



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

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

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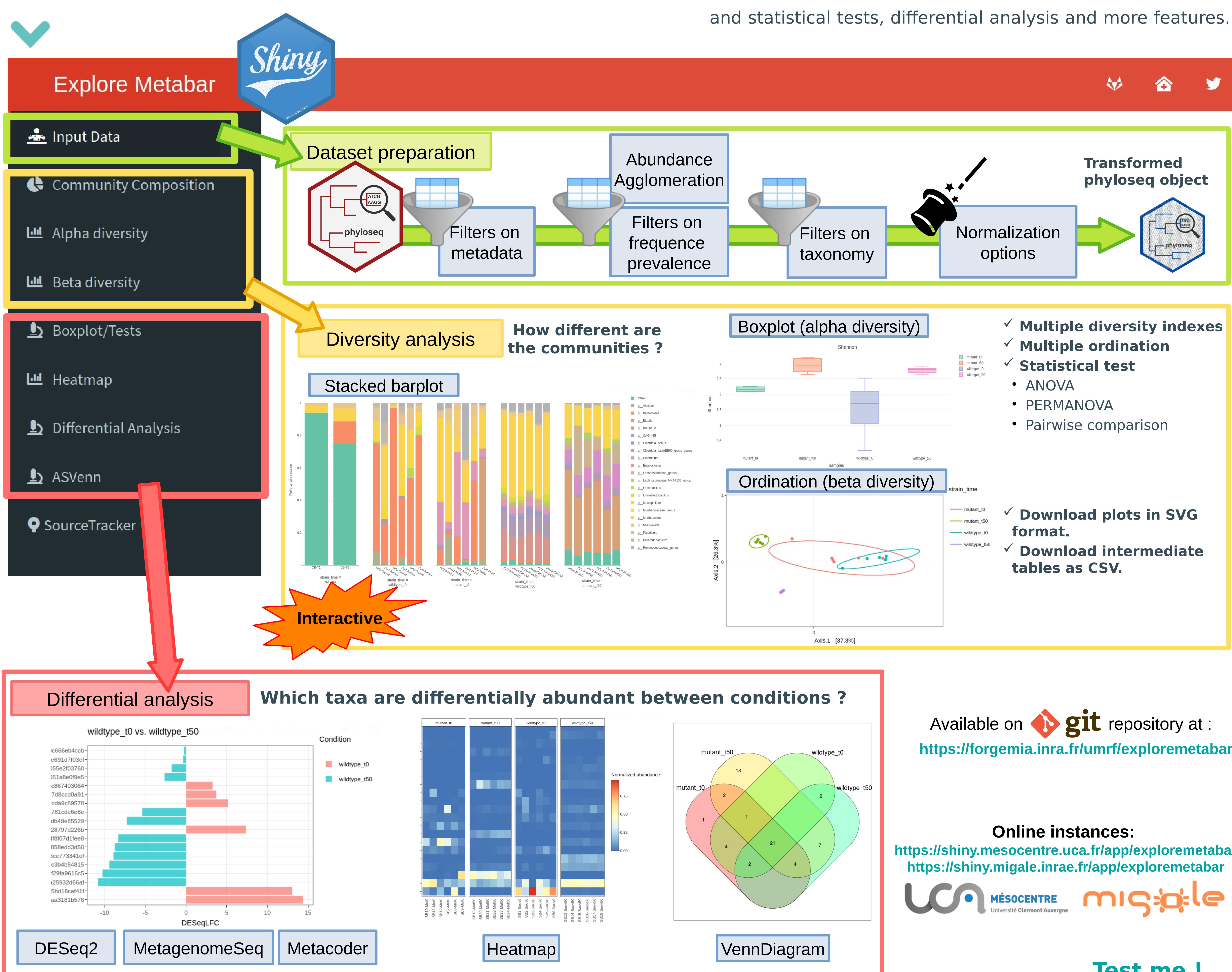
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Context

- 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.



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 !



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