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# Easy16S: a user-friendly Shiny interface for analysis and visualization of metagenomic data

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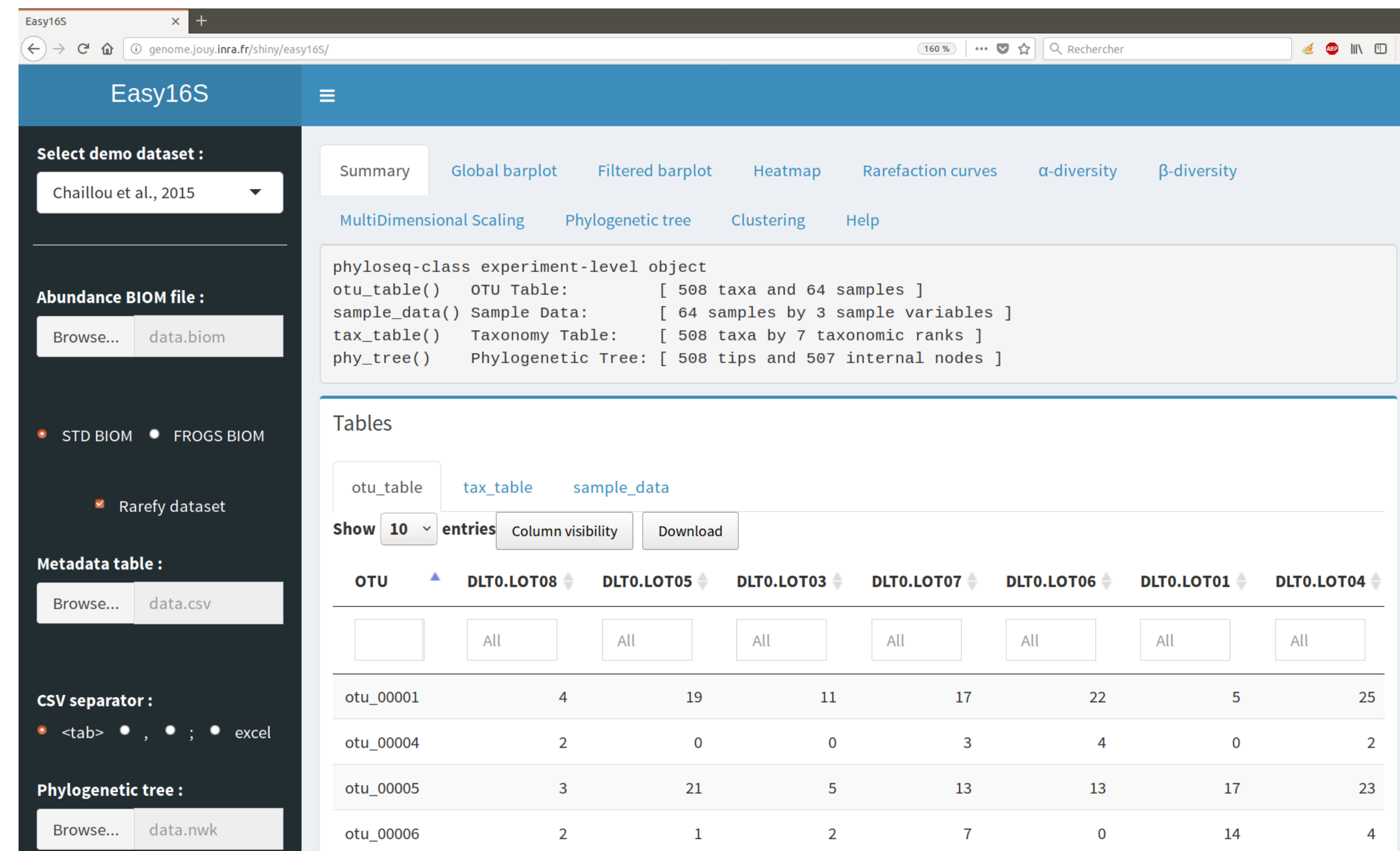


## Introduction

Microbiome data investigation has become a crucial step of recent studies of microbial diversity and dynamics. For the first step of metabarcoding analysis, bioinformatic treatment, user friendly tools like FROGS are available through the Galaxy platform. We developed a user friendly application for statistical analysis and data visualization, the second step of metabarcoding analysis: an interactive R-shiny interface named "Easy16S". It is based on two main packages: shinydashboard and phyloseq. Easy16S is intended for biologists eager to explore their data and create figures rapidly and interactively. It is simple, easy-to-use and specifically focused on the mapping of covariates of interest. This tool is available online: [genome.jouy.inra.fr/shiny/easy16S/](http://genome.jouy.inra.fr/shiny/easy16S/)

## Inputs

- Dataset created with:
  - BIOM (ie: from FROGS)
  - Table of metadata
  - Phylogenetic tree
 → Possibility to rarefy data
- Simple and facilitated import



## Data table output

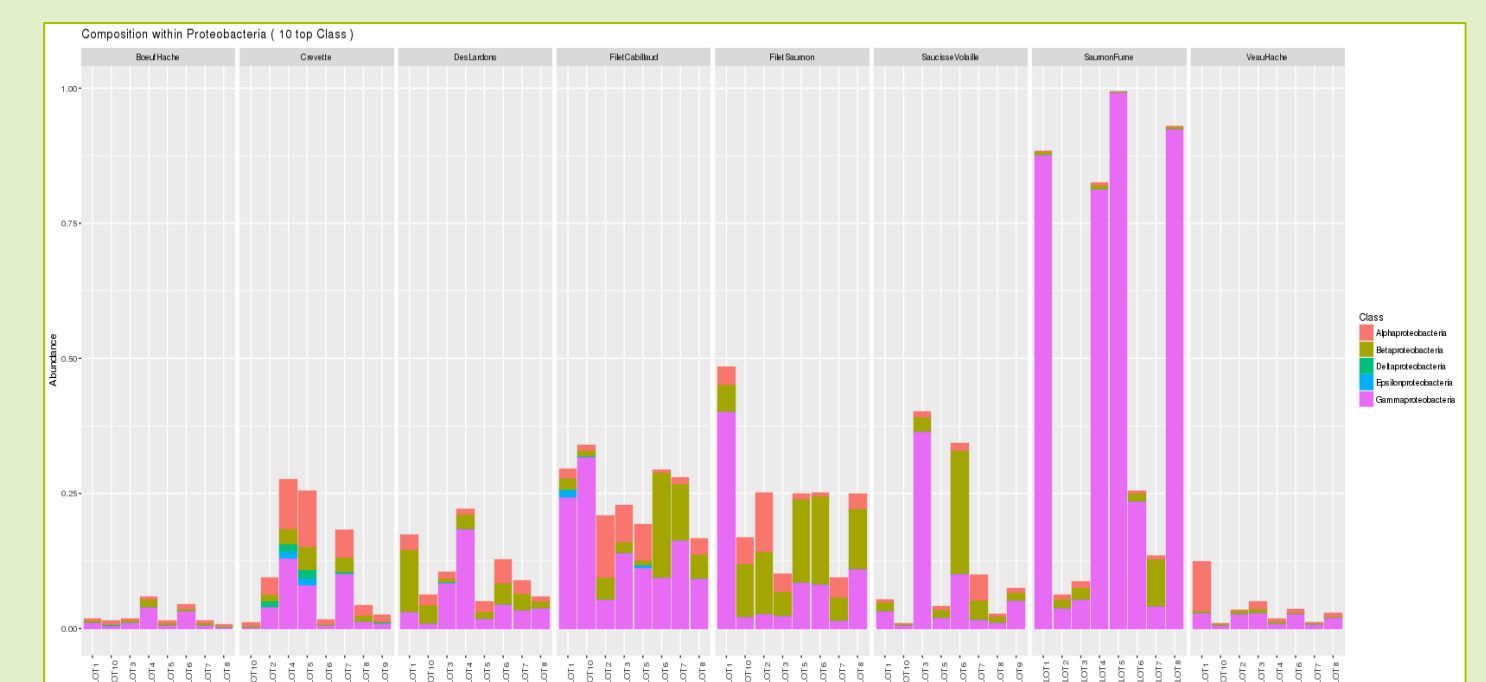
- Phyloseq object
  - OTU table
  - Taxonomic table
  - Sample table
- The user can filter, sort and download tables

## Examples of graphical outputs

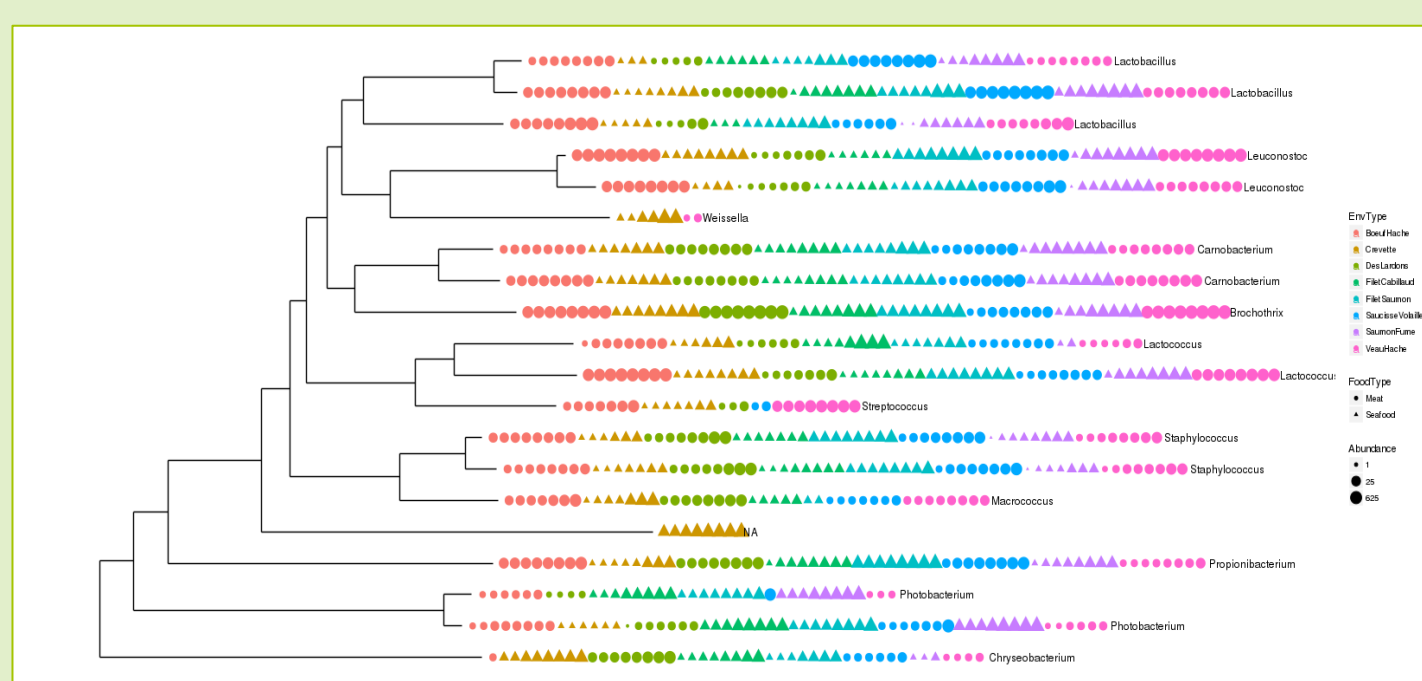
Thanks to the tabs on the top side, the user can visualize the different plots

→ Each plot can be subplotted, colored and ordered based on sample metadata

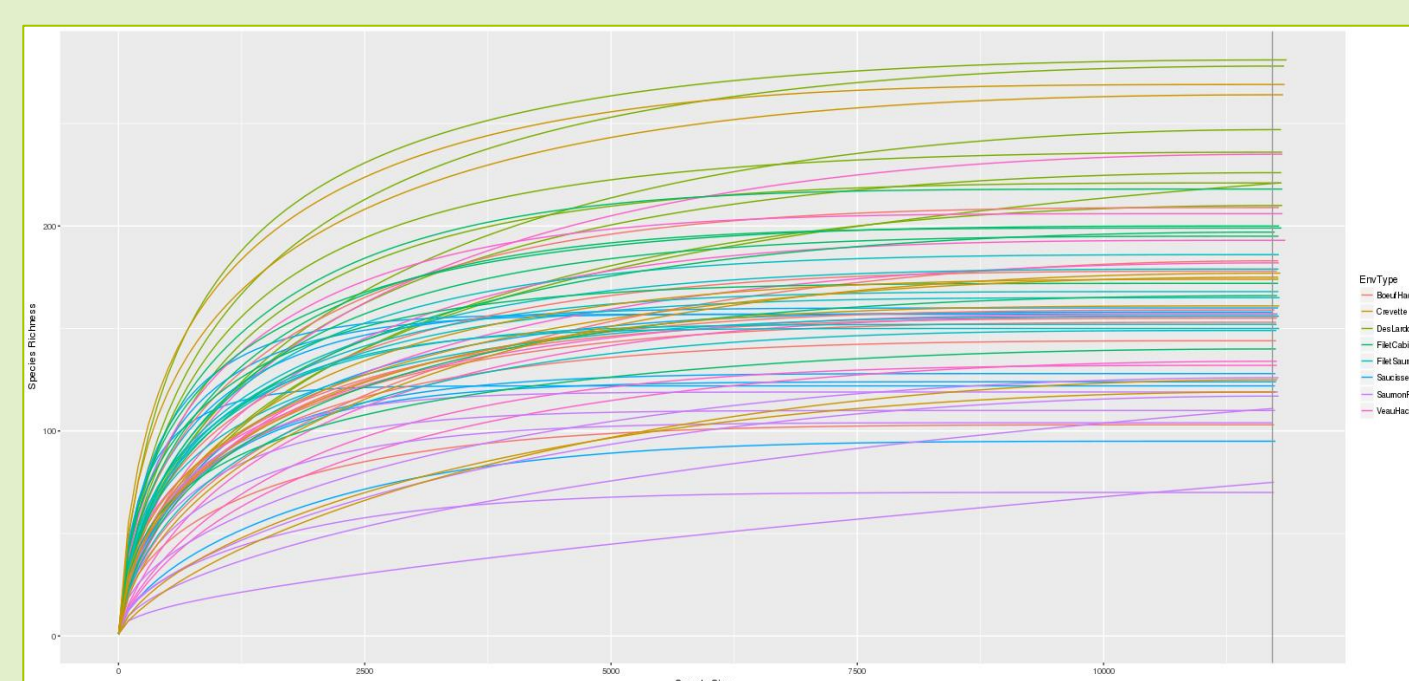
→ Each graphical parameter can be adjusted dynamically



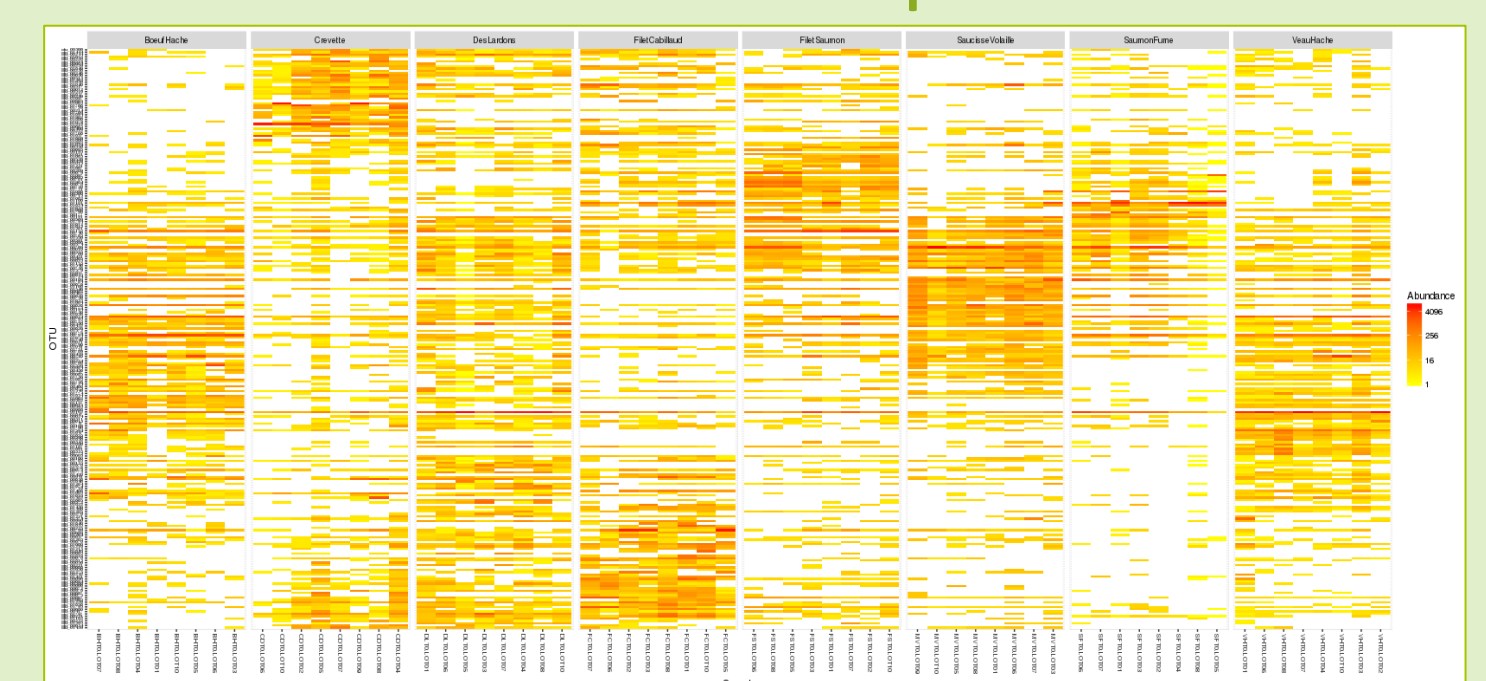
Filtered barplot



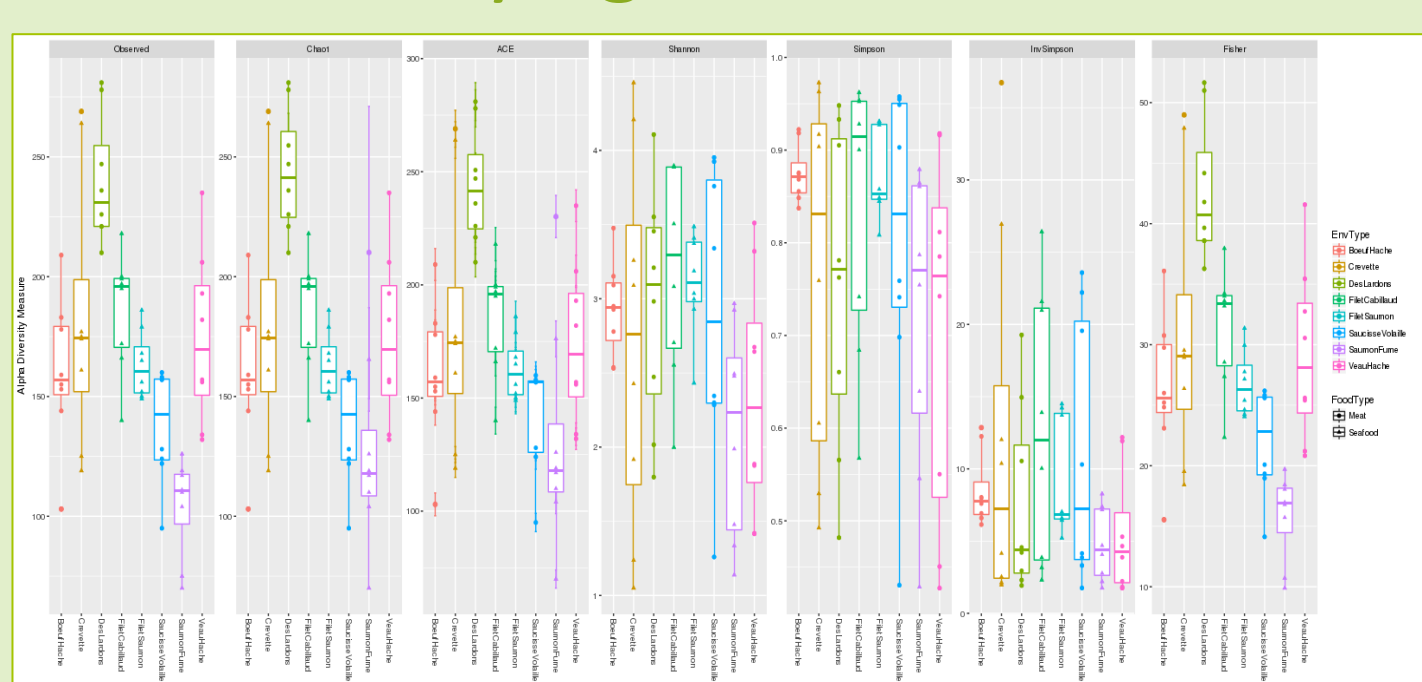
Phylogenetic tree



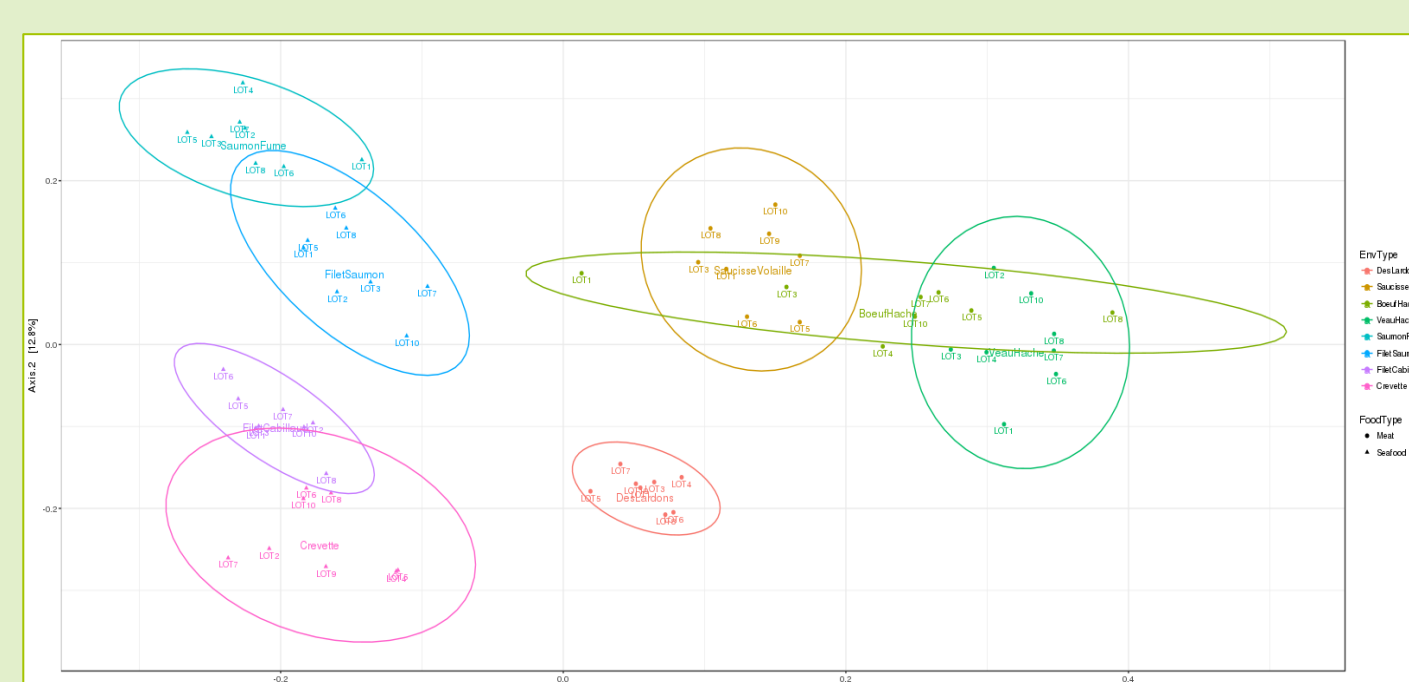
Rarefaction curves



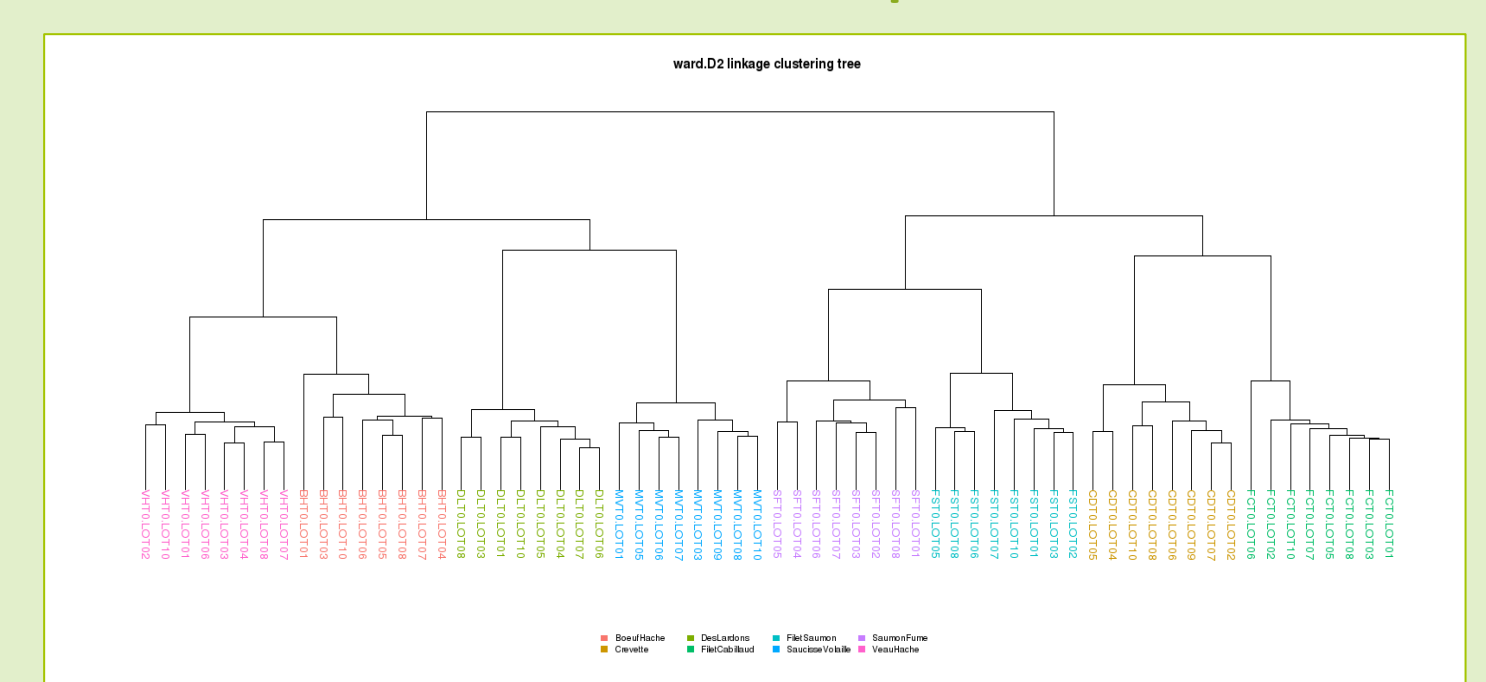
Heatmap



α-diversity: box plot



β-diversity: PCoA



β-diversity: clustering

## Upcoming

- Continuous addition of features as requested by users:
  - Download of Rcode to rebuild outputs
  - RData object upload/download
  - Multidimensional scaling settings
  - Additional multivariate analysis methods
  - and many more...
- LDAP user management
- Server resource optimization
- User manual

## Technological choices

- <http://genome.jouy.inra.fr/shiny/easy16S/>
- Open source shiny server
- INRA MIGALE bioinformatics platform
- GitLab repository



- F. Escudié *et al.*, FROGS: Find, Rapidly, OTUs with Galaxy Solution. *Bioinformatics* **34**, 1287-1294 (2018).
- W. Chang *et al.*, shiny: Web Application Framework for R. (2017).
- P. J. McMurdie, S. Holmes, phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS One* **8**, e61217 (2013).

