

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

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

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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, 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.

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## UX/UI Design

## **Front-End Development**

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.

# **Deployment / DevOps**

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

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).
- boostrap, robust and widely mastered CSS framework
- NGL, Plotlyjs, d3.js, as specialized visualization components

Shiny,

**Back-End Development** 

BJ

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

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

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

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	and 41	780	100	100		22944	22622		ctre	

HELM

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

Welcome to the	AMR Spread	user interface!	of activity content barraria simular	
Bacterial specificities Within-host dynamics	e. Within-country dynamics Between-host model	Between-country dynamics Travel network	Select the emergent resistant E. consumption levels, international trave starts. Then, simulate for 20 years the scenario. After simulation, visualize two outputs: • a map of antibiotic resistance pro • a timeline to visualize at what year resistant infections by country	coli characteristics, national antibiot I flows and index country where emergen a emergence corresponding to the select portion for healthy carriage r surveillance system detects 5 antibiotic
		RUN SIA	AULATION	
EMERGENT RES	ISTANT BACTERIA C	HARACTERISTICS Choose	the characteristics of the emergent res	istant bacteria for simulations.
NORM carbapenem-resista transmissible as ESS	AL BUG nt Escherichia coli - 31-producing E. coli	SUPER BUG super-transmissible carbapenem-resistant Eschenichie coli	FITNESS COST BUG carbapenem-resistant <i>Escherichia</i> coli with carbapenem resistance coming with a fitness cost where bug is less transmissible.	MULTI-DRUG RESISTANT BUG and a strabagenem-resistant. Eicherichia coli selected by both carbageneme consumption and extended B-lactams consumption (cephalosporins, monobactam, broad secture periciliar)

**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.

- 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.

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**DenfenseFinder** 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 Alphfold ).







**Bioflow-Insight** analyses Nextflow

workflow, automatically reconstructs the

structure without manual configuration or

execution, and detect different types of

errors in the code.

**BioFlow-Insight** 

vour Nextflow workflow

uidelines, please refer to the Specification Li

o different types of araphs generated by BioFlow-Ins







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 Biostatitics 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

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ONCODASH A DECIDER data-driven decisions tool				
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	Q Search by patient ID or st	age	Patient status 🐱	
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PATIENT 1 Cohort D333 Age 18 Status DEATHUNKNOWN Stage - Read more	PATIENT 2 Cohort D335 Age 65 Status DEATHUNKNOWN Stage - Read more	PATIENT 3 Cohort M003 Age 70 Status Deceased Stage IIIB Read more	PATIENT 4 Cohort M004 Age 61 Status Deceased Stage IVB Read more	PATIENT 5 Cohart M005 Age 78 Status Alive Stage IVB Read more
PATIENT 6 Cohort M006 Age 55 Status Deceased Stage IIIC Read more	PATIENT 7 Cohort M007 Age 71 Status Deceased Stage IIIC Read more	PATIENT 9 Cohort M009 Age 79 Status Deceased Stage IVA Read more	PATIENT 12 Cohort M012 Age 76 Status Deceased Stage IIIC Read more	PATIENT 13 Cohort M013 Age 74 Status Deceased Stage IVB Read more
PATIENT 14 Cohort M014 Age 59 Status Deceased Stage IVB Read more	PATIENT 17 Cohort M017 Age 65 Status Deceased Stage IIIB Read more	PATIENT 18 Cohort M018 Age 64 Status Deceased Stage IIIC Read more	PATIENT 19 Cohort M019 Age 63 Status Deceased Stage IVB Read more	PATIENT 22 Cohort M022 Age 66 Status Deceased Stage IIIC Readimote

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





