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## ExploreMetabar: a user-friendly Shiny application to explore the drivers of microbial communities

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## Context

- Metabarcoding is widely used for community composition studies of complex samples (food, gut, environment)
- Existing tools for the analysis of these data needs some coding knowledge
- We present a Shiny application for metabarcoding data with interactive features allowing user to explore and analyse them.

## Features

- A free and easily accessible web application
- R package for local installation
- Use of phyloseq object (output from rANOMALY, FROGS)
- Interactive filters, to focus on a specific group of samples.
- Complete diversity analysis with advanced visualizations and statistical tests, differential analysis and more features.

Explore Metabar
🏠

Input Data

Community Composition

Alpha diversity

Beta diversity

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Boxplot/Tests

Heatmap

Differential Analysis

ASVenn

SourceTracker

Dataset preparation

Diversity analysis **How different are the communities ?**

Stacked barplot

Boxplot (alpha diversity)

Ordination (beta diversity)

Interactive

**Differential analysis** **Which taxa are differentially abundant between conditions ?**

wildtype\_10 vs. wildtype\_150

Heatmap

VennDiagram

DESeq2 MetagenomeSeq Metacoder

Available on repository at :  
<https://forgemia.inra.fr/umrf/exploremetabar>

Online instances:  
<https://shiny.mesocentre.uca.fr/app/exploremetabar>  
<https://shiny.migale.inrae.fr/app/exploremetabar>

Test me !