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Web development, expertise of the Web INTEgRation group in the Bioinformatic and Biostatistics Hub

Juliette Bonche^{1,2}, Bryan Brancotte¹, Elodie Chapeaublanc¹, Amanda Dieuaide^{1,3}, Simon Malesys¹, Fabien Mareuil¹, Rémi Planel¹, Marie Schmit¹, Raphaël Tackx^{1,3}, Rachel Torchet¹



1 Bioinformatics and Biostatistics Hub, Institut Pasteur, Université de Paris, Paris, F-75015, France
2 Université Claud Bernard, Lyon 1 - Master IMST EISO, 69100, Villeurbanne, France
3 Institut Français de Bioinformatique, Evry, F-91000, France

The group Web INTEgRation is a software development team whose aim is to build websites and apps using Web technologies. We provide our expertise to the scientists on campus, covering a broad range of services to design, develop, deploy, maintain web interface and databases creating fully functional dedicated tools for publishing and sharing analysis, data, scientific tools, and workflows.

Several competencies and informatic languages are necessary to create a complete user-friendly web tool following dynamic and iterating process with 4 essential steps: UX/UI design, Front-end and Back-end development and Deployment - DevOps. Depending on the project's needs and size, Winter team members can work alone as full-stack DevOps members or contribute specifically to a stage as domain experts in close collaboration with the other team members.

UX/UI Design

Starting with an exploration phase where we benchmark existing solutions, other related softwares and websites, we conduct different rounds of interviews with stakeholders to define more precisely users' needs.

Following this, we start to ideate the future product and design mock-ups and prototypes.

Once we have a clear vision of the final product, we will begin implementation.

The collaborative design tool Figma permit at UX/UI designer and developers to interact on the web design.



Front-End Development

To develop responsive and dynamic web interface, according to prototype designed previously, we define the most relevant tech stack including technologies, frameworks, tools, and best development practices to ensure that the product is developed in the most efficient way. We use:

- Javascript, that rely on recent and industry-grade frameworks (VueJs, React).
- bootstrap, robust and widely mastered CSS framework
- NGL, Plotlyjs, d3.js, as specialized visualization components



Back-End Development

To develop back-end, we focus on building an effective website architecture, scripting, and writing code that serves as a means of communication between the website's database (structured data storage) and the browser using by visitor. We use:

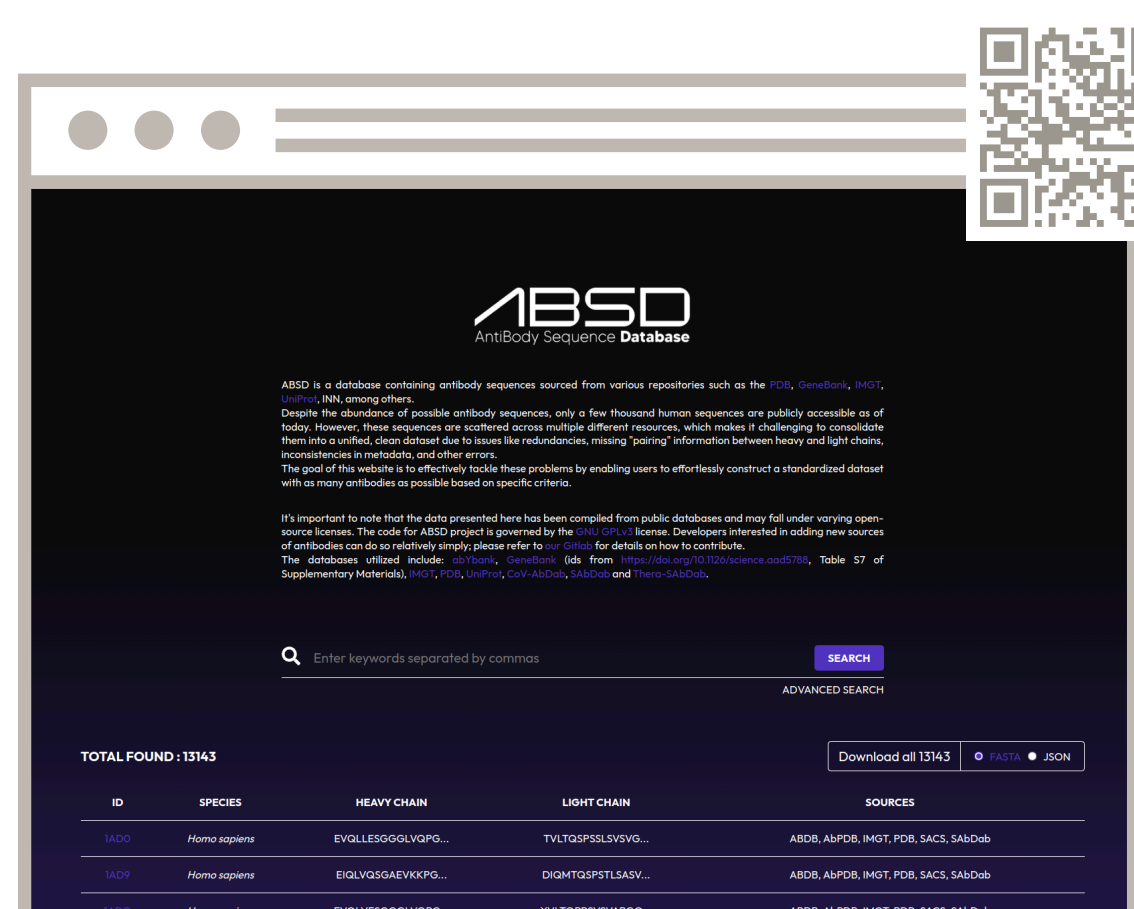
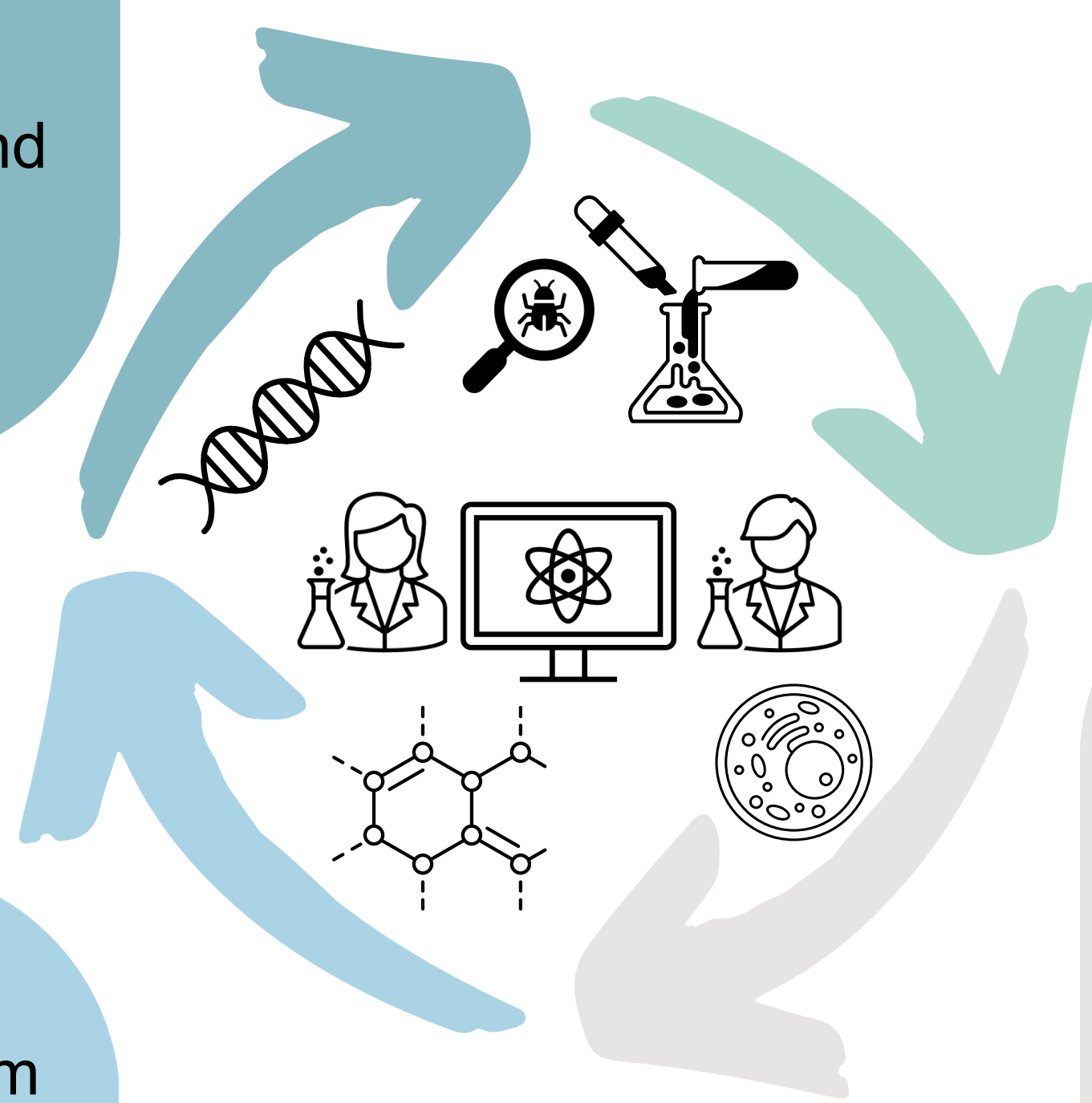
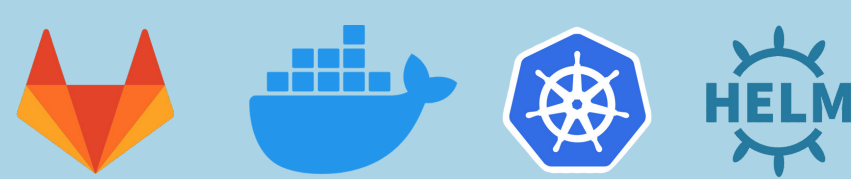
- Python-based frameworks like Django and Flask, to provide seamless access to scientific libraries (Pandas and BioPython) ensuring enhanced analytical capabilities.
- For CPU-intensive tasks, bioblend and Celery for accessing to computing cluster leverage the Galaxy platform.
- robust APIs (Application Programming Interfaces) to facilitate us seamless communication between frontend and backend components, ensuring efficient data exchange and enabling third-party integrations.



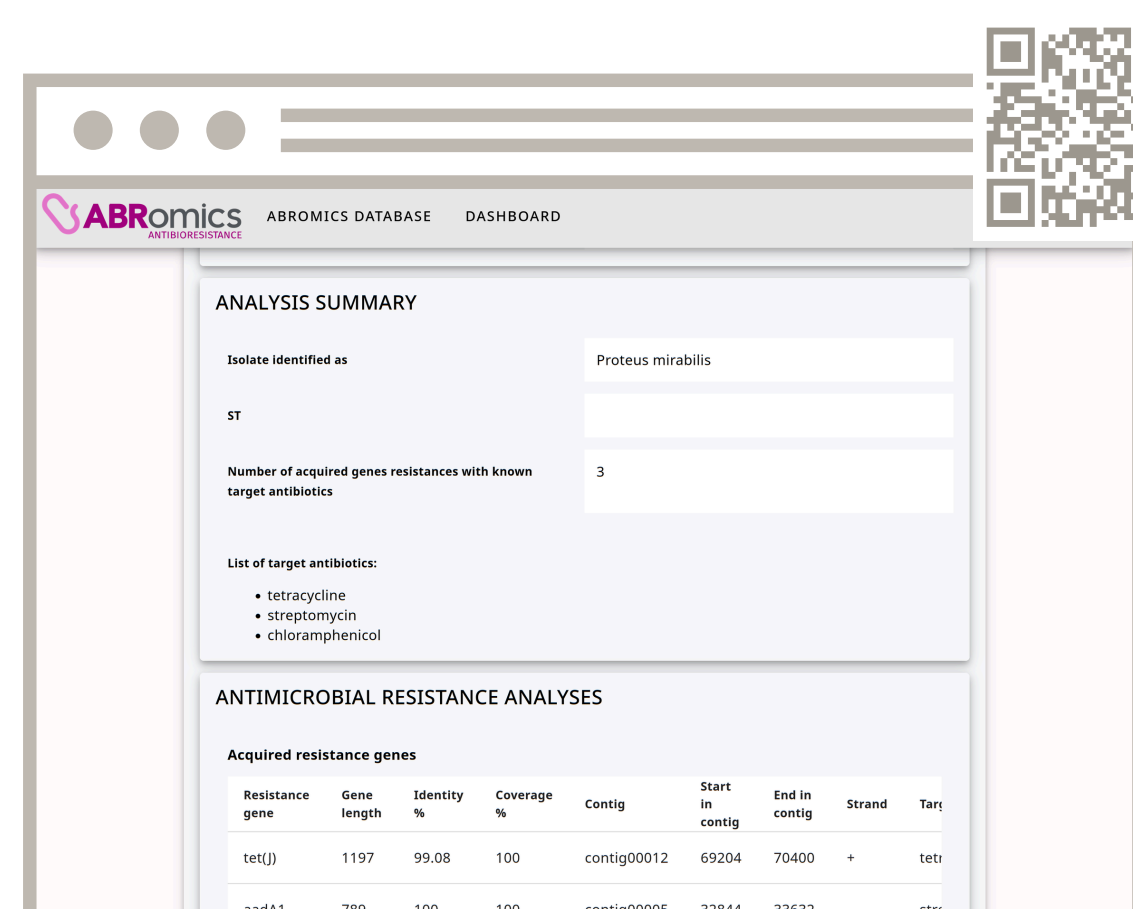
Deployment / DevOps

To facilitate the deployment, and enable the long-term maintenance and scalability of Web applications, we mostly rely methodologies and dedicated tools, all running on infrastructures provided by the IT department:

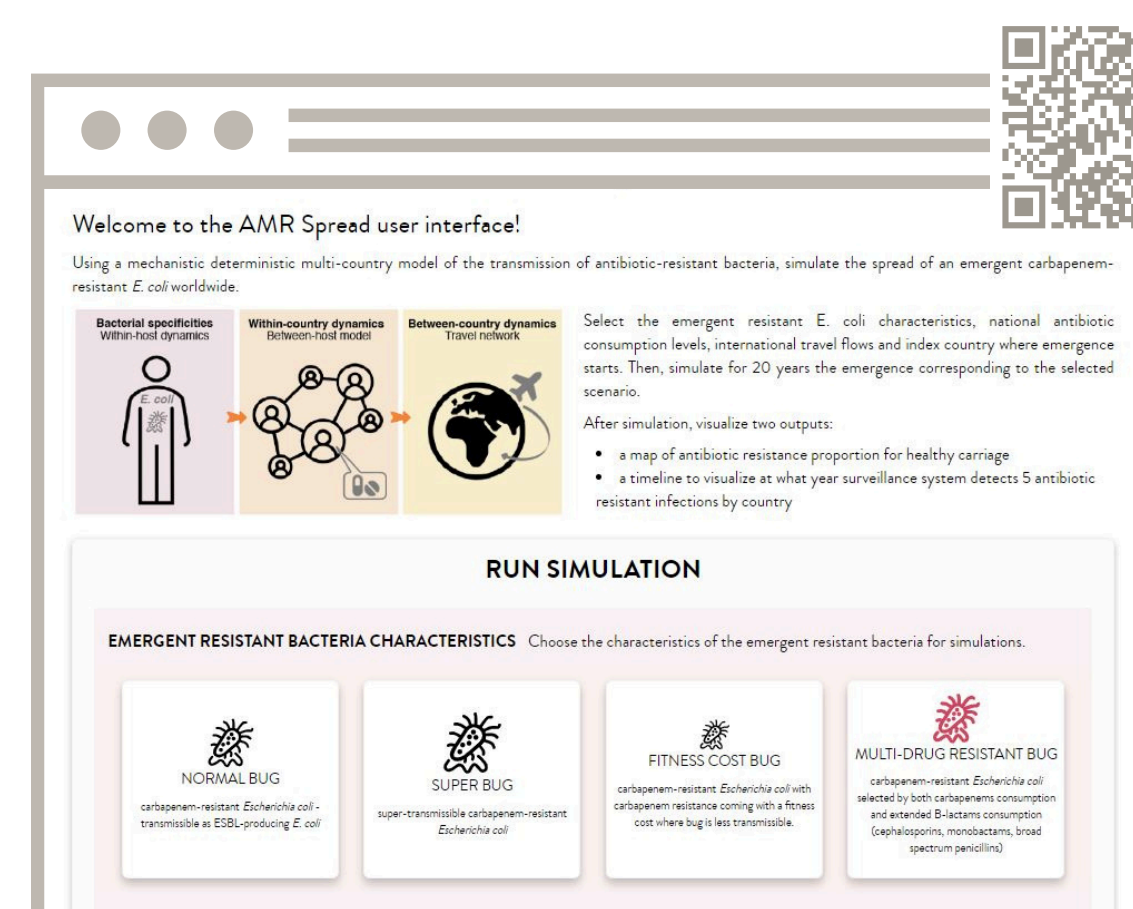
- Development code with using code versioning (gitlab) on container technologies (Docker, Kubernetes),
- continuous integration and deployment including unit testing and automated release in dev/staging or production environment.



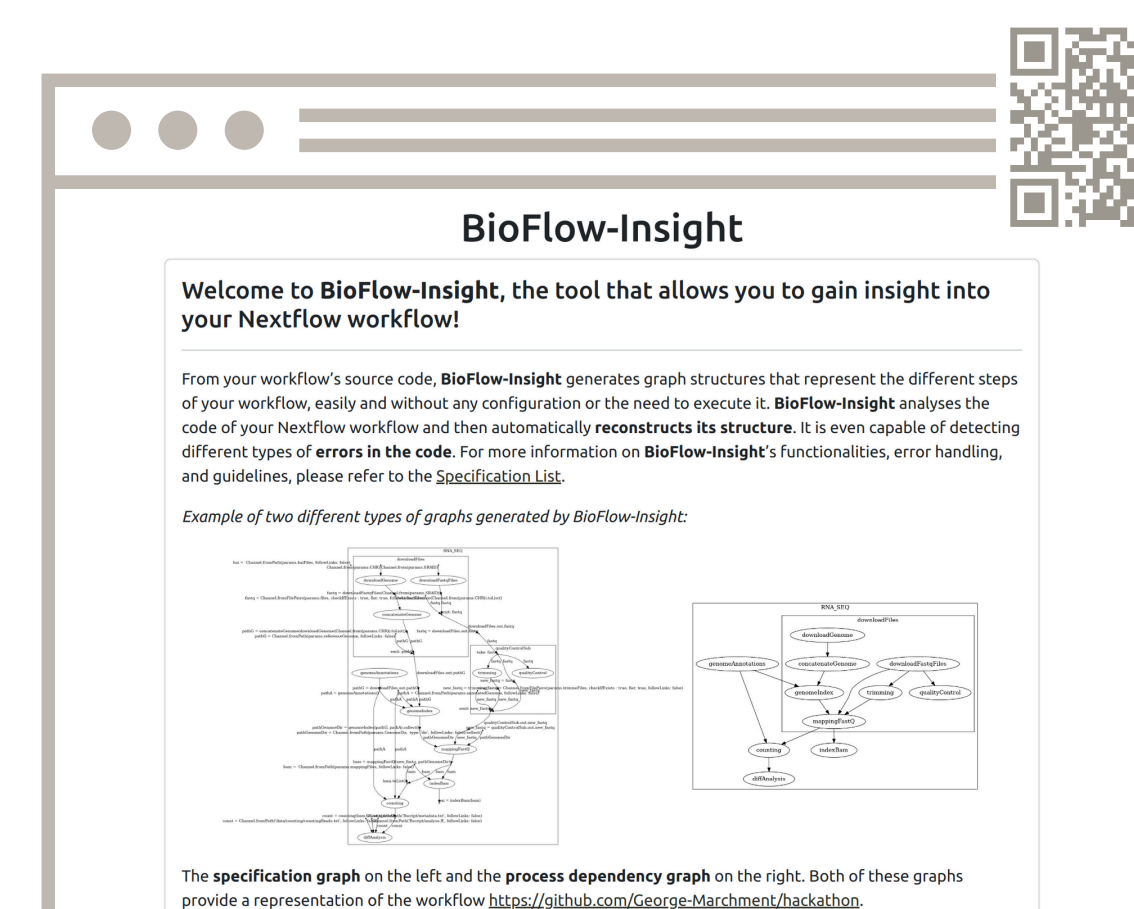
ABSD is a database containing antibody sequences sourced from various repositories such as the PDB, GeneBank, IMGT, UniProt, INN, among others.



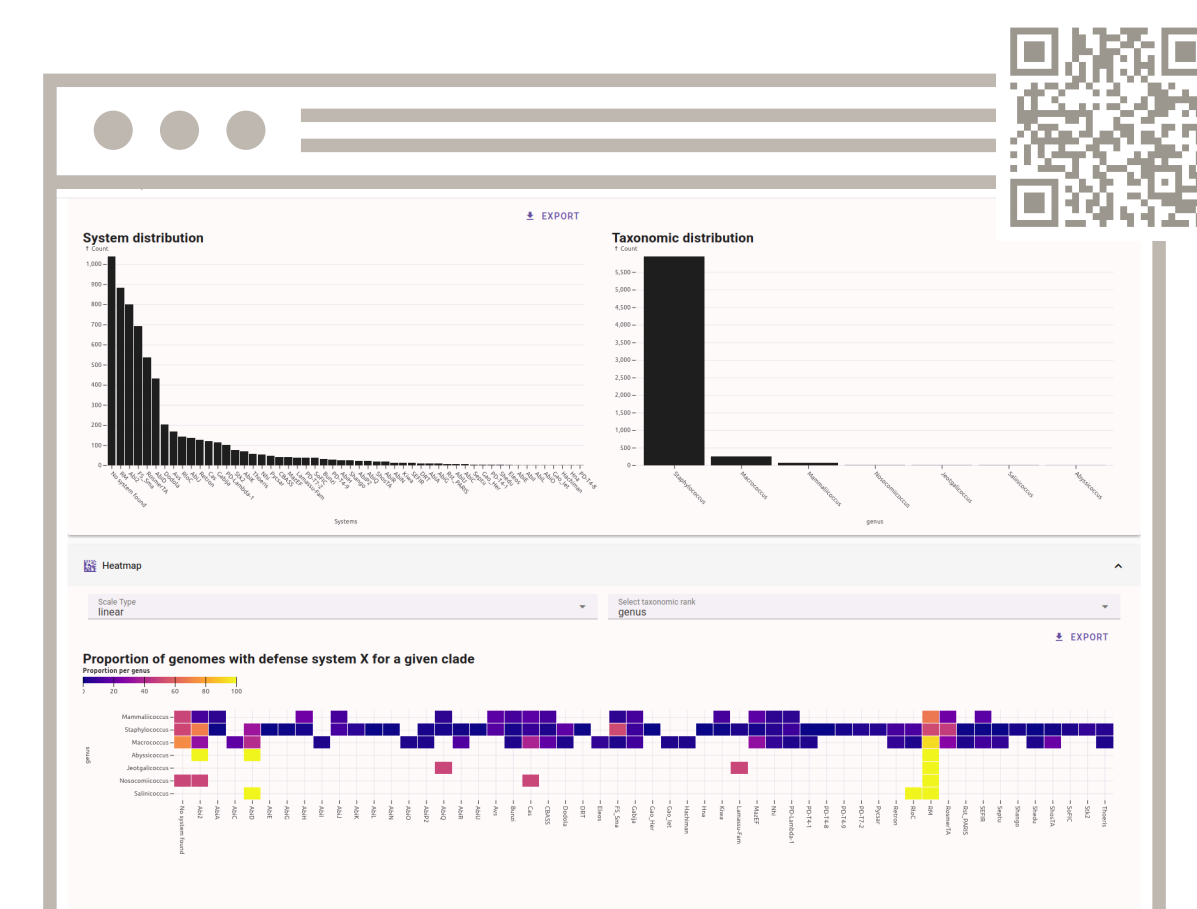
ABRomics is an online community-driven platform to scale up and improve surveillance and research on antibiotic resistance from a One Health perspective.



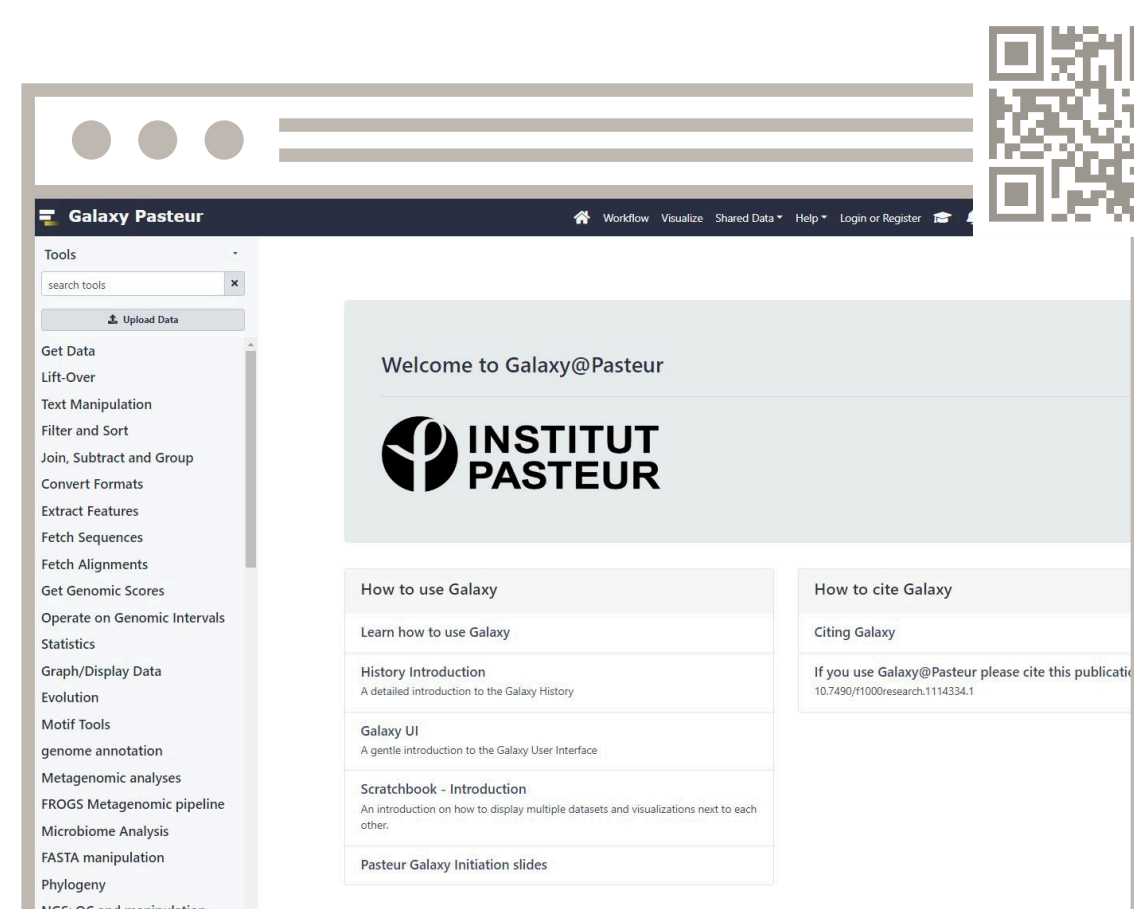
AMR Spread, using a mechanistic deterministic multi-country model of the transmission of antibiotic-resistant bacteria, simulate the spread of an emergent carbapenem-resistant *E. coli* worldwide.



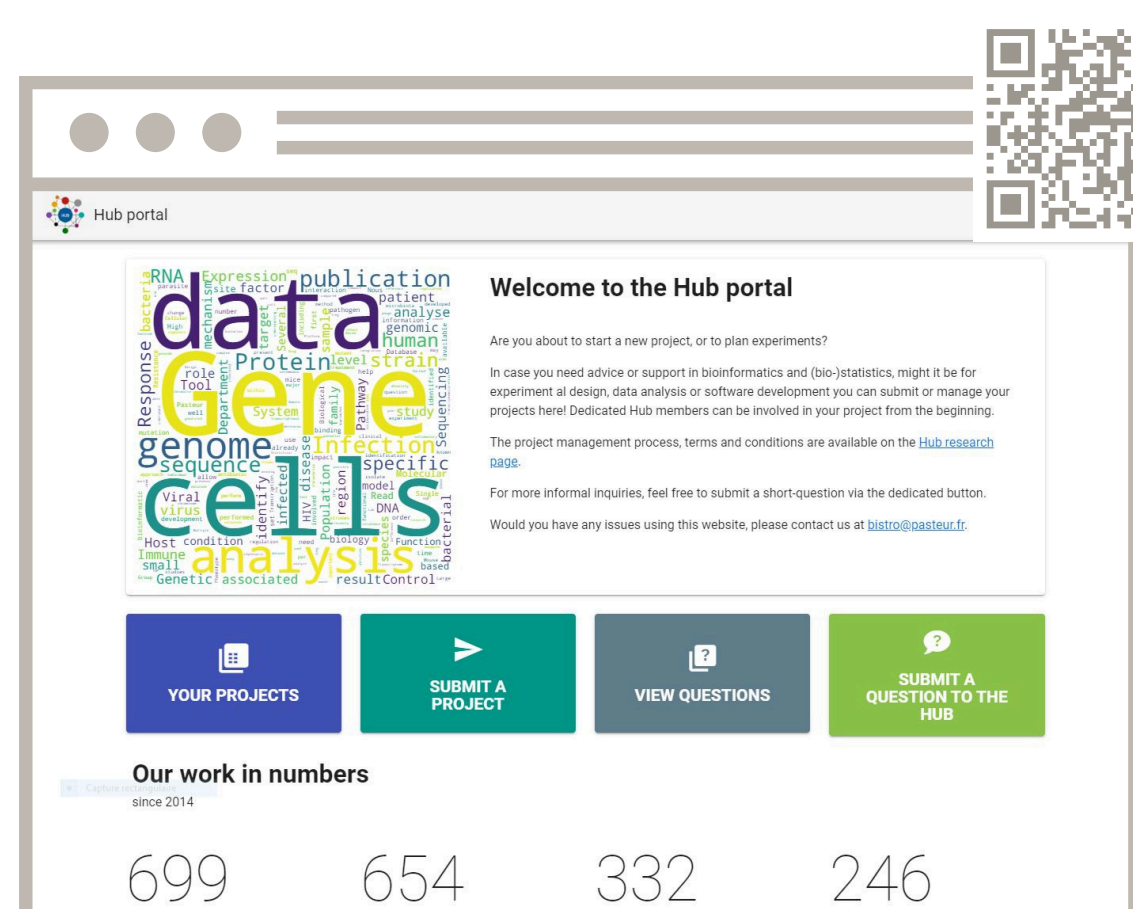
Bioflow-Insight analyses Nextflow workflow, automatically reconstructs the structure without manual configuration or execution, and detect different types of errors in the code.



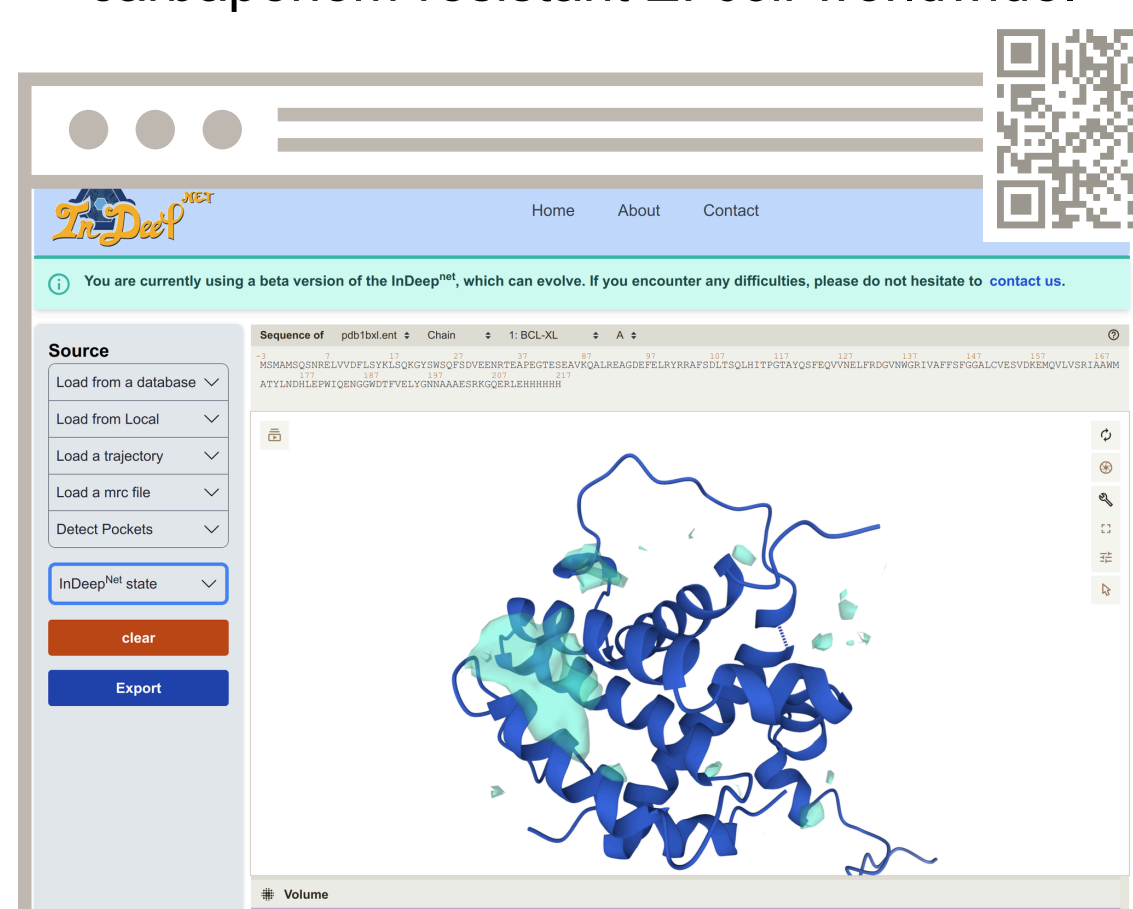
DefenseFinder is a resources on defense systems including: an online search tool, a knowledge database and a computational databases (results on RefSeq, predicted structure computed with Alphafold).



The **Institut Pasteur Galaxy server** is an advanced bioinformatics platform providing powerful features for the analysis and manipulation of biological data.



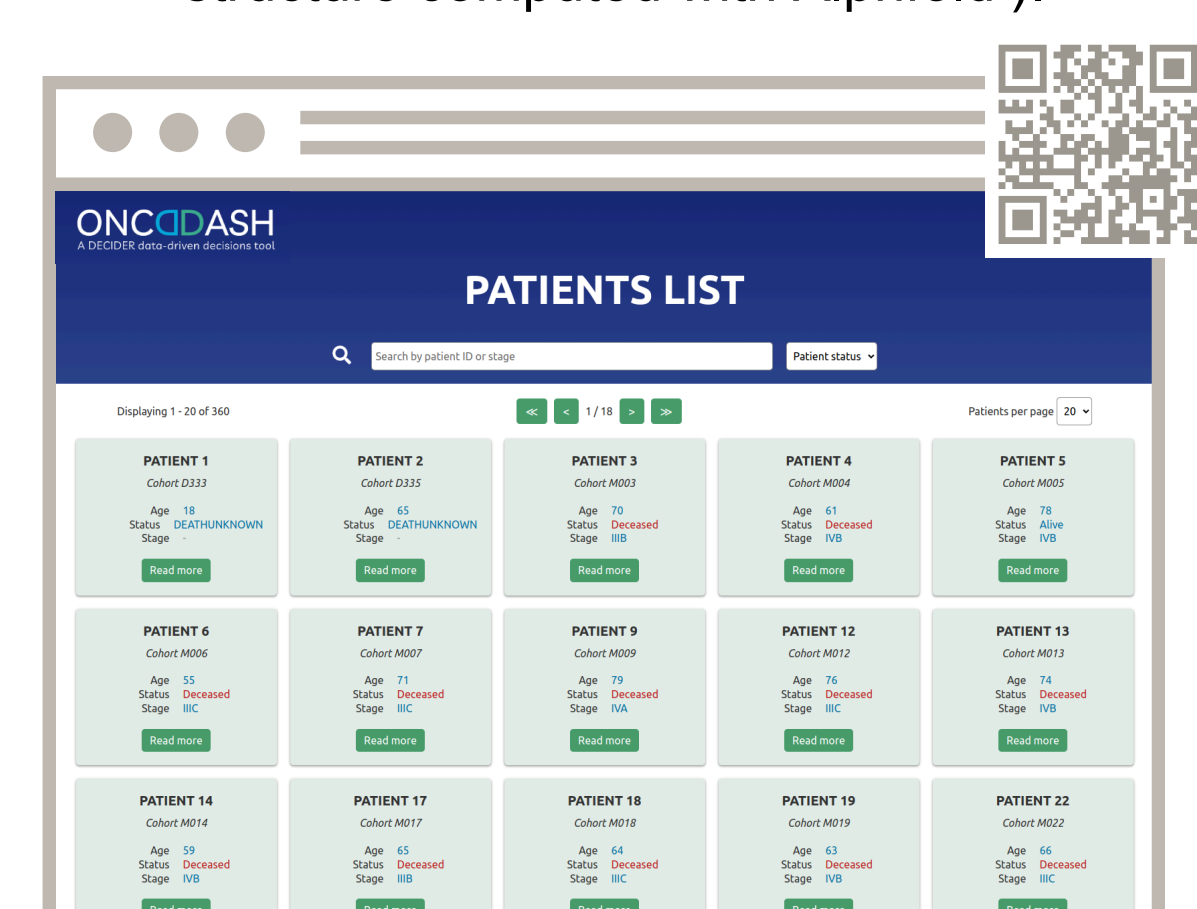
Hub Portal is the web site where you can submit your project or your question to the Bioinformatic and Biostatistics Hub



InDeep-net is a powerful tool that enables the prediction of functional binding sites within proteins, including those involved in protein-protein interactions (PPIs).



The **JASS** web interface efficiently compute multi-trait genome-wide association study (GWAS) and enable user to interactively explore results



Oncodash is a decision support system that helps tumour boards to come up with the best decisions for their patients.

