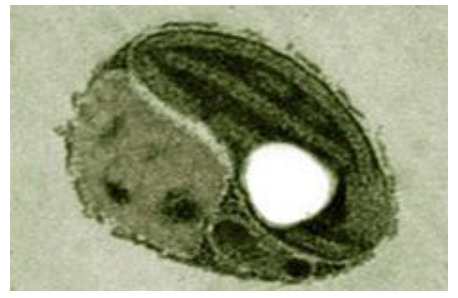


## Marine Genomics Observatories

Marine Genomics Observatories provide tools and protocols for long-term monitoring of marine ecosystems located in a well-defined and usually limited geographical area, in order to allow the study of their evolution over time. Hence, they yield a significant amount of heterogeneous and complex data (metabarcoding data, "classical" (morphology-based) biodiversity data, supplemental physico-chemical data), which needs to be organized and stored to enable interested parties to carry out downstream analyses.



Ostreococcus lucimarinus



Cryptophyta



Dinoflagellata

## MyGOD project

The MyGOD project (Manipulate Your Genomic Observatory Data) aims to explore and interpret the data of genomic observatories projects, by providing an integrated and user-friendly web-based visualization tool.

The key component of the interface is a dashboard enabling users to assemble various graphical representations according to their needs. The user interface taps into a database for which specific integration tools, as well as (meta)data formats have been developed and/or adapted in the framework of the MyGOD project, aiming to achieve a high degree of automated ingestion.

Third party tools are used to compute relevant biological and ecological indicators.

## Development tools

MyGOD

Data storage/processing



Dashboard

The dashboard uses the **Vue.js** Javascript framework with the **vue-grid-layout** plugin. Graphical representations are generated dynamically generated with the **D3.js** Javascript library.



## An Interactive Dashboard

### How the dashboard works

The MyGOD dashboard is a multi-taxonomic search tools with save/reload functionality

#### 1 Search Panels

- Provide high level search criteria such as dataset, date range and taxon
- Multiple criteria sets allow easy data comparison
- Search panels are automatically linked to dashboard plots

#### 2 Dashboard Controls

- Allow selection of graph types to be displayed in the dashboard
- For authenticated users, allow saving and loading of dashboards

#### 3 Plot Area

- User controls size and position of plots
- For each plot, user can modify specific parameters (taxon, physico-chemical parameter, fraction size...)
- Plots can be exported as png or svg, associated with a metadata file
- Two types of representations are provided: R generated plots (suitable for publication) and D3.js plot (resizable, perfect for data exploration)

Flash QR code to access a short dashboard demo

### Quick reminder : What is metabarcoding ? :

- Analysis of Taxonomical DNA sequences in environmental samples
- Characterization of biodiversity
- Rapid detection of impacts of environmental change

### Data

#### Metabarcoding series :

- Astan 18S (Eukaryota)
- Astan 16S (Bacteria, Archaea)

#### Taxonomical reference databases :

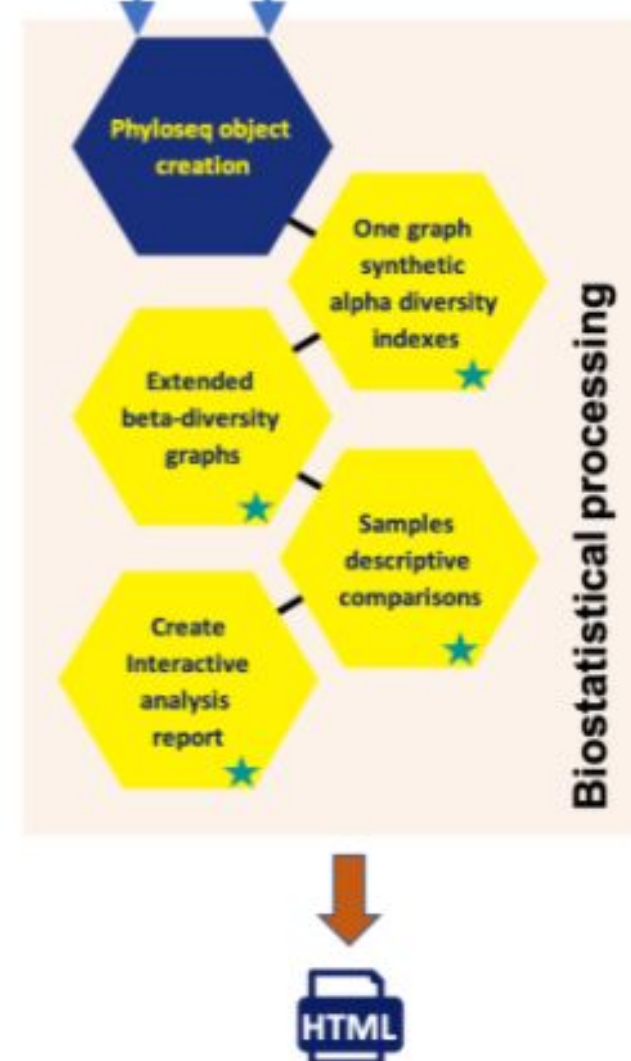
- PR2 (Eukaryota)
- SILVA (Bacteria, Archaea)

## SAMBA integration

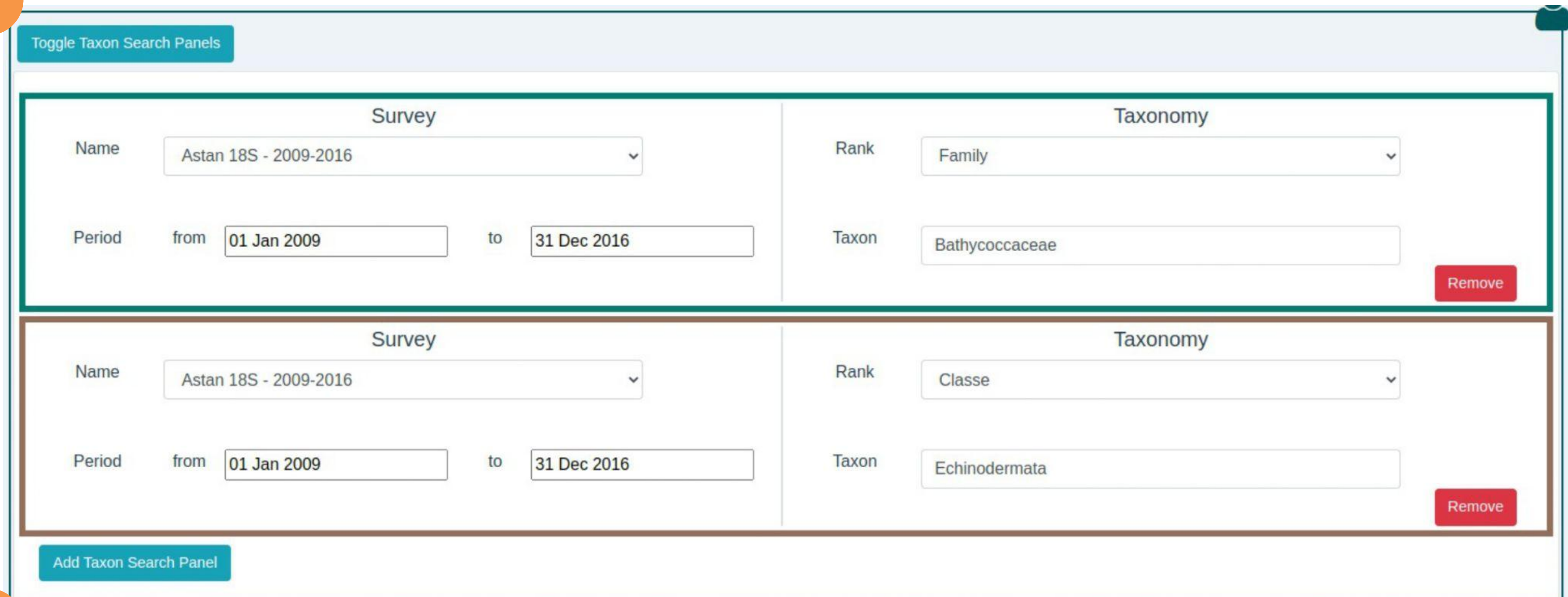
<https://github.com/ifremer-bioinformatics/samba>

Samba is a metabarcoding analysis workflow developed by SeBimer. Collaboration on MyGOD project, leads to integration of biostatistical processing part of the pipeline in visualisation tool.

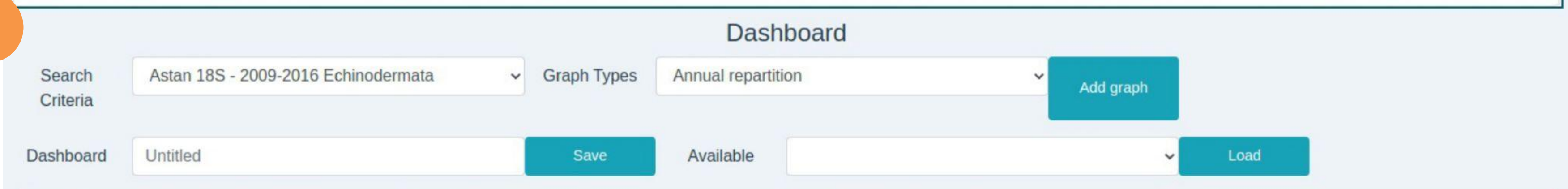
- Data are send from database to R script,
- Distance matrix is computed for  $\beta$ -diversity
- Generated GGplot are integrated in dashboard



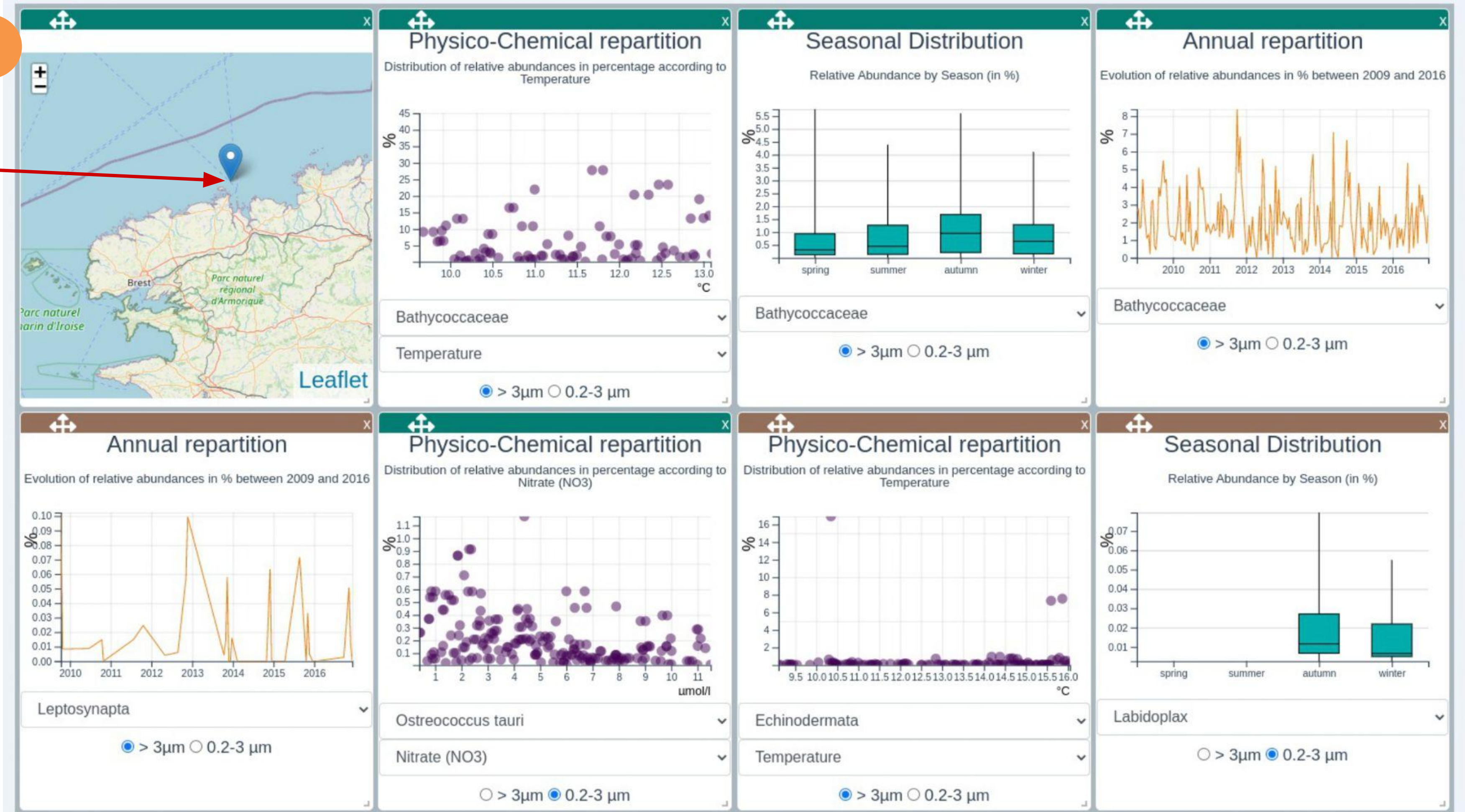
1



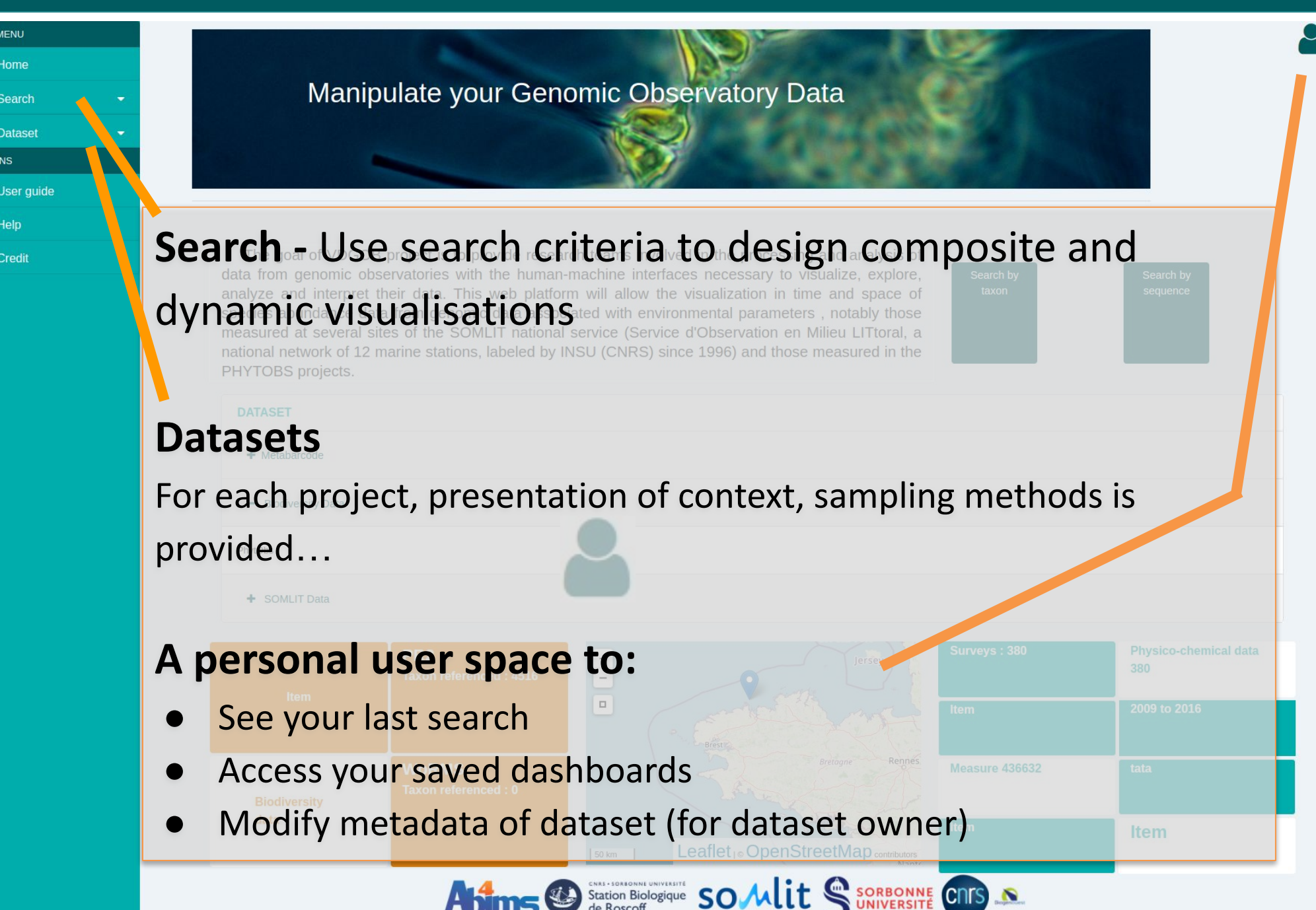
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## The Web Portal



## Challenges

### Non-Technical Challenges:

- Defining the nature of the data and metadata needed for the visualization tool
- Defining the relevant types of representations for the data
- Handling varying taxonomical frameworks (fixed or variable number of levels, explicitly named ranks or unnamed ranks)

### Technical Challenges:

- Making the best of the reactive framework : Vue/vuex/grid layout.
- Integrating third-party (R) components for analysis and visualisation.

## What's Next ?

### Active Developments:

- Addition of graphical representations of normalized data : Alpha &  $\beta$ -diversity (with R and Javascript)
- Addition of spatial data (Tonga cruise)
- Enhance genericity of data integration tools
- Integration of PetB metabarcoding dataset : CyanoMARKS Taxonomy

### Upcoming Developments:

- Addition of sequence similarity based search (Blast)
- Addition of "classical" (morphology-based) biodiversity data
- Enable promotion of "showcases" (dashboards with extensive comments) on portal

