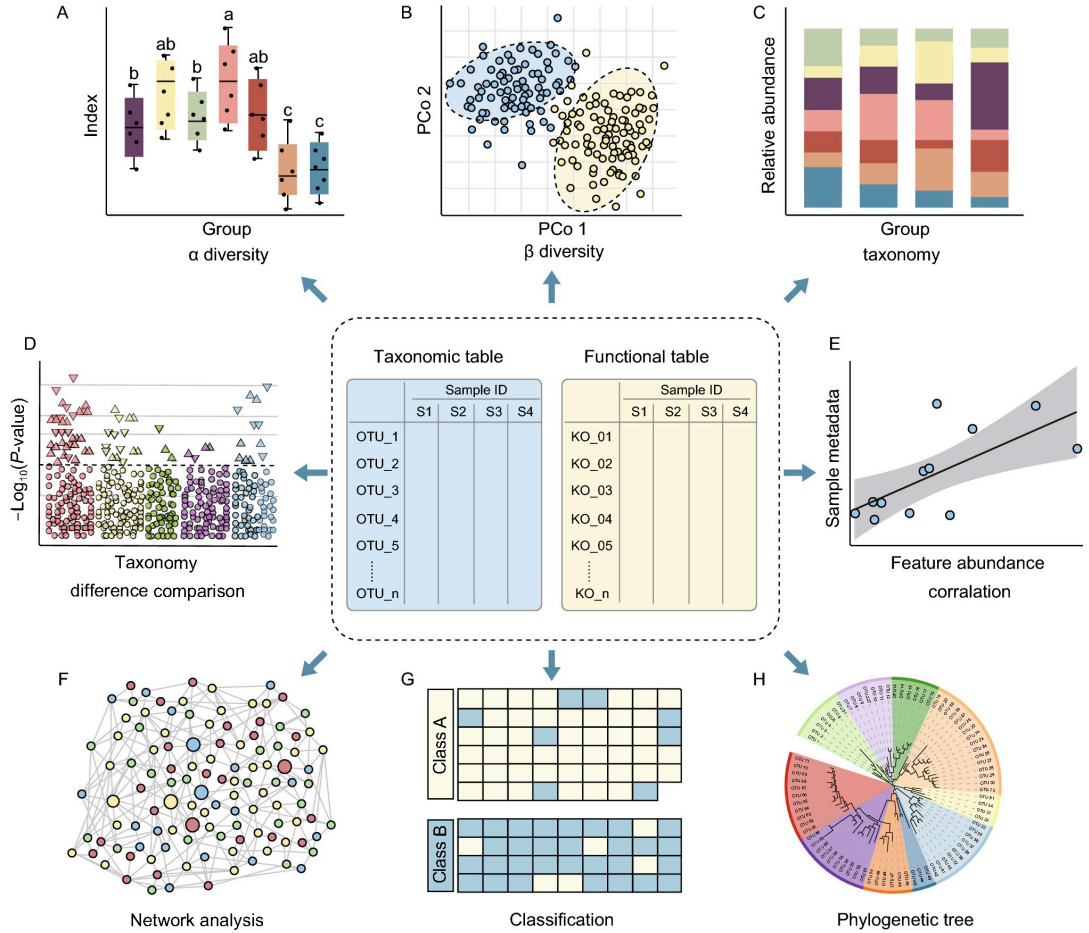


Alvaro (2017)

RÉPUBLIQUE FRANÇAISE
Liberté
Égalité
Fraternité

INRAE

Exploration and visualization?



With R?

⇒ Hard to master

Users need an interactive and user-friendly tool!

Liu et al. (2020)

Let me introduce `{easy16S}`

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

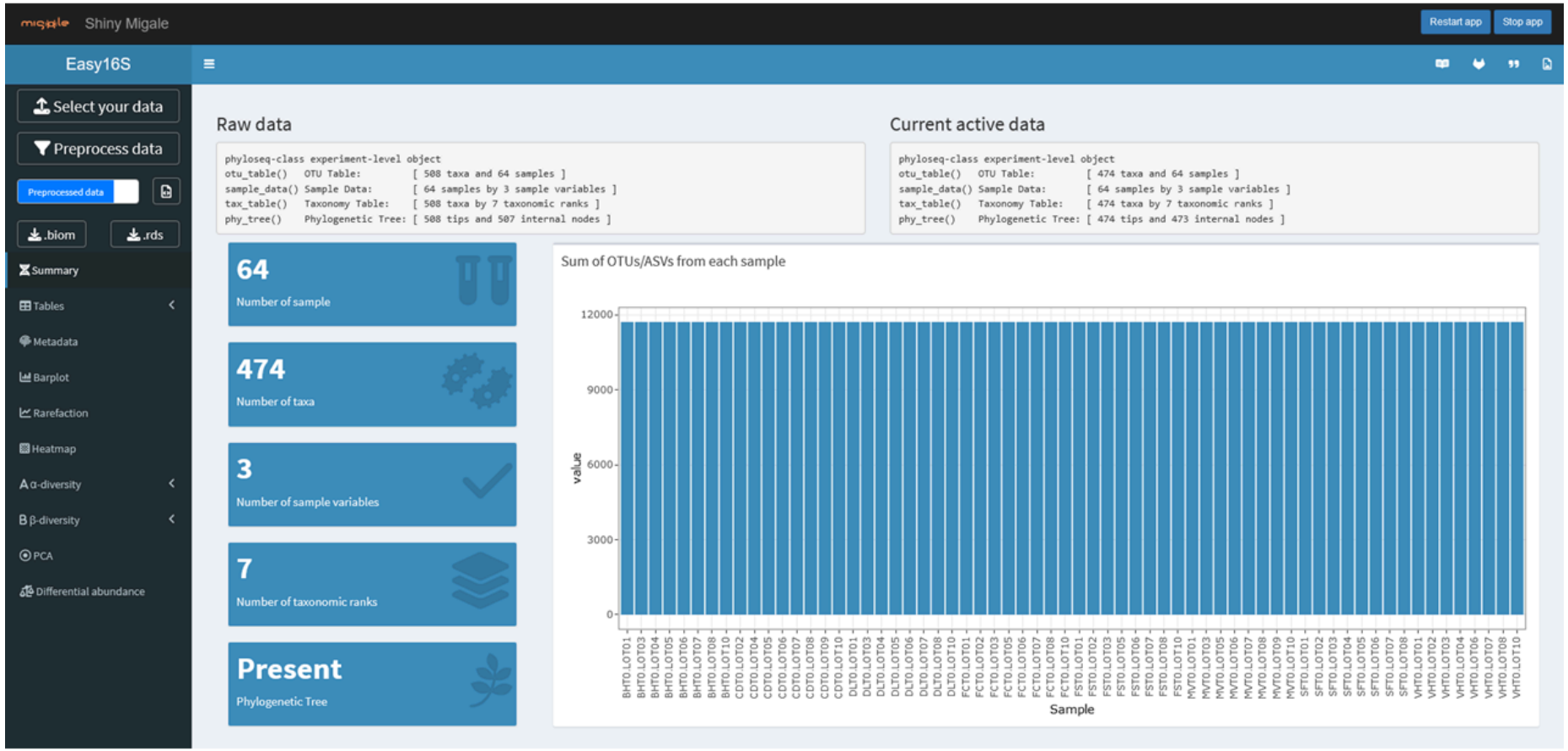
- User-friendly interactive web application with **Shiny**
- Explore, visualize, and analyze metabarcoding data
- Built with R and based on the `phyloseq` package
- Convenient functions and default settings

Behind the scenes

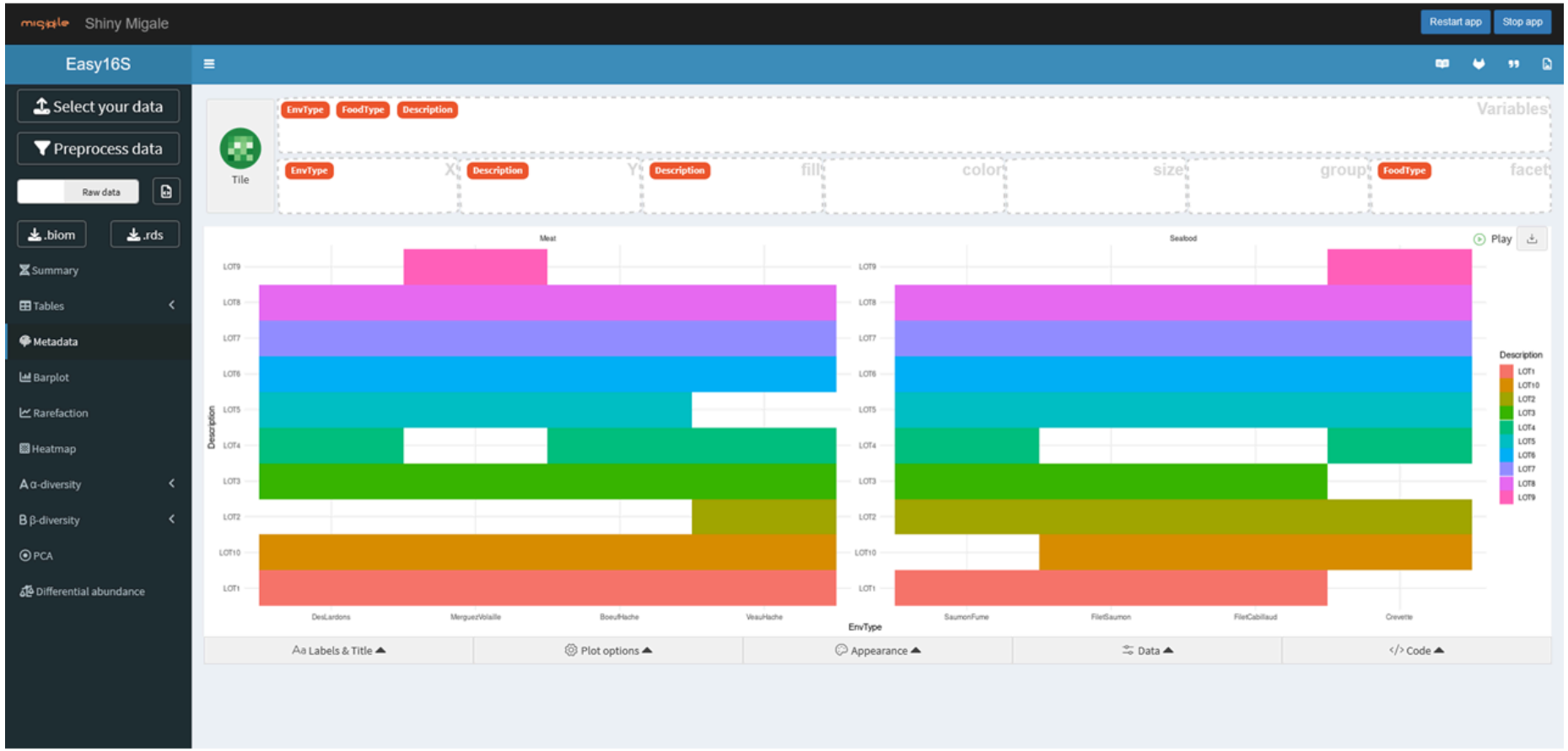
- Built like a package with **`golem`**
- Hosted online on the MIGALE instance of **`shinyproxy`**
- Containerized with **Docker**, **CI/CD** deployed with `.gitlab-ci.yml` in a **`renv`** reproducible environment
- Documented with **`pkgdown`** **pages**
- Licensed under **GNU AGPLv3**

~~Live~~ Demo

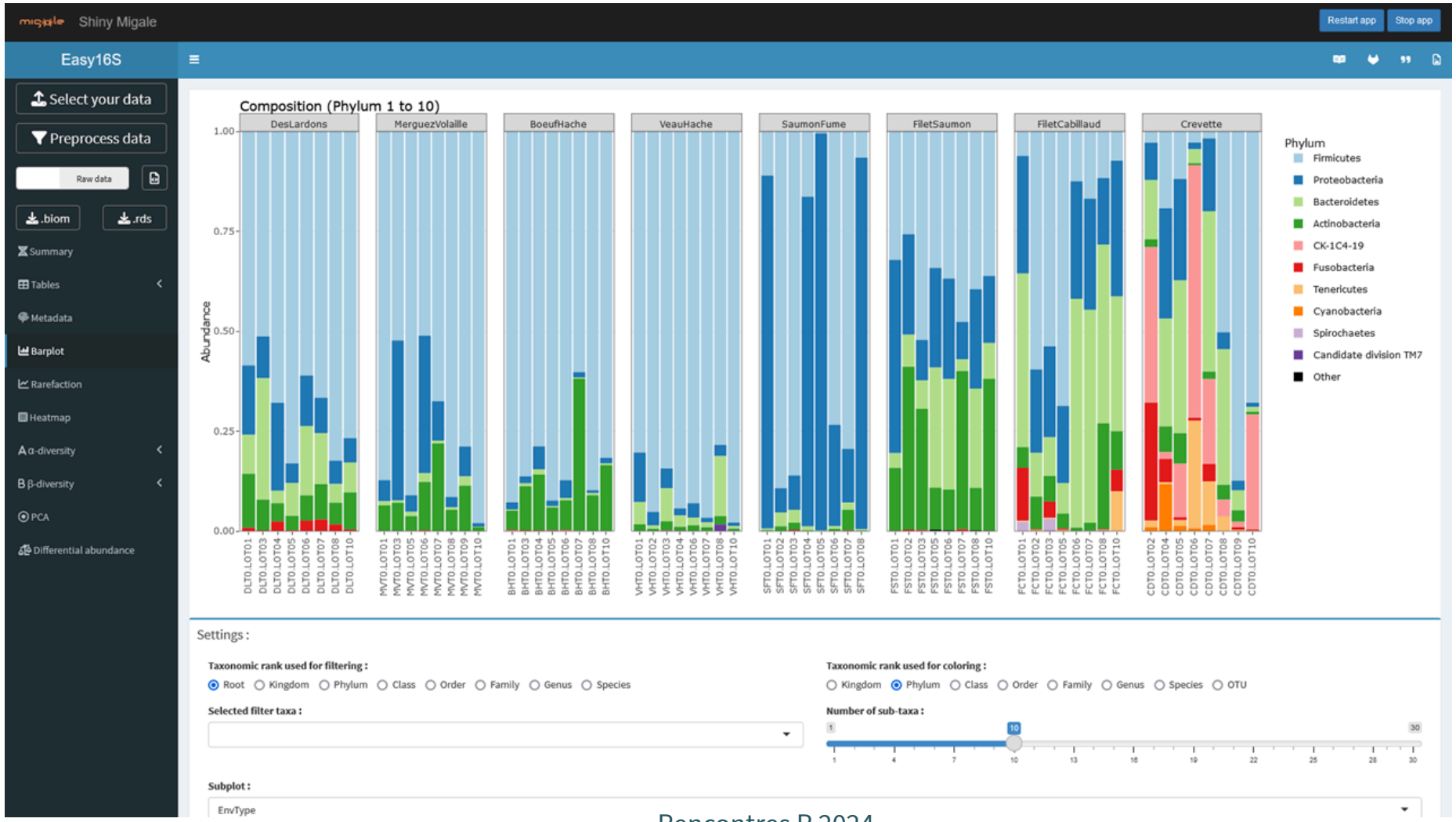
Interface


Shiny Migale
Restart app
Stop app
Easy16S
Select your data
Preprocess data
Preprocessed data
.biom
.rds
Summary
Tables
Metadata
Barplot
Rarefaction
Heatmap
α-diversity
β-diversity
PCA
Differential abundance
Raw data
phyloseq-class experiment-level object
otu_table() OTU Table: [508 taxa and 64 samples]
sample_data() Sample Data: [64 samples by 3 sample variables]
tax_table() Taxonomy Table: [508 taxa by 7 taxonomic ranks]
phy_tree() Phylogenetic Tree: [508 tips and 507 internal nodes]
Current active data
phyloseq-class experiment-level object
otu_table() OTU Table: [474 taxa and 64 samples]
sample_data() Sample Data: [64 samples by 3 sample variables]
tax_table() Taxonomy Table: [474 taxa by 7 taxonomic ranks]
phy_tree() Phylogenetic Tree: [474 tips and 473 internal nodes]
64
Number of sample
474
Number of taxa
3
Number of sample variables
7
Number of taxonomic ranks
Present
Phylogenetic Tree
Sum of OTUs/ASVs from each sample
value
Sample

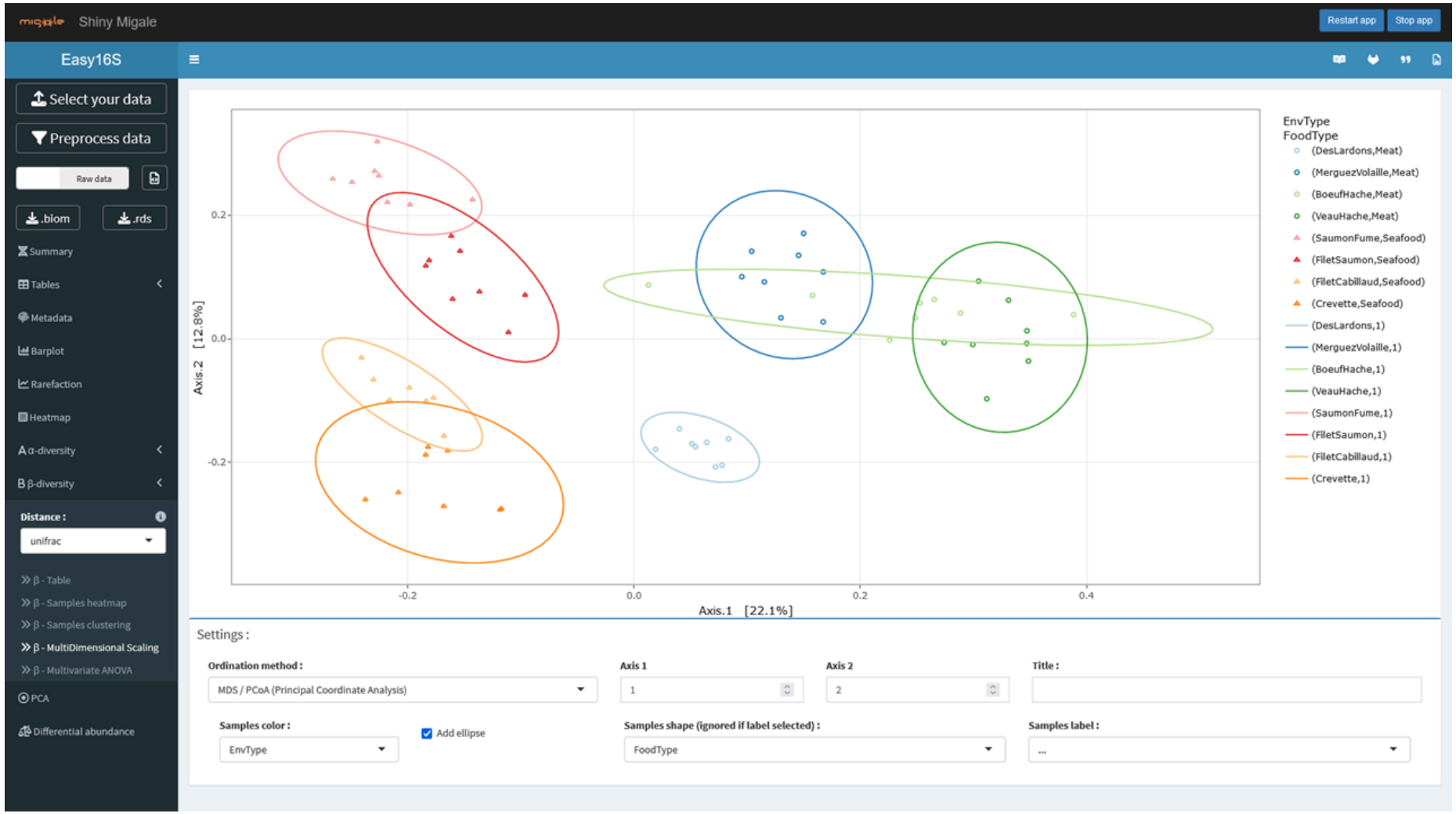
Metadata (with `esquisse`)



Compositional Barplots



Beta Diversity Visualization



Differential Abundance

Use-Case

- **Beginner users**: Autonomous analyses without any technical skills
- **Advanced users**: Swiftly explore data and identify patterns
- **Training sessions**: Focus on biological concepts without being limited by programming challenges

Publication: JOSS Under Review

Take Home Message

- Online instance
  - shiny.migale.inrae.fr/app/easy16S
- Documentation
  - easy16s.migale.inrae.fr
- GitLab (issues and contributions)
  - forgemia.inra.fr/migale/easy16s
- Docker image
  - `registry.forgemia.inra.fr/migale/easy16s:latest`

Thank you for your attention

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Bibliography

Alvaro, Sebastian. 2017. “Amplicon Sequencing and High-Throughput Genotyping – Metagenomics.” http://www.sixthresearcher.com/amplicon-sequencing-and-high-throughput-genotyping-metagenomics/.

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.