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

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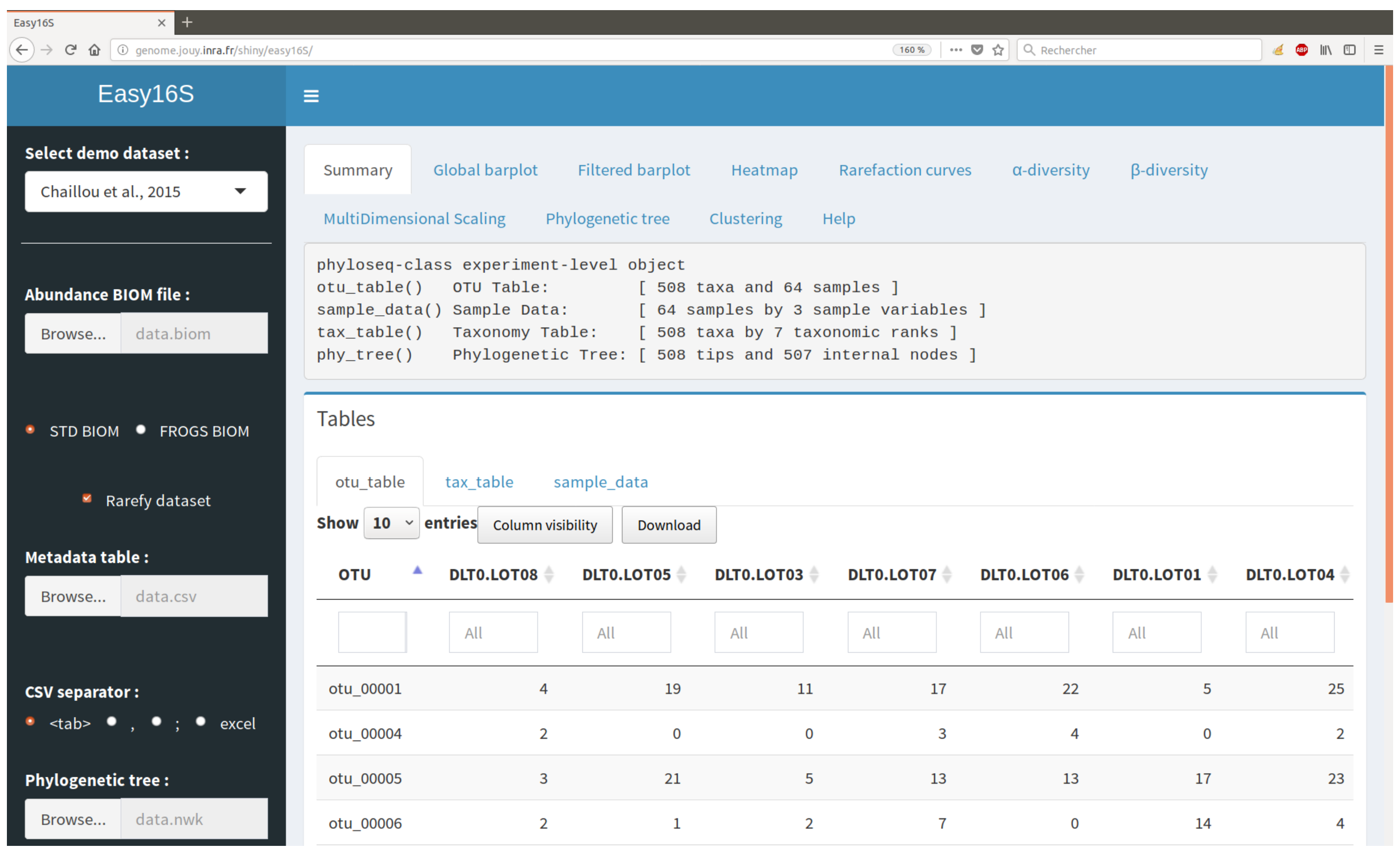
Introduction

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/**

Inputs

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



Select demo dataset : Chaillou et al., 2015

Abundance BIOM file : data.biom

● STD BIOM ○ FROGS BIOM

☑ Rarefy dataset

Metadata table : data.csv

CSV separator : ● <tab> ○ , ○ ; ○ excel

Phylogenetic tree : data.nwk

```
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 ]
```

Tables

otu_table | tax_table | sample_data

Show 10 entries

OTU	DLT0.LOT08	DLT0.LOT05	DLT0.LOT03	DLT0.LOT07	DLT0.LOT06	DLT0.LOT01	DLT0.LOT04
	All	All	All	All	All	All	All
otu_00001	4	19	11	17	22	5	25
otu_00004	2	0	0	3	4	0	2
otu_00005	3	21	5	13	13	17	23
otu_00006	2	1	2	7	0	14	4

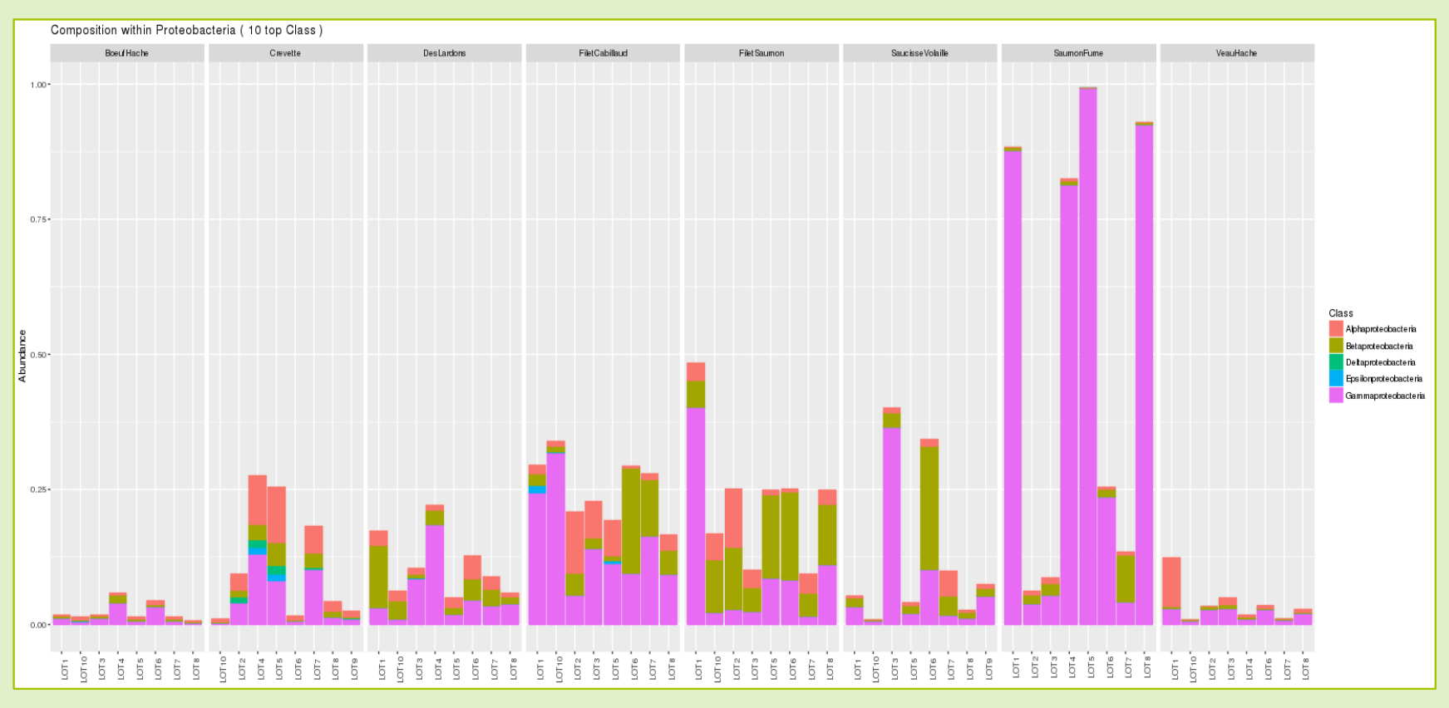
Data table output

- Phyloseq object
- OTU table
- Taxonomic table
- Sample table

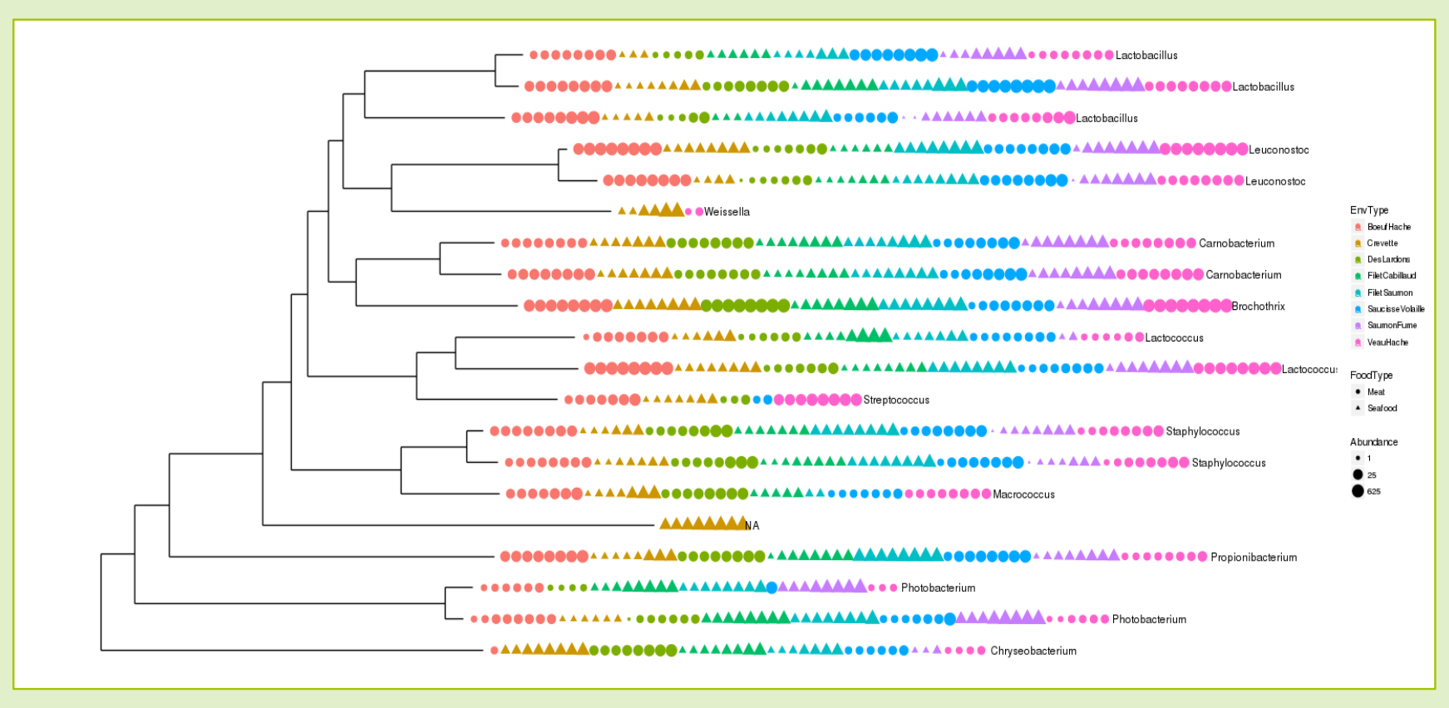
→ The user can filter, sort and download tables

Examples of graphical outputs

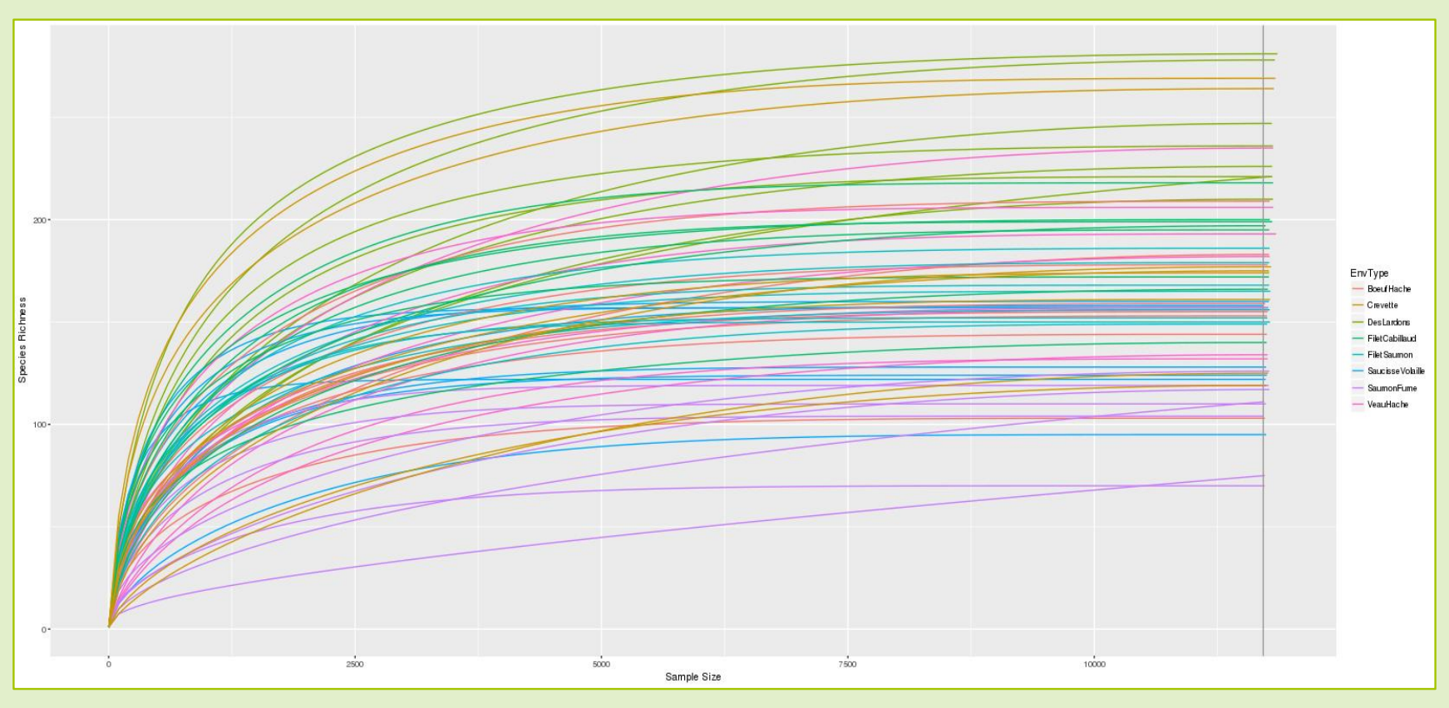
Thanks to the tabs on the top side, the user can visualize the different plots
→ **Each plot can be subplotted, colored and ordered based on sample metadata**
→ **Each graphical parameter can be adjusted dynamically**



Filtered barplot

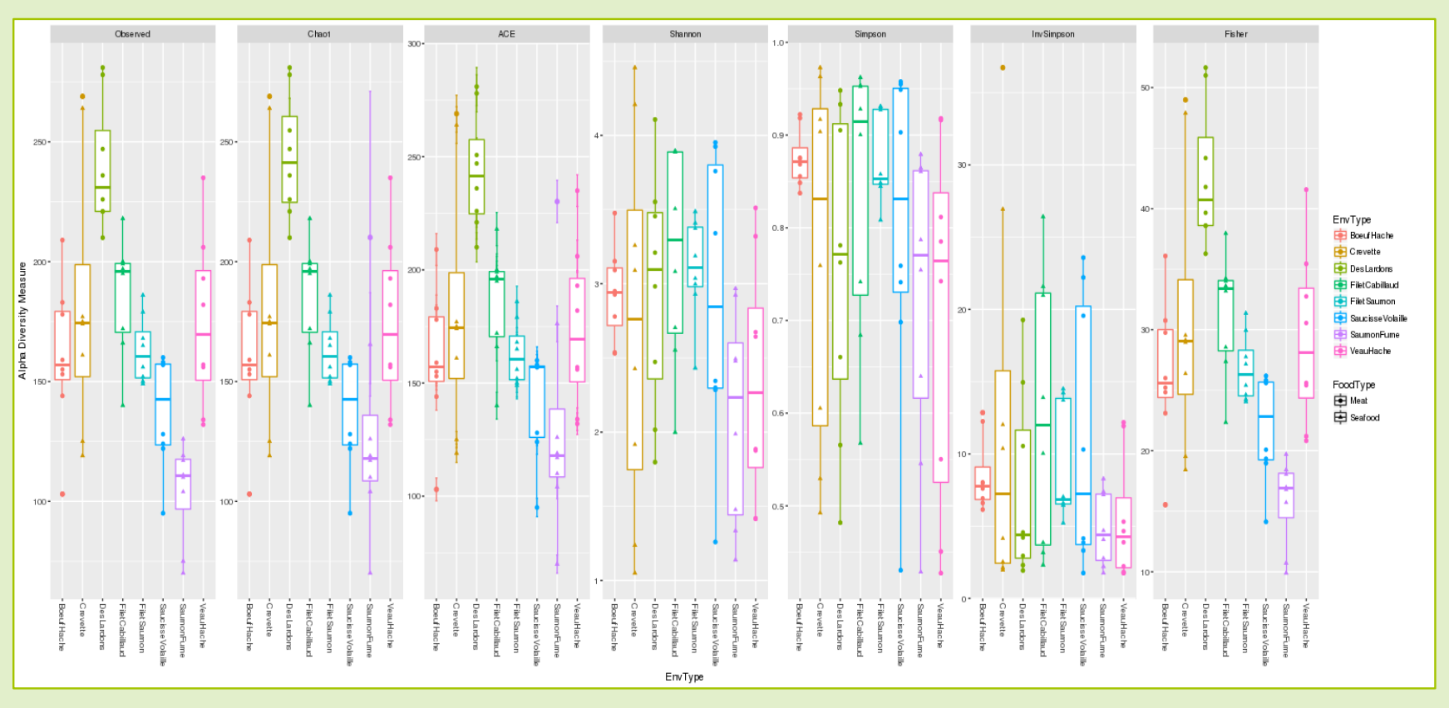


Phylogenetic tree

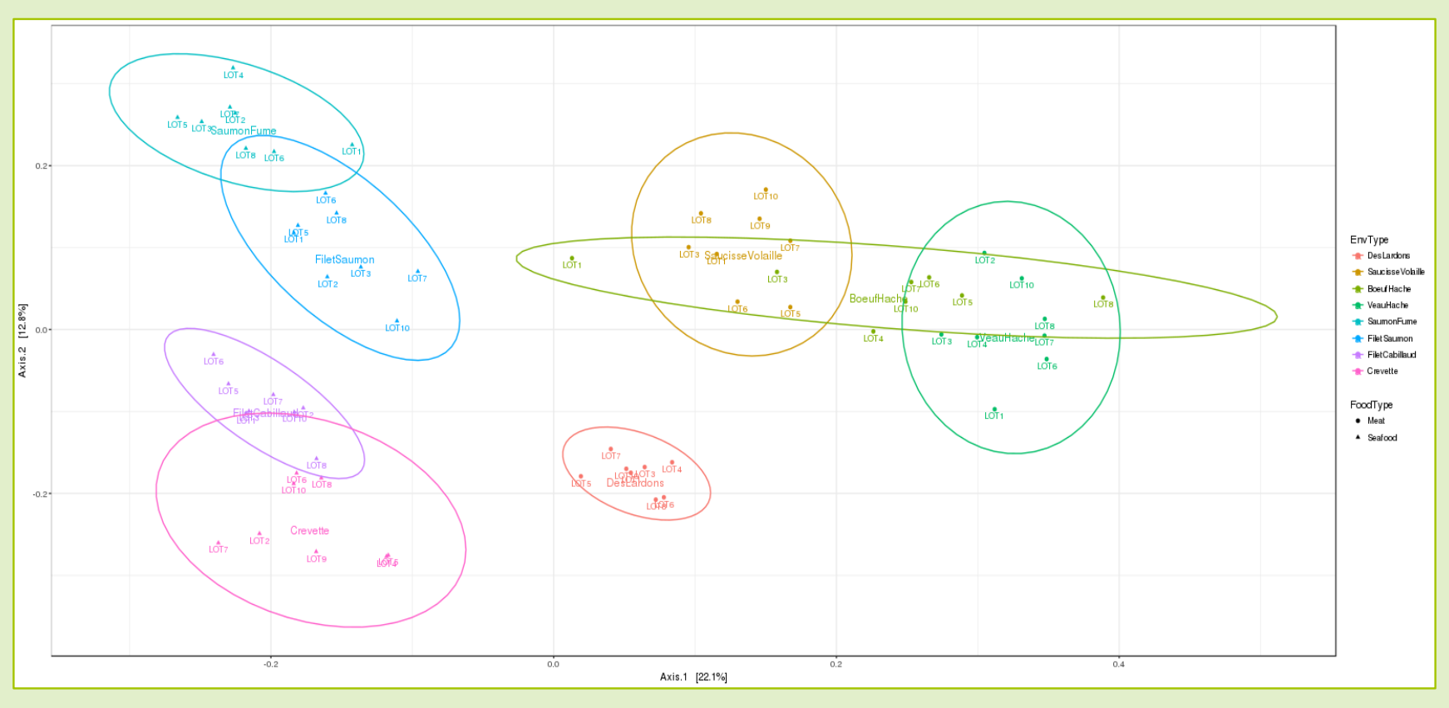


Rarefaction curves

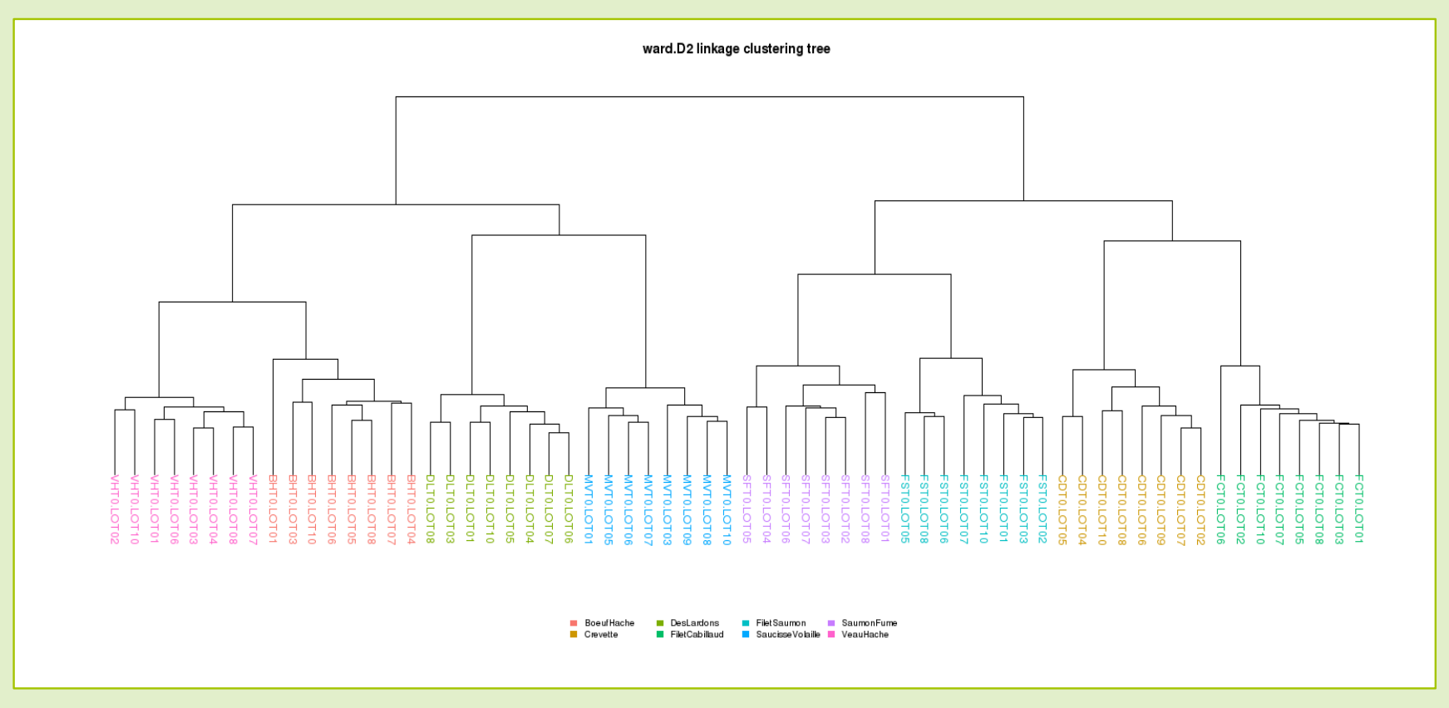
Heatmap



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).