Design and production of a plug-in tool facilitating the submission of microbial meta-omics data to an international repository

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DeepOmics Submission, a plug-in tool to facilitate the submission of meta-omics data to the ENA

DeepOmics

- **Storage** and interrogation of project **data** and **metadata**, from laboratory reactors and pilots or industrial plants
- **Import** and **export** data in standard formats (biom, fastq, fasta, CSV…) according to the nature of the data
- **Statistical analysis** and **data visualization** of 16S metabarcoding and metagenomic data thanks to coupling with the user-friendly application Easy16S - genome.jouy.inra.fr/shiny/easy16S/

Technological choices

Shiny:

- Easy and fast to develop, suited for a POC
- Does not need extra knowledge of *DeepOmics* architecture
- Facilitates the deployment with an INRAE in-house solution, SK8

Metark:

- Data-brokering requires specific skills and a precise expertise
- Ensures the quality of the data and metadata submitted to the ENA
- Guarantees process stability by absorbing potential changes in the submission process

Development best practices

Versioning

git→ https://forgemia.inra.fr/prose/deepomics-submission

Virtual environments and dependency

docker renv attachment

Development tools

Shiny golem devtools roxygen2 test that covr plumber

Context

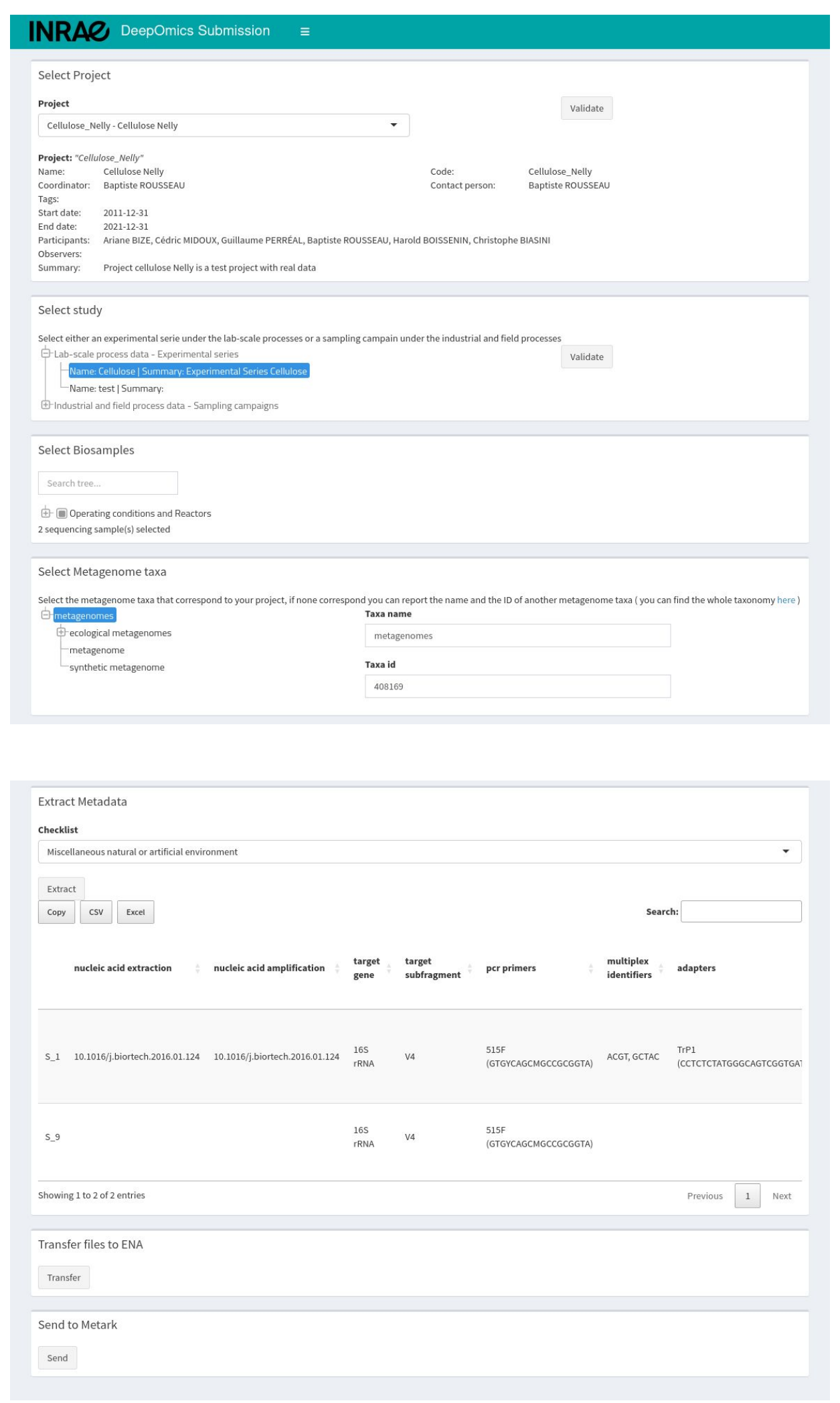
INRAE PROSE has coordinated the development of ***DeepOmics***, an information system dedicated to **meta-omics** datasets in the field of **environmental biotechnology.** *DeepOmics* offers the possibility to upload, query and export **16S metabarcoding data** from several environmental biotechnologies, together with many relevant associated metadata, especially regarding operating conditions and process design. To date, *DeepOmics* has all the data and metadata necessary for submission of the datasets to international repositories such as the European Nucleotide Archive (**ENA**), but submission remains a manual and rather complex process.

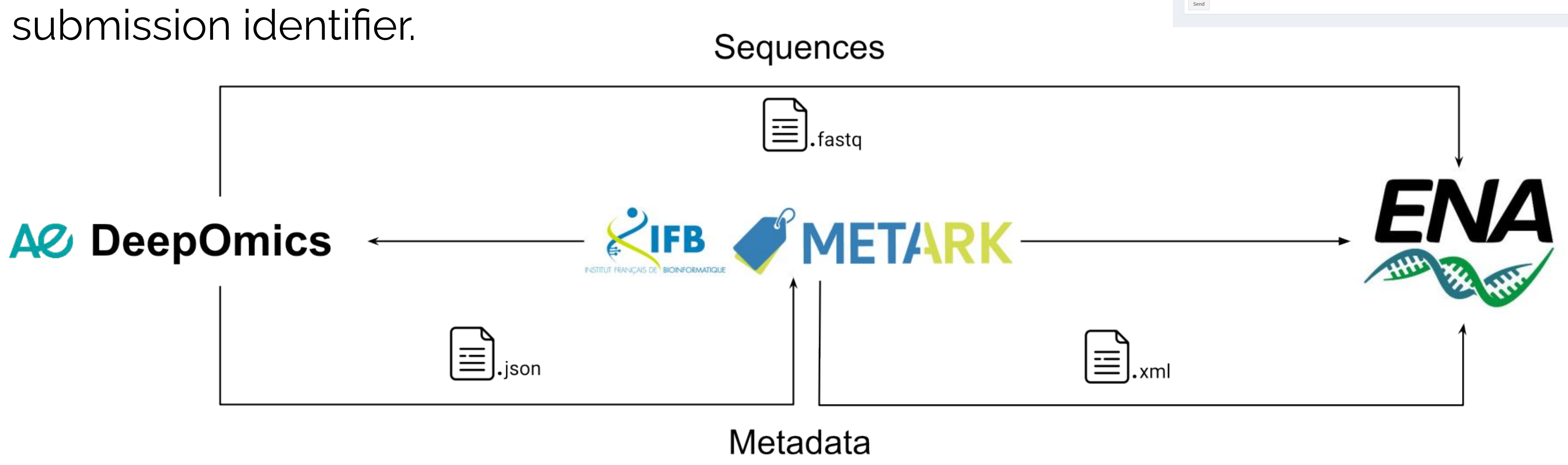
In collaboration with the French Institute of Bioinformatics (**IFB**), we designed and developed a R-shiny plug-in application, ***DeepOmics Submission***, to prepare and automate raw sequencing data submission to the ENA. We will also guarantee the quality of the associated metadata with an IFB data brokering application prototype.

DeepOmics Submission

A proof-of-concept (POC) application plugging into *DeepOmics* to cover:

- Mapping of *DeepOmics* concepts onto ENA checklists;
- Extracting the architecture of a *DeepOmics* project;
- Enabling the selection of biological samples;
- Extracting and transmitting to ENA the raw sequence files for these samples;
- Extracting and transmitting to *Metark* the metadata for these samples;
- Managing errors and comments from ENA;
- Finalizing the submission and retrieving the ENA submission identifier.





Conclusion

Most objectives of the **POC** have been **completed**. ***DeepOmics*** is currently in the pre-production phase and is now entering **production**. *DeepOmics Submission* works with the development version of *DeepOmics* and will thus need some modifications to work with the production version, especially regarding user account management. *DeepOmics Submission* will also need to be **deployed**, by relying on **SK8** at this stage.

The realization of this POC raised many **conceptual** and **technological challenges**, from **concept mapping** to developing a **headless** and **stateless application**.

All in all, it gives rise to **optimism** regarding the prospects of **FAIR data** and contributing to **Open Science**.

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