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

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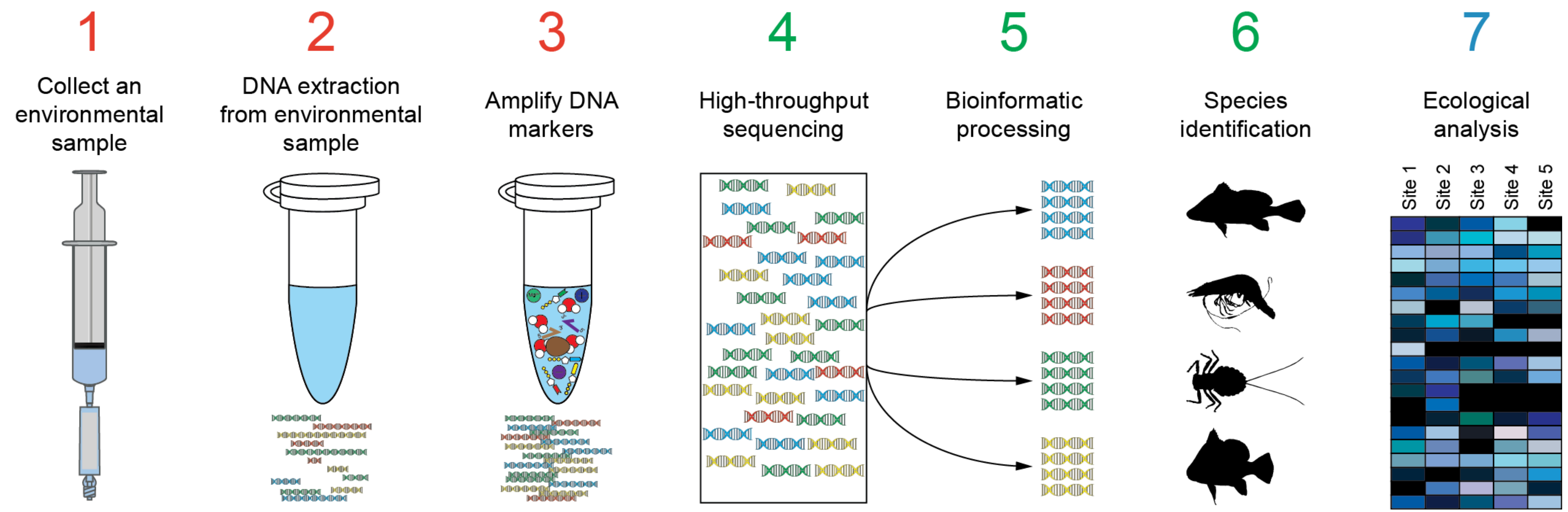
Rencontres R 2024

Cédric Midoux

PROSE & MaIAGE

June 13, 2024

Metabarcoding (16S) workflow



1 Collect an environmental sample

2 DNA extraction from environmental sample

3 Amplify DNA markers

4 High-throughput sequencing

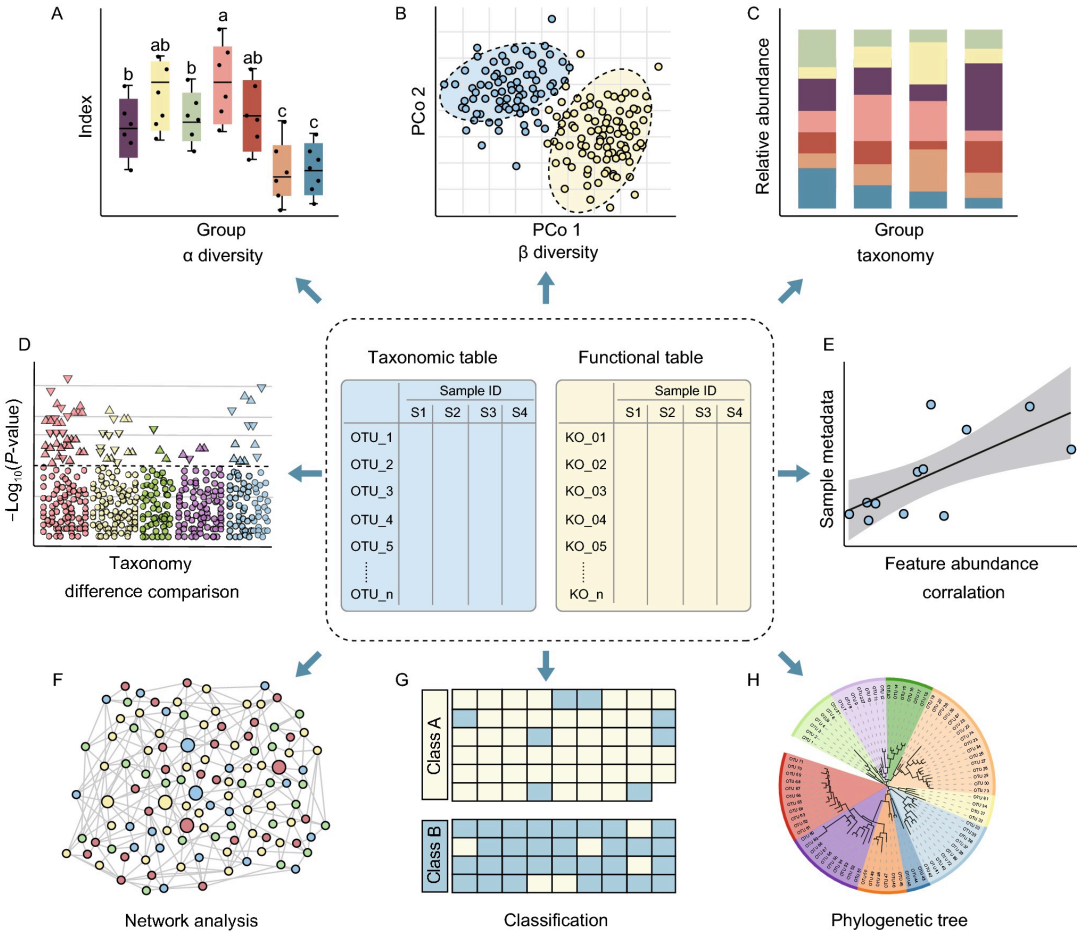
5 Bioinformatic processing

6 Species identification

7 Ecological analysis

Alvaro (2017)

Exploration and visualization?



Liu et al. (2020)

With R?

⇒ Hard to master

Users need an interactive and user-friendly tool!

Let me introduce `{easy16S}`

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

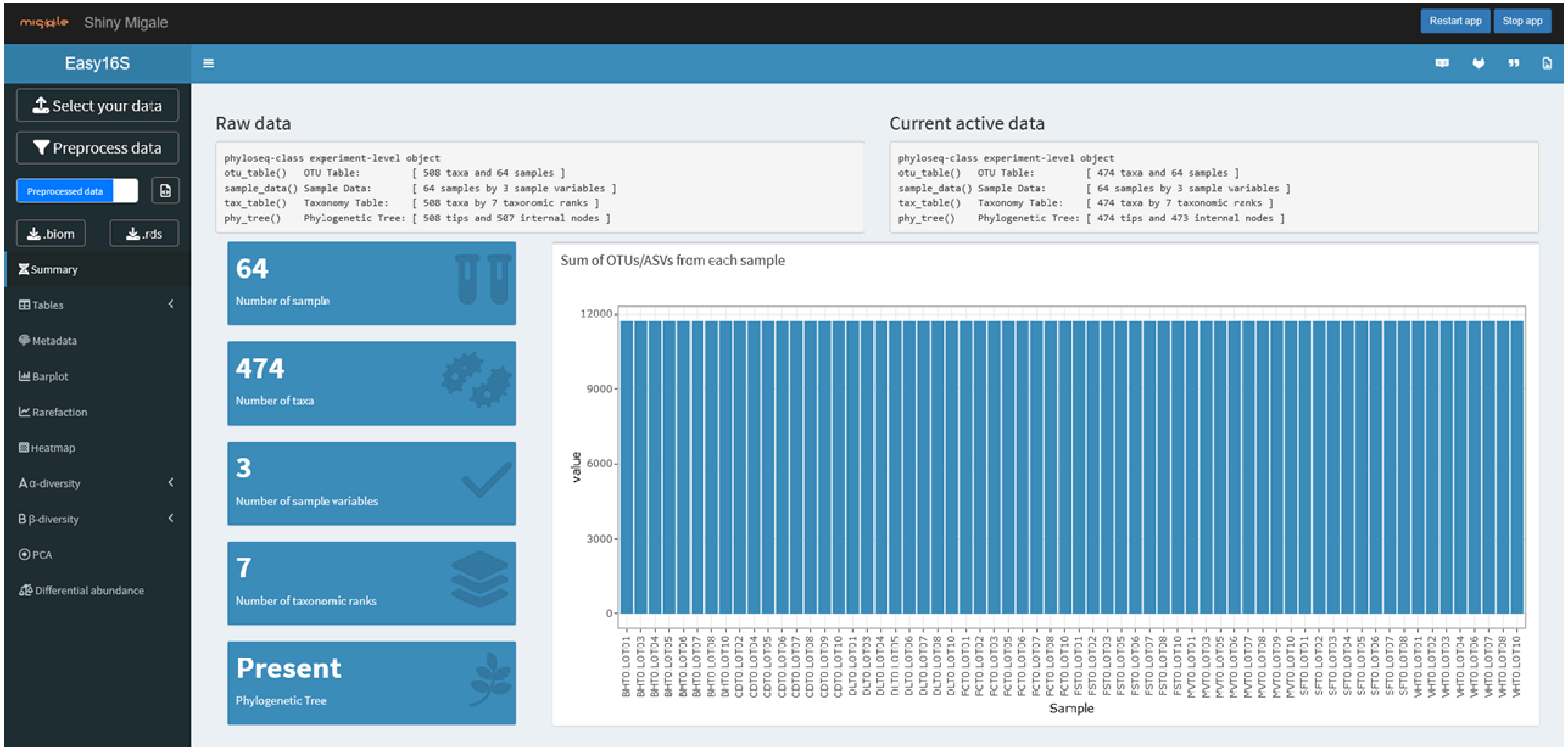
- User-friendly interactive web application with **Shiny**
- Explore, visualize, and analyze metabarcoding data
- Built with R and based on the `phyloseq` package
- Convenient functions and default settings

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



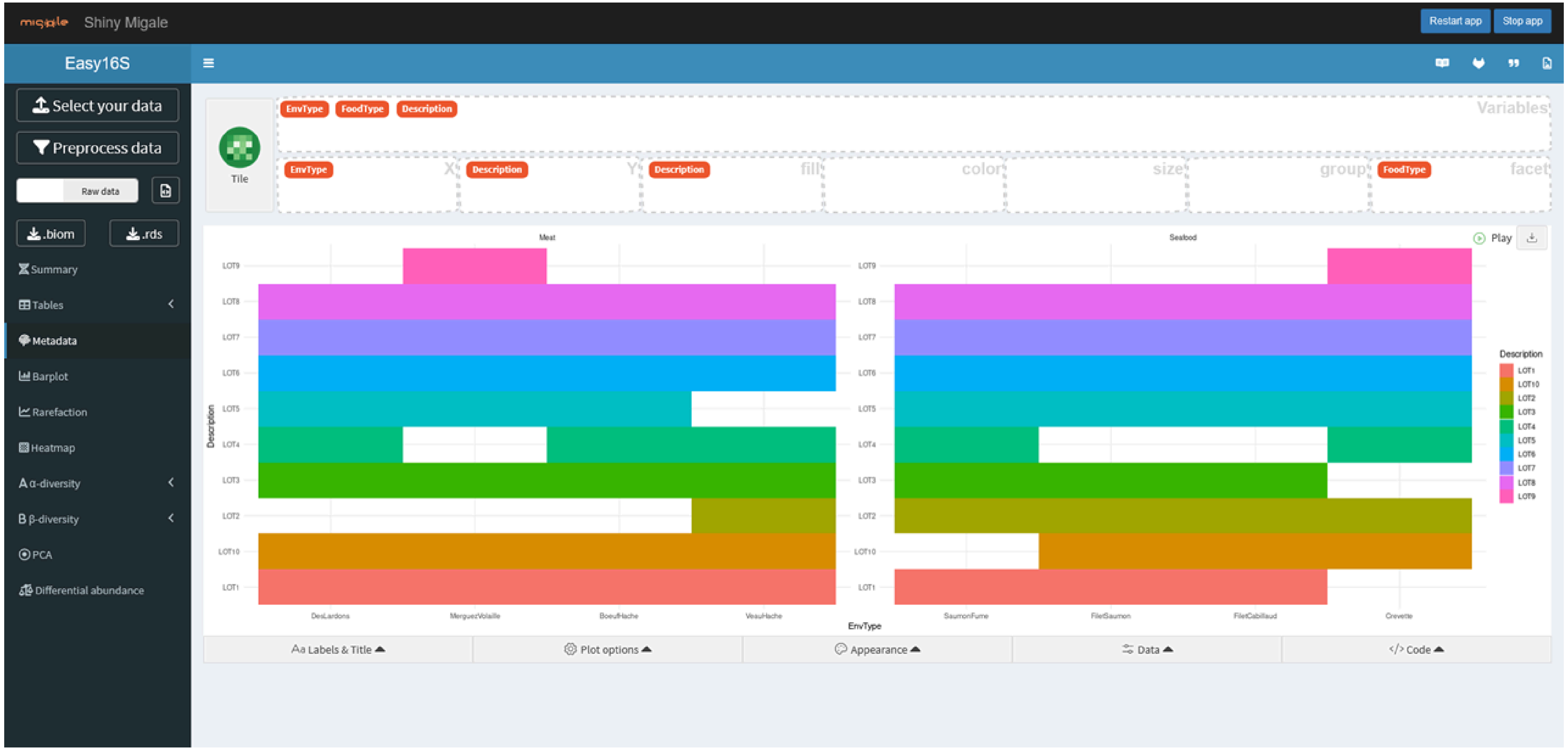
Raw data

```
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 ]
```

Metadata (with `esquisse`)



Variables: EnvType, FoodType, Description

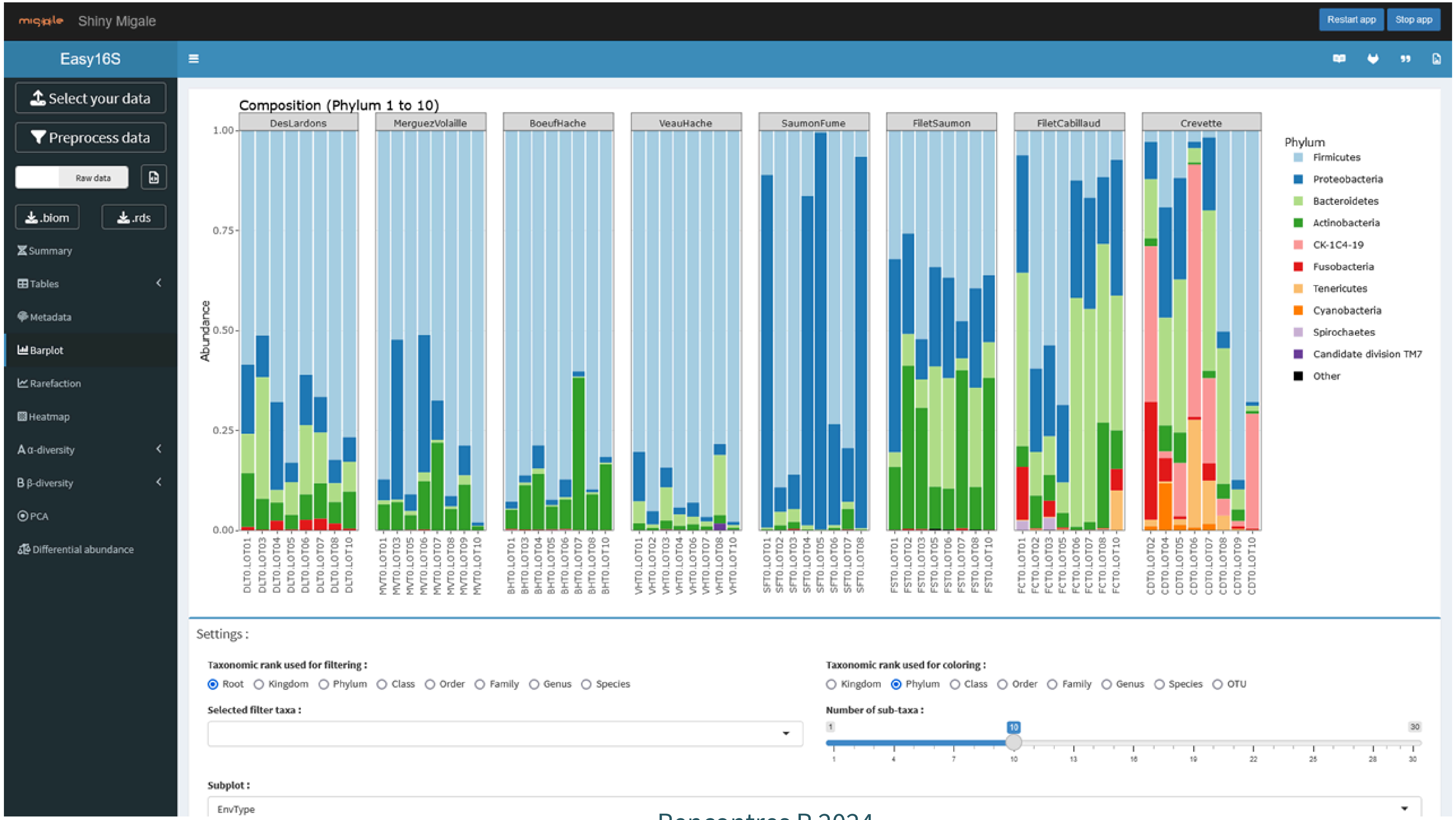
X: EnvType

Y: Description

fill: Description

facet: FoodType

Compositional Barplots



Settings :

Taxonomic rank used for filtering :
● Root ○ Kingdom ○ Phylum ○ Class ○ Order ○ Family ○ Genus ○ Species

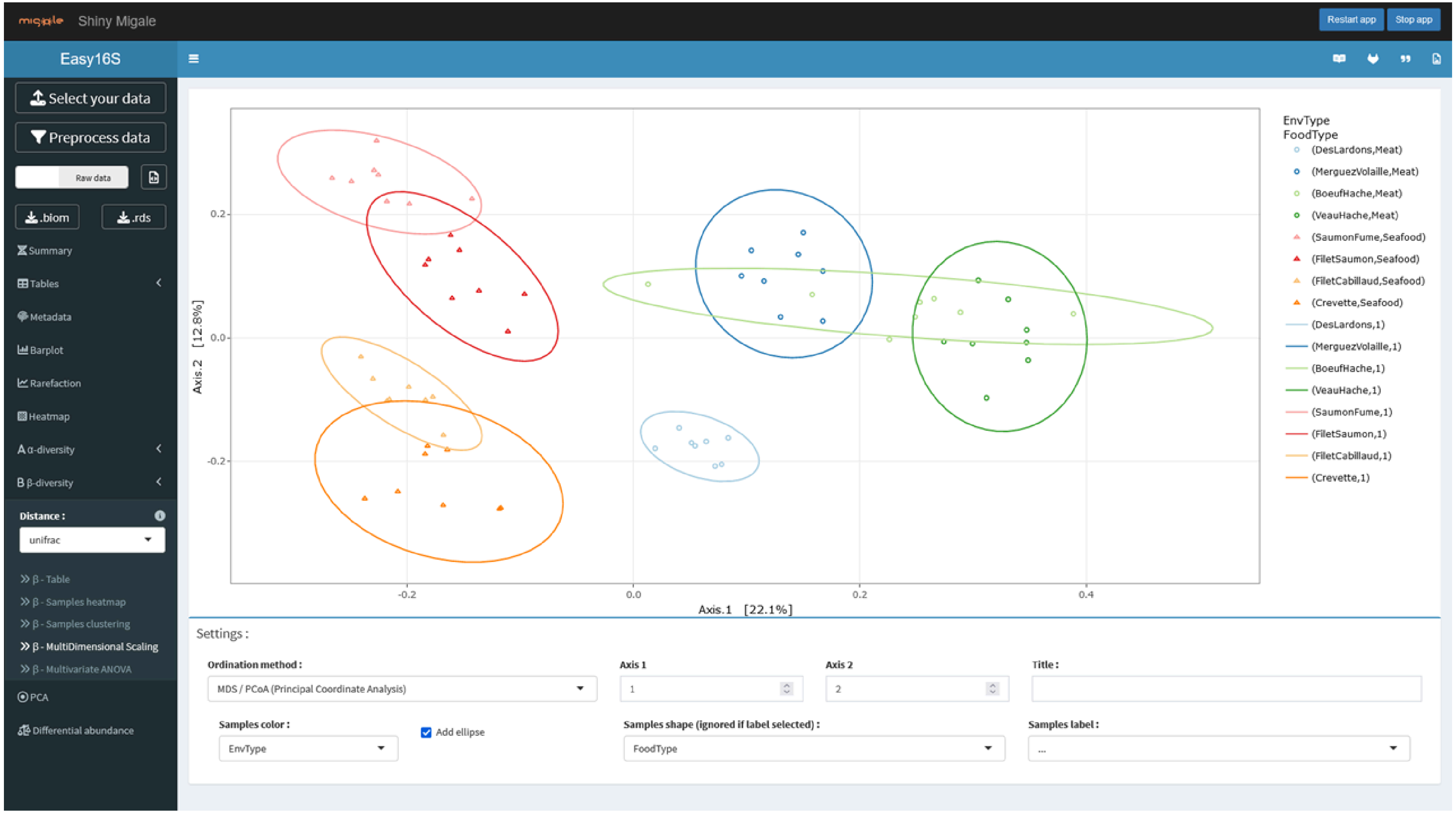
Selected filter taxa :

Subplot :
EnvType

Taxonomic rank used for coloring :
○ Kingdom ● Phylum ○ Class ○ Order ○ Family ○ Genus ○ Species ○ OTU

Number of sub-taxa : 10

Beta Diversity Visualization



Distance : unifrac

Settings :

Ordination method : MDS / PCoA (Principal Coordinate Analysis)

Axis 1 1

Axis 2 2

Title :

Samples color : EnvType

☑ Add ellipse

Samples shape (ignored if label selected) : FoodType

Samples label : ...

Differential Abundance

Settings :

Experimental design : FoodType

Contrast left : Meat

Contrast right : Seafood

Title : Volcano plot

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

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

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

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.