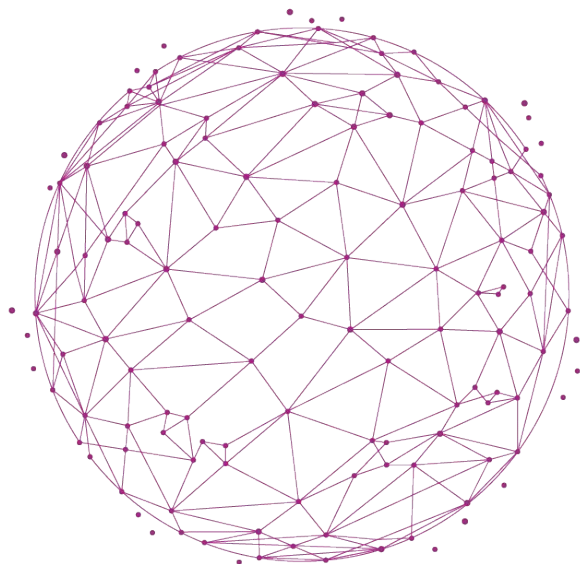




Plateforme d'analyse ABRomics

Un retour d'expérience sur le développement
d'une plateforme web nationale d'analyse
bioinformatique

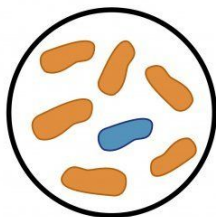
Julie Lao

*Institut Français de Bioinformatique (CNRS)
Hub de Bioinformatique (Institut Pasteur)*

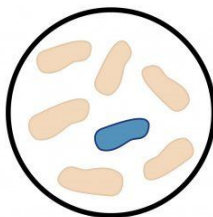


Les bactéries, virus, champignons et parasites ne réagissent plus aux antimicrobiens.

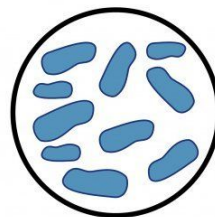
Comment la résistance aux antibiotiques apparaît ?



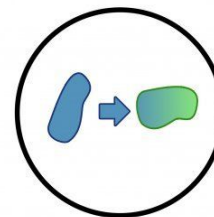
Plusieurs bactéries et une est résistante à l'antibiotique



L'antibiotique tue les bactéries responsables de la maladie ainsi que de bonnes bactéries protégeant l'organisme des infections



La bactérie résistante peut maintenant se développer et devenir majoritaire



Certaines bactéries transfèrent leur résistance à d'autres bactéries



Bactérie sensible



Bactérie résistante



Bactérie morte

Source : AdobeStock

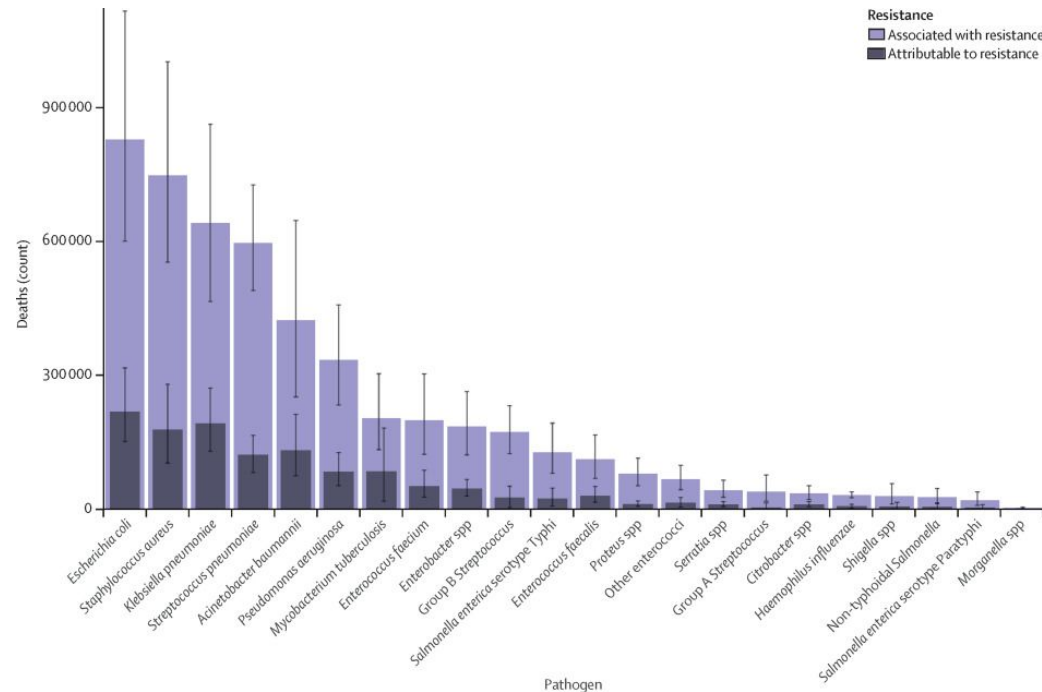


Figure 2 - Antimicrobial Resistance Collaborators *et al*, The Lancet, 2022.

- Amélioration des connaissances sur la circulation des bactéries résistantes aux antibiotiques (gènes de résistance aux antibiotiques et éléments génétiques mobiles)
- Simplification des analyses à travers des pipelines standardisés et contrôlés :
 - Utilisable par les non bio-informaticiens et les experts en analyses des résistances antimicrobiennes (AMR) et de l'antibiorésistance (ABR)
- Intégration/interopérabilité des outils et des données (multi-omiques) pour limiter les analyses d'échantillons (méta) génomiques bactériens cloisonnées/individuelles
- Assurer la pérennité du stockage et de partage de données ; soumission dans les « entrepôts » internationaux (ENA)



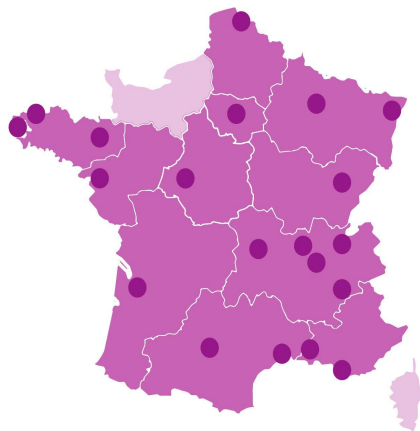
⇒ AAP « structurants » du PPR antibiorésistance

2 M€ pour 4+1 ans

4 projets dont **ABRomics** « A multi-omics data platform »

début 01/11/2021

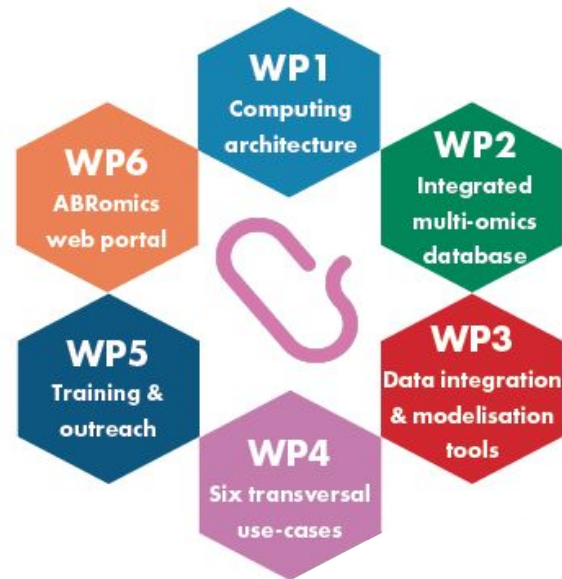
⇒ Conception d'une plateforme web partagée pour améliorer la surveillance et la recherche en AMR dans un objectif « One Health »



Co-coordination :
C. Médigue
(Institut Français de Bioinformatique)
&
P. Glaser
(Institut Pasteur)

Consortium multidisciplinaire national de 43 partenaires

- Microbiologistes
 - Centres nationaux de référence (CNR)
 - Hospitalo-universitaires
 - Vétérinaires (ANSES)
 - Chercheurs
- Bioinformaticien·nes et mathématicien·nes
 - Plateforme d'ingénierie
 - Équipes de R&D



WP1, **WP2** et **WP3** : objectifs en relation avec l'AAP du PPR

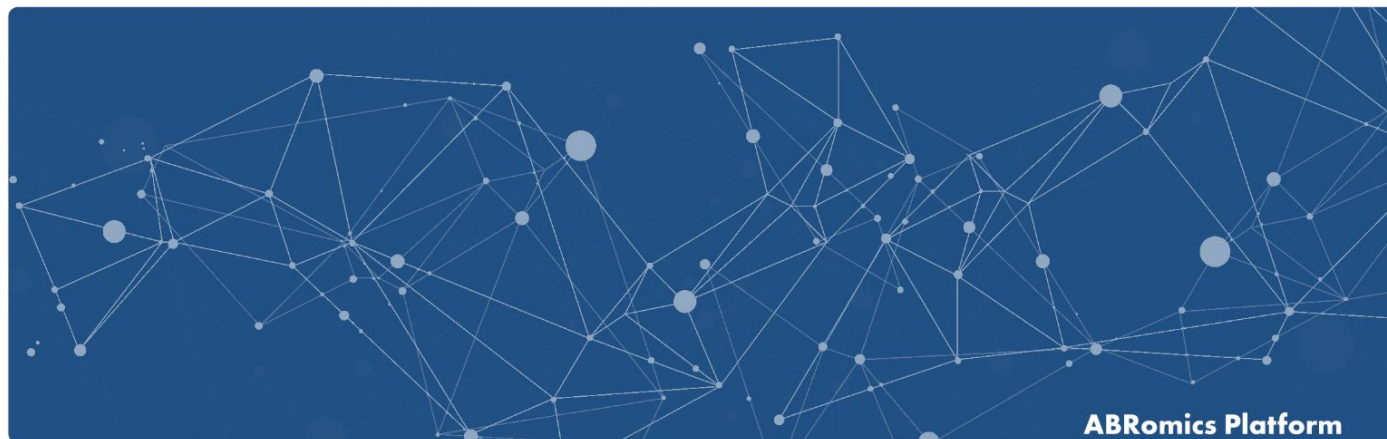
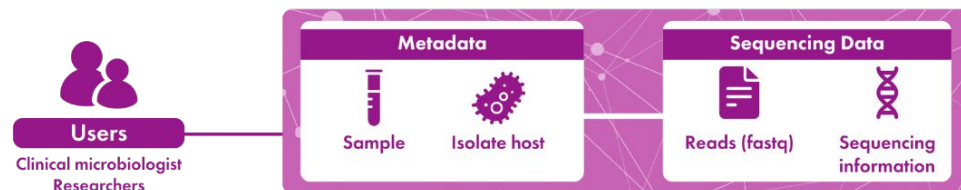
- Utilisateurs des trois secteurs : **humain, animal et environnement**
- **Laboratoires de microbiologie** (Clinique, vétérinaire, agroalimentaire, environnement ...)
 - Analyser les données et les stocker
- **Les laboratoires de santé publique** pour **aider** à la surveillance
 - Intégrer les données génomiques globales à la surveillance et assurer un suivi spatio-temporel (sur plusieurs années et de manière rétrospective)
- **Laboratoires de recherche**
 - Stocker, partager, soumettre les données, notamment pour les plans de gestion des données
 - Utiliser des méthodes développées par le consortium

Portail ABRomics : Information sur le projet et le consortium <https://www.abromics.fr/>

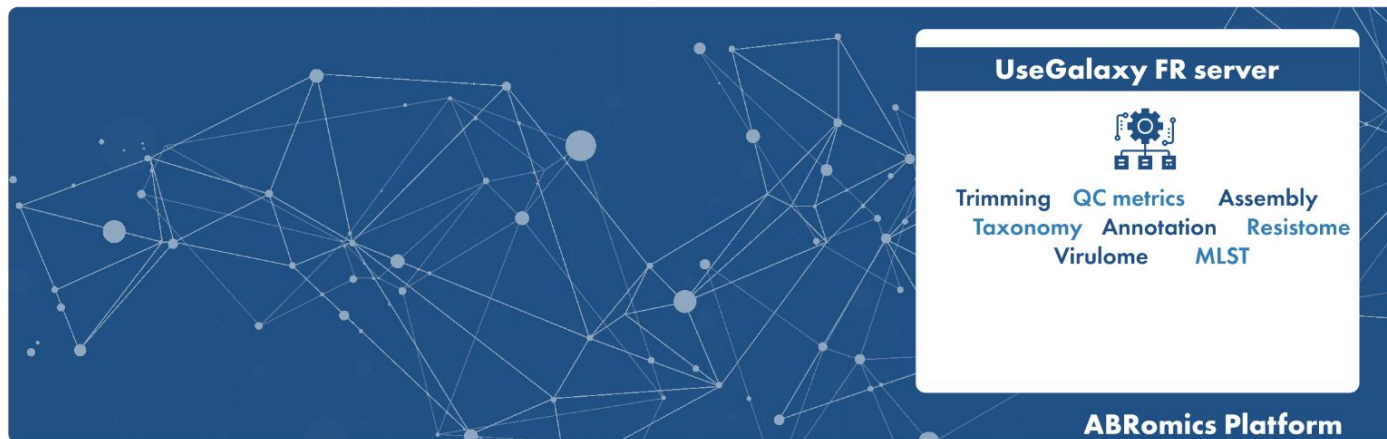
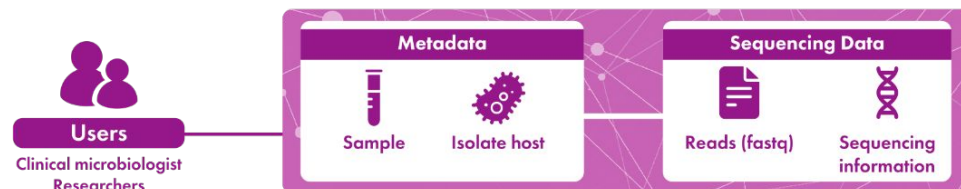
The screenshot shows the ABRomics portal homepage. At the top, there's a navigation bar with the ABRomics logo, a search bar, and links to 'ABRomics Platform', 'Project', 'News', 'Events', 'Publications', and a 'Go To Platform' button. The main heading reads 'The French national multiomics platform for antibiotic resistance research and surveillance'. Below this, a paragraph states: 'ABRomics is an online community-driven platform to scale up and improve surveillance and research on antibiotic resistance from a One Health perspective.' A call-to-action box says 'Let's go to the data analysis platform'. At the bottom, three statistics are displayed: 1483 Analysis, 166 Public samples, and 49 Projects. The footer mentions 'ABRomics - The French national multiomics platform for Antibiotic Resistance research and surveillance'.

ABRomics analysis : La plateforme web d'analyse <https://www.analysis.abromics.fr/>

The screenshot shows the ABRomics analysis platform homepage. The navigation bar includes 'ABOUT', 'SERVICES', 'TEAMS', 'CONTACT', and a 'LOG IN' button. The main section is titled 'Explore' and describes the platform's capabilities: 'Discover global antimicrobial resistance patterns through our interactive visualization tools. Explore geographical distribution, track resistance trends, and gain insights from our comprehensive database of bacterial genomes and AMR genes across different environments, hosts, and regions.' It lists three main features: 'Geographic Mapping' (Visualize AMR distribution across countries and regions), 'Trend Analysis' (Track resistance patterns over time with interactive charts), and 'Comparative Analysis' (Compare AMR profiles across different bacterial species). A 'Learn more' button is present. Below this, the 'Most common species' section is introduced, stating 'Follow the evolution of species in our worldwide database for resistance surveillance.' Three species are highlighted with images and analysis counts: Escherichia (Found in 998 analyses), Campylobacter (Found in 296 analyses), and Acinetobacter (Found in 122 analyses).



Core Cluster



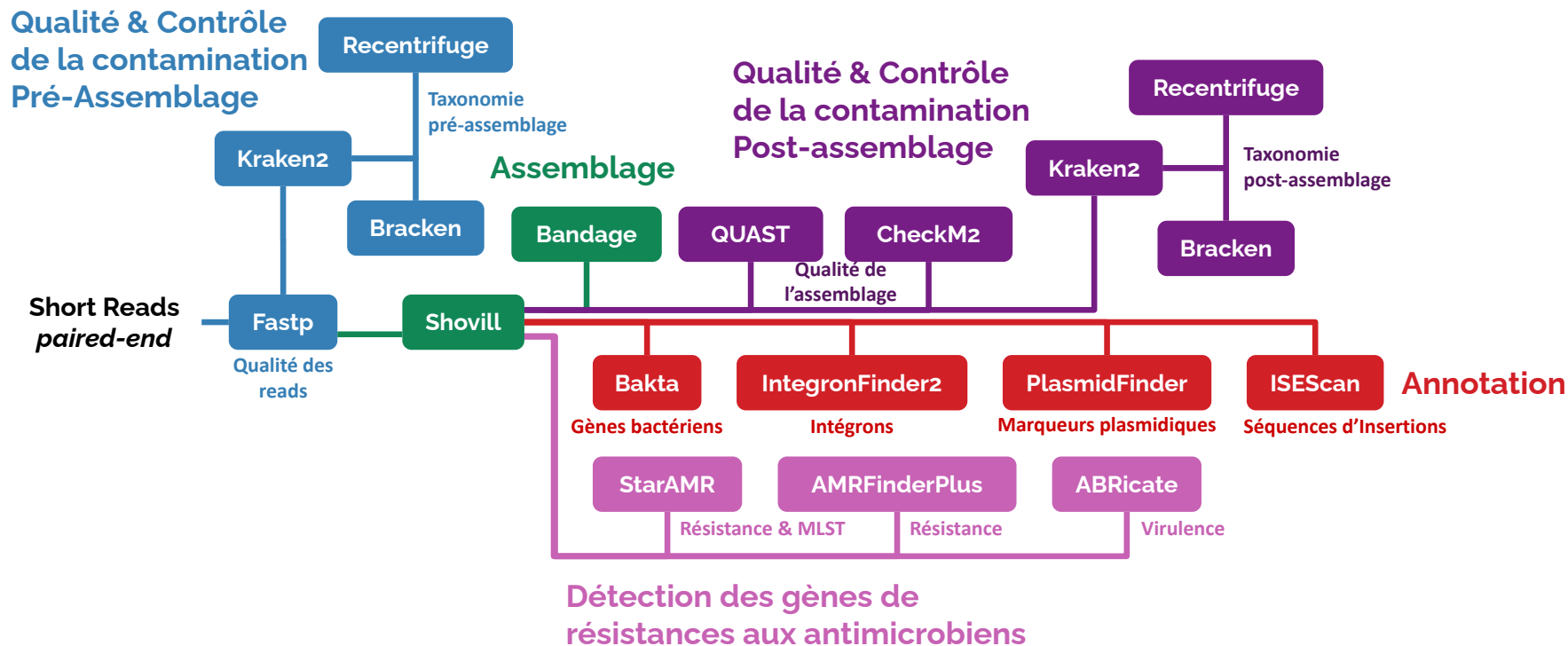
Galaxy workflows

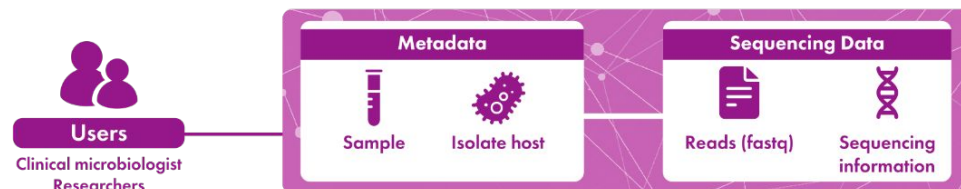


Pierre Marin



Core Cluster

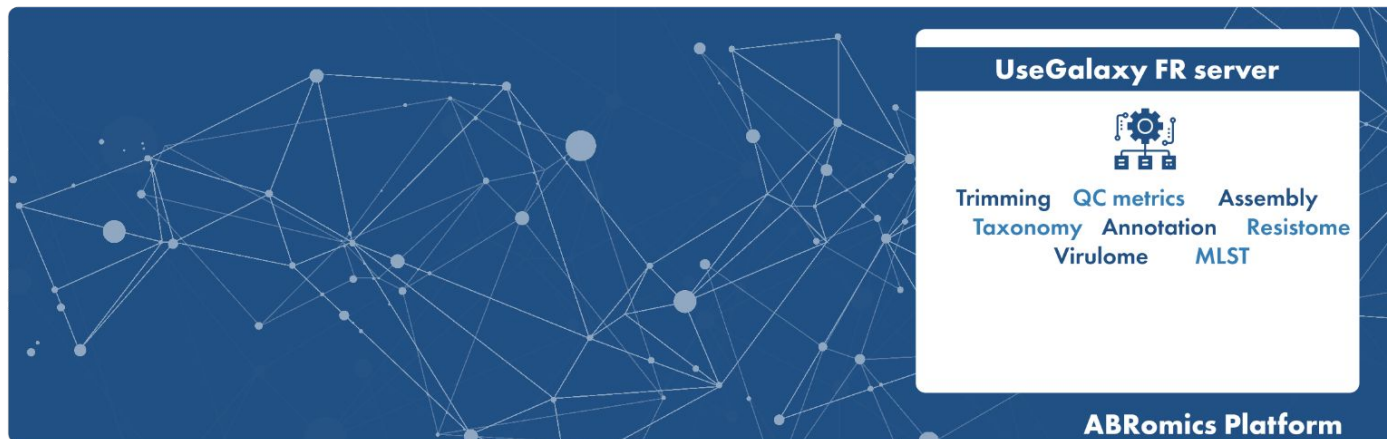




Metadata referential



Julie Lao



Galaxy workflows



Pierre Marin



Core Cluster

Métadonnées pour les données de séquençage short read paired-end

Sample ID
Strain ID
Sample type
Sample source
Host species
Country
Region
Place
Collected date
Travel countries
Accession(s) number
Sample comment

16 champs décrivant l'échantillon biologique, l'isolat et les données de séquençage pour 1 échantillon

- 11 champs obligatoires et 5 optionnels

Utilisation de vocabulaires contrôlés

- pour le stockage dans notre base de données
- formatés pour la publication des données et résultats sur l'ENA (*ENA prokaryotic pathogen minimal sample checklist*)

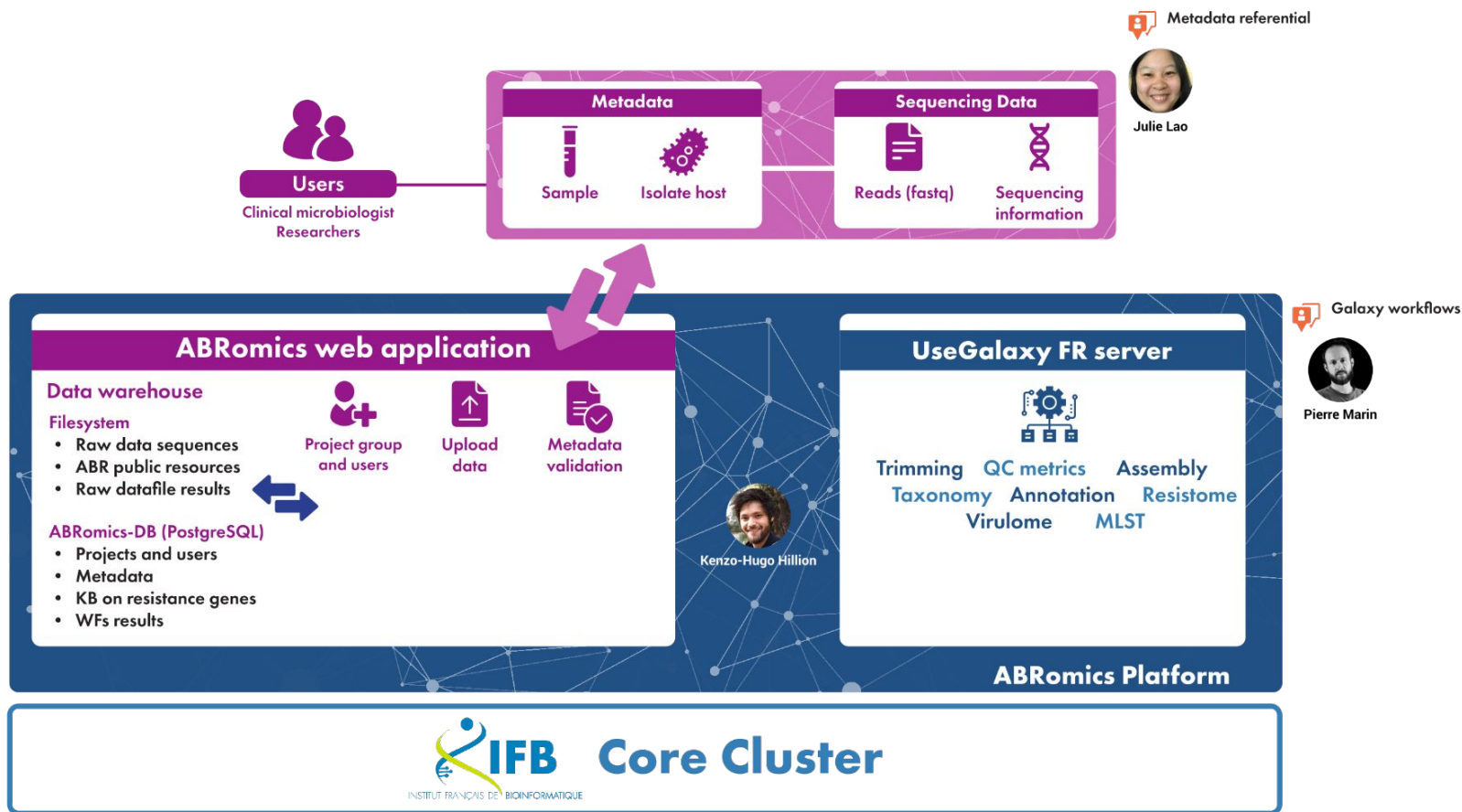
Microorganism scientific name

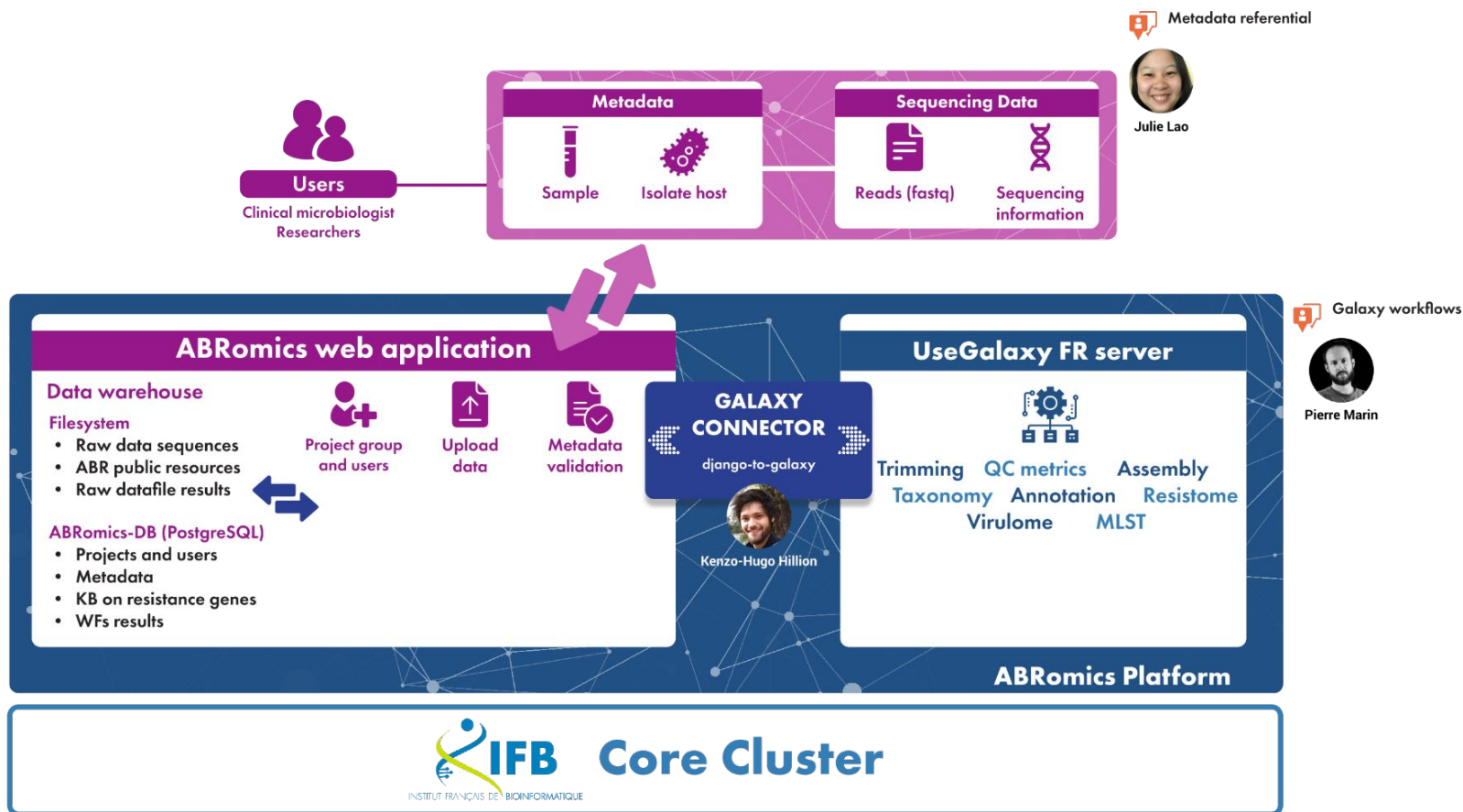
Instrument model

R1 fastq filename

R2 fastq filename

<https://www.abromics.fr/home/abromics-platform/metadata-referential/>





Django-to-Galaxy: *Django extension* that eases communication with Galaxy instance to execute workflows.

<https://gitlab.com/ifb-elixirfr/abromics/django-to-galaxy>

<https://pypi.org/project/django-to-galaxy/>

Django to Galaxy

The extension might be similar to [this project](#).

Django extension that eases communication with Galaxy instance to execute workflows.

This should includes:

- List available workflows on a Galaxy instance
- Add selected workflow from Galaxy instance to the app for execution from admin panel
- Run workflow from a Galaxy instance

For more information, please check the [Wiki](#)



django-to-galaxy 0.7.0.1

```
pip install django-to-galaxy
```



Dernière version

Dernière version : 24 nov. 2025



Kenzo-Hugo Hillion



Fabien Mareuil



Julie Lao



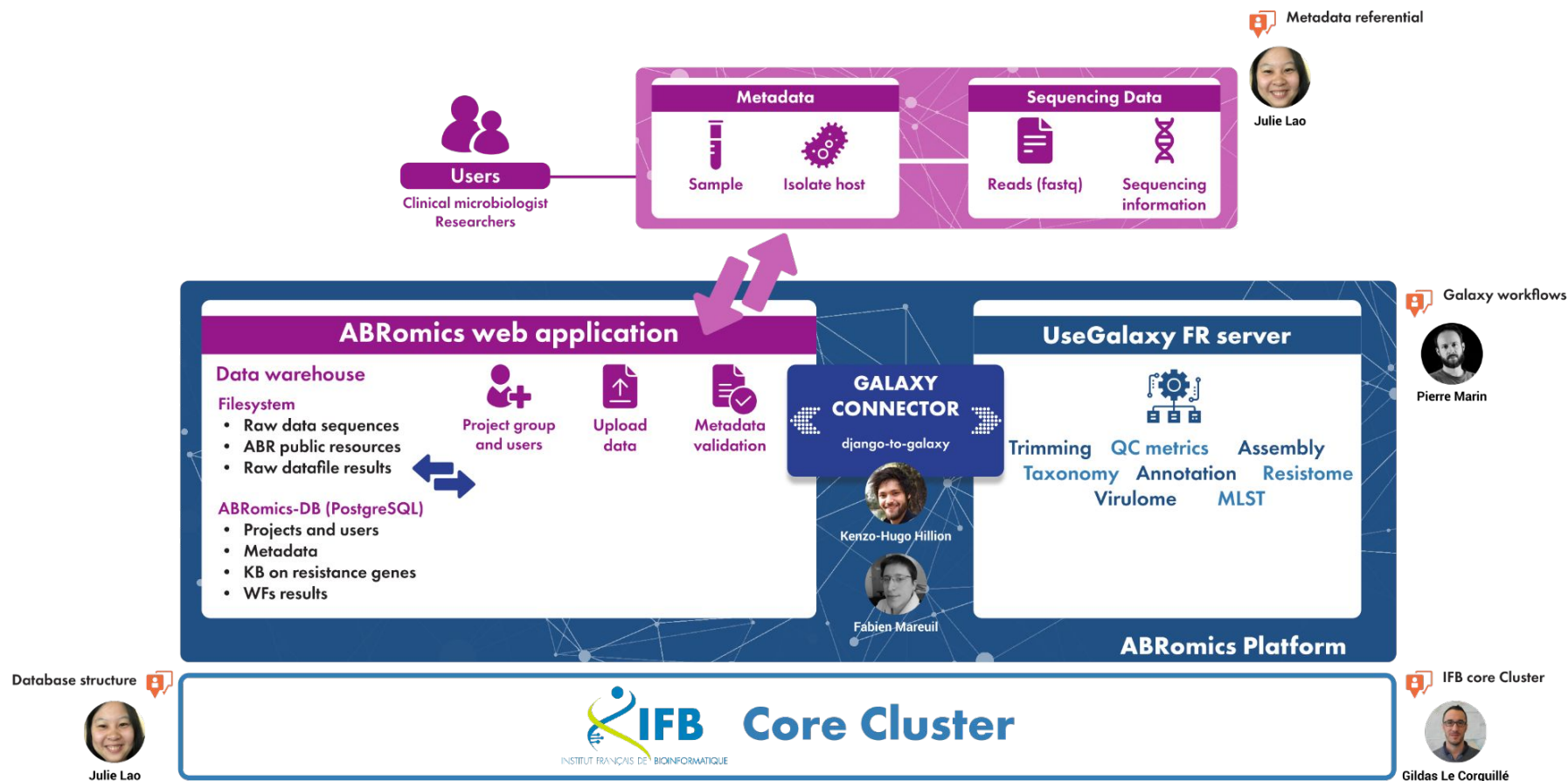
Romain Dallet

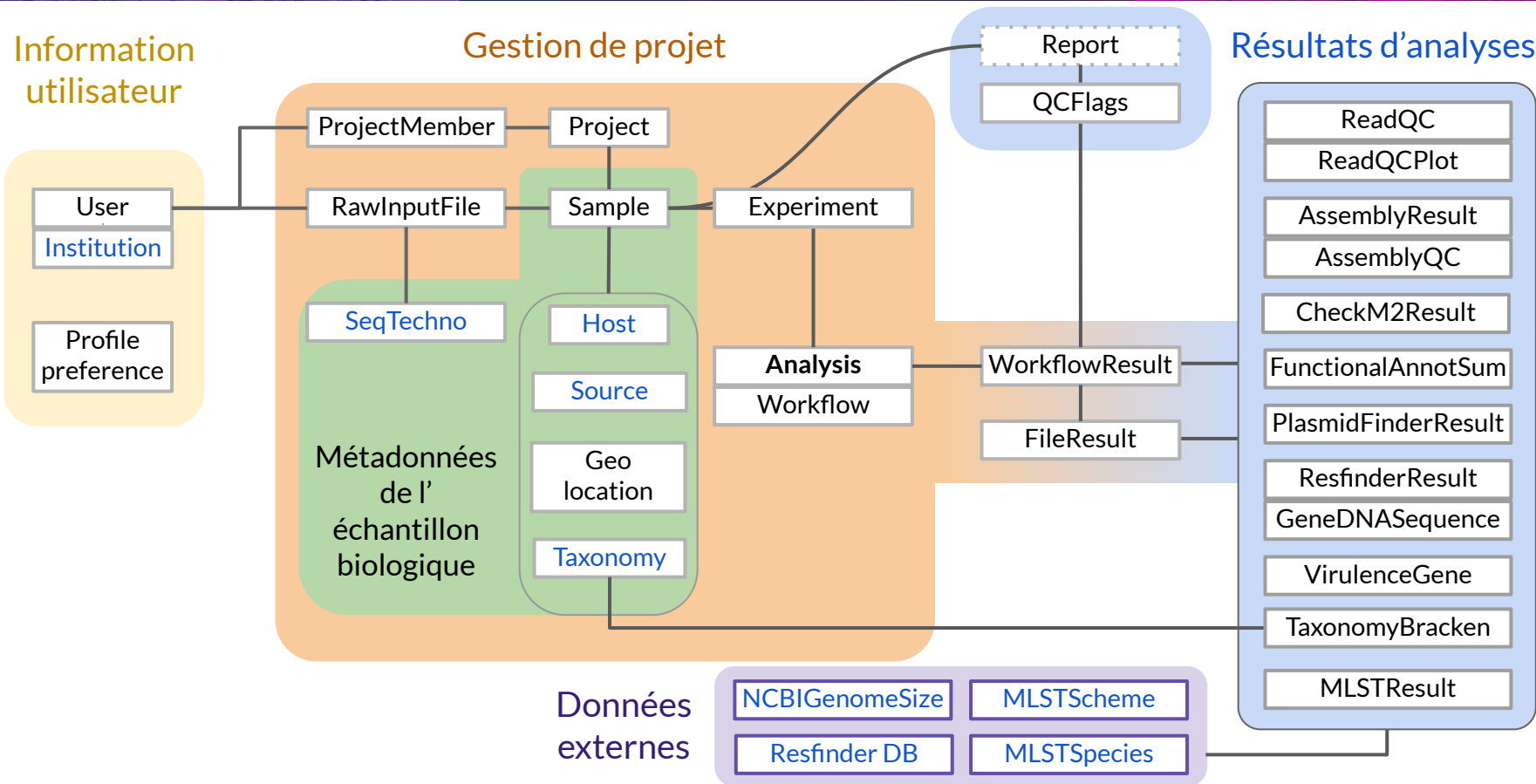


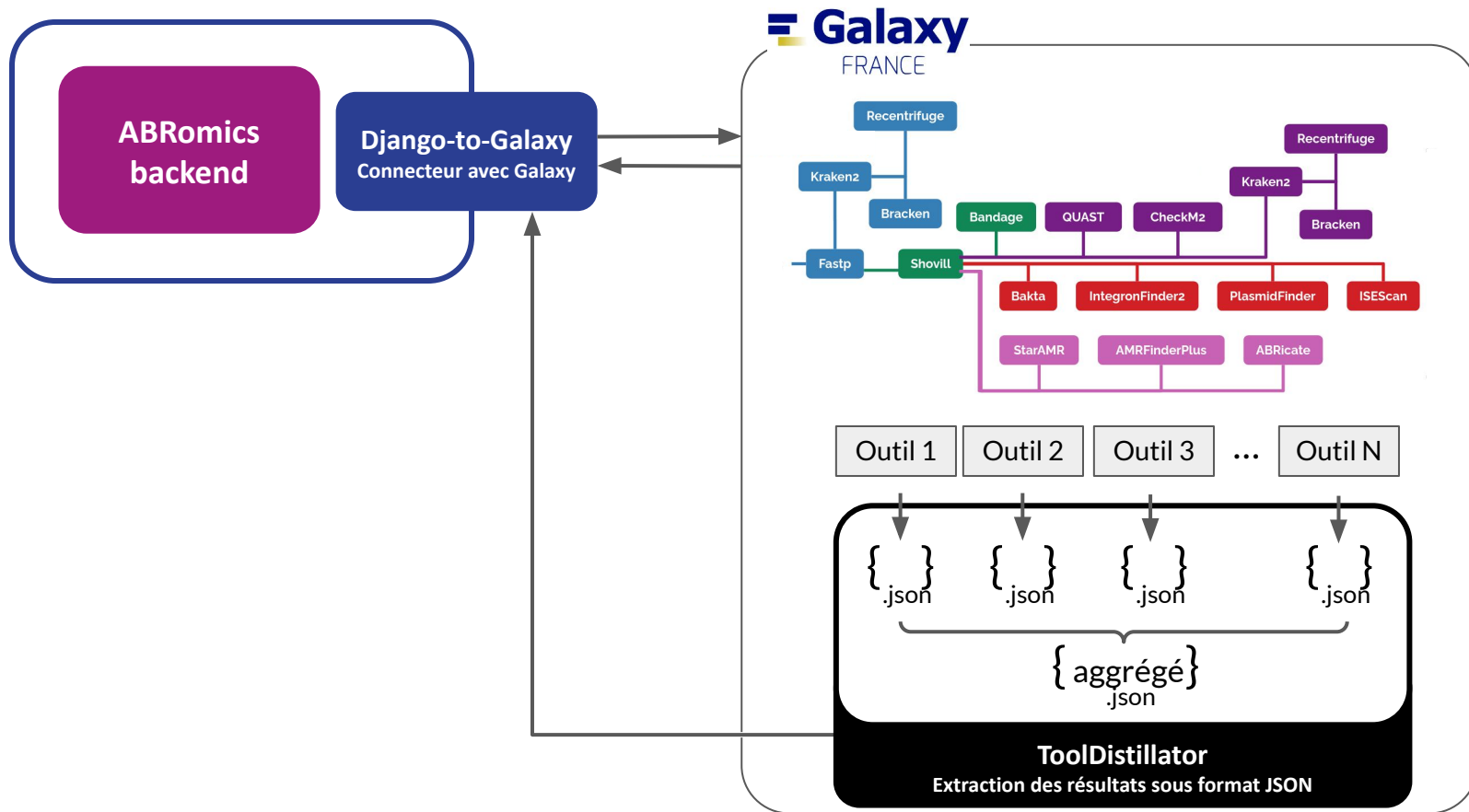
Amanda Dieuaide



Raphaël Tackx







ABRomics consortium (2023). ToolDistillator: a tool to extract and aggregate information from different tool outputs to JSON parsable files.

<https://gitlab.com/ifb-elixirfr/abromics/tooldistillator>

ToolDistillator: a tool to extract and aggregate information from different tool outputs to JSON parsable files

License **GPL v3** Python **3.9** release **1.0.4**

ToolDistillator is a tool to extract information from output files of *specific tools*, expose it as JSON files, and aggregate over several tools.

It can produce both a single file to each tool or a summarized file from a set of reports.

It was initially developed to be used on Galaxy and some options are only available on Galaxy (e.g. extract the historic ID from a galaxy analysis).

Tool was inspired from the hAMRonization project (author: @dfornika, @fmaguire, @raphenya, @jodyphelan, @pvanheus)

<https://bio.tools/tooldistillator>

ToolDistillator (biotools:tooldistillator)

<https://gitlab.com/ifb-elixirfr/abromics/tooldistillator>

Available versions

0.8.4.1 **0.8.5.0** **0.9.0** **0.9.1** **0.9.2** **0.9.3**

Microbiology > Bioinformatics > Sequence analysis >



BIOCONDA



Pierre Marin



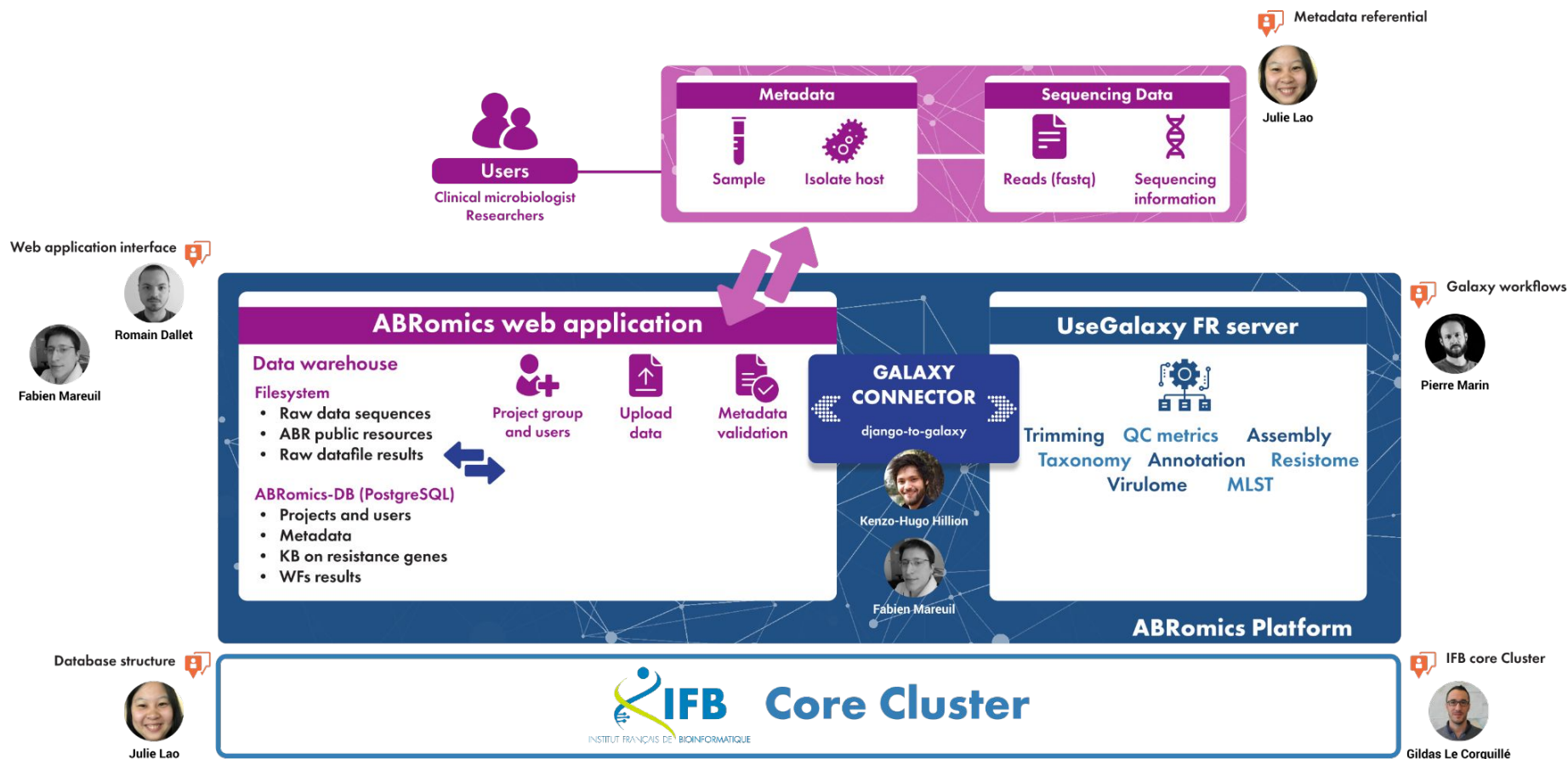
Cléa Siguret



Julie Lao



Hugo Lefevre



ABRomics

ABRomics DB

Dashboard

Submit data

Upload Metadata

Choose a metadata file (.xlsx)
metadata_A...0.1.2.xlsx (143.7 kB)
1 files (143.7 kB in total)
SUBMIT

✓ The file was successfully uploaded at http://localhost/mediafiles/metadata_Abromics_GENOMIC-WGS_v0.1.2_b63Rw00.xlsx

Upload Data

Choose a data file (.fastq)
r1_forward.fastq (54 B)
1 files (54 B in total)
SUBMIT

✓ The file was successfully uploaded at http://localhost/mediafiles/r1_forward_AZ6kbeJ.fastq

Running a workflow

Workflow
ABR_QC_TEST1
Version test pour abromics to galaxy django

Read1_forward
r1-forward

Read2_reverse
r2-reverse

EXECUTE

ABRomics. Work funded by IEB.

GitLab

ABRomics

LOGIN/REGISTER

ABRomics DB

Dashboard

Submit data

Samples

Search

Sample ID	Sequencing partner	Collected date	Comments	Submission date
ec-01	Toto agency	2022-10-20		2022-10-20
SE-01	Test user university	2022-10-12		2022-10-20
EF-01	Toto agency	2022-10-02		2022-10-20

Rows per page: 10 1-3 of 3

Projects

Here is a list of your projects

- Project 1
- Project 2

Workflow status

Search

Workflow	Galaxy state	Status	Create time
ABR_QC_TEST1	new	running	2022-11-08 09:20:54
ABR_QC_TEST1	new	running	2022-11-08 10:16:35

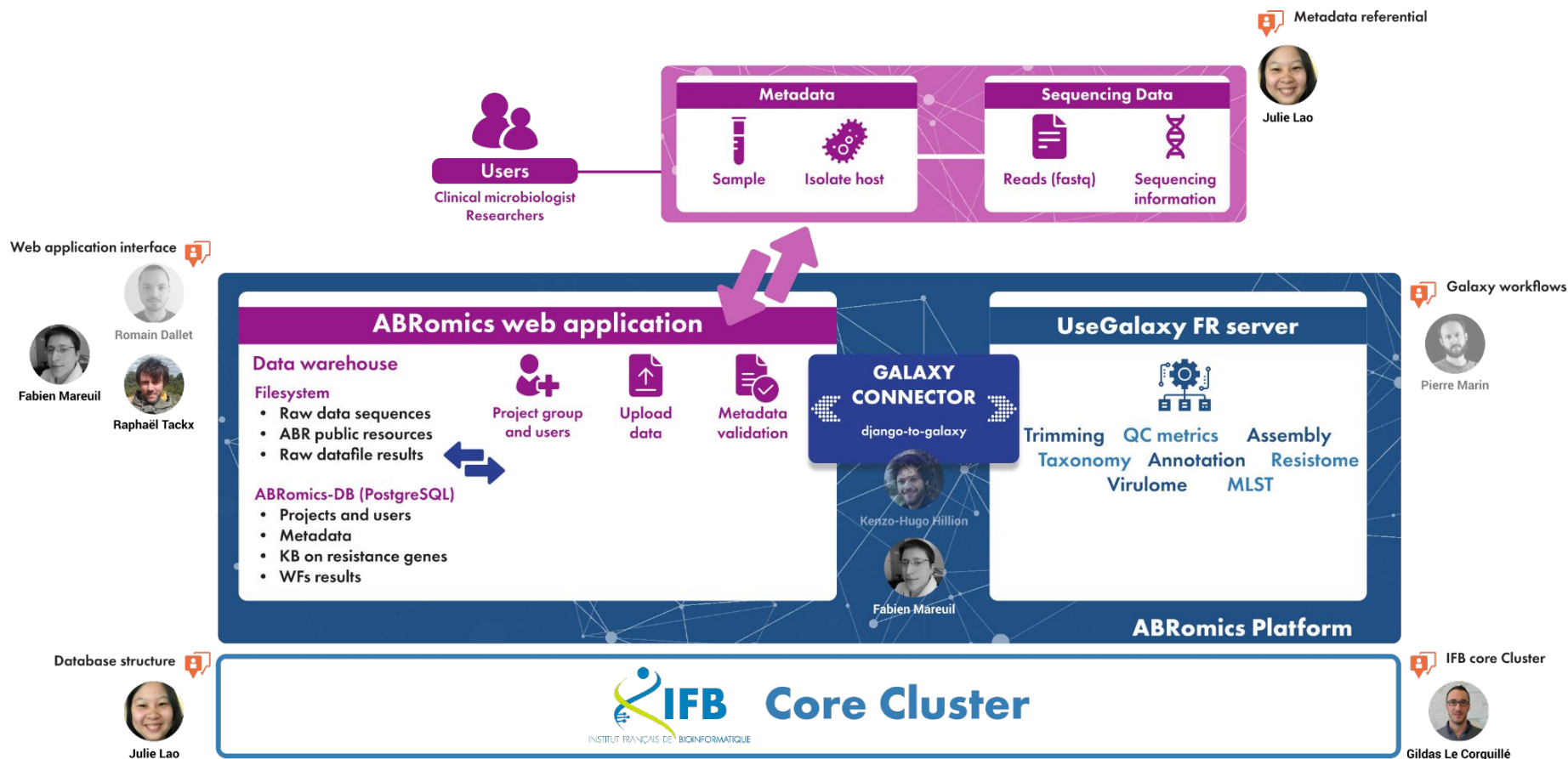
Rows per page: 10 1-2 of 2

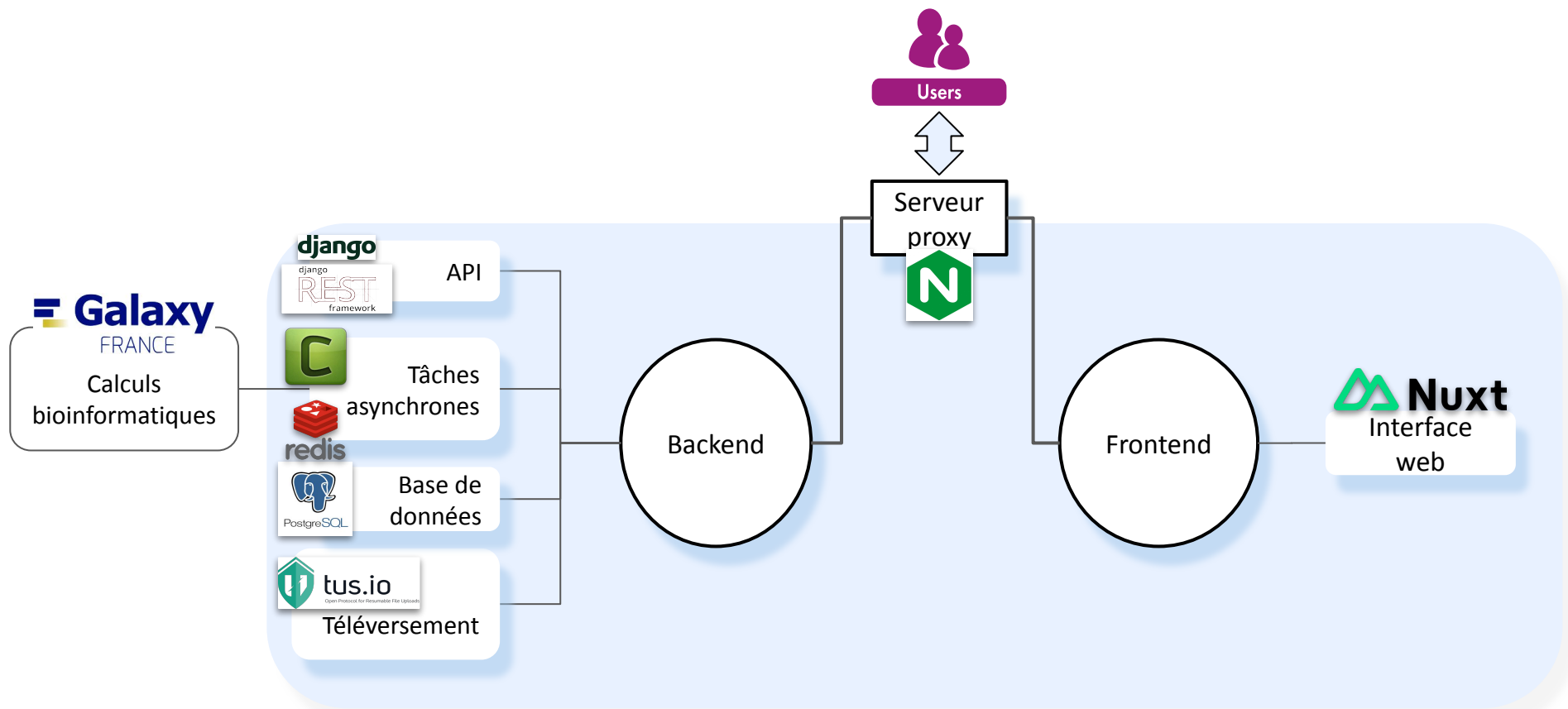
ABRomics. Work funded by IEB.

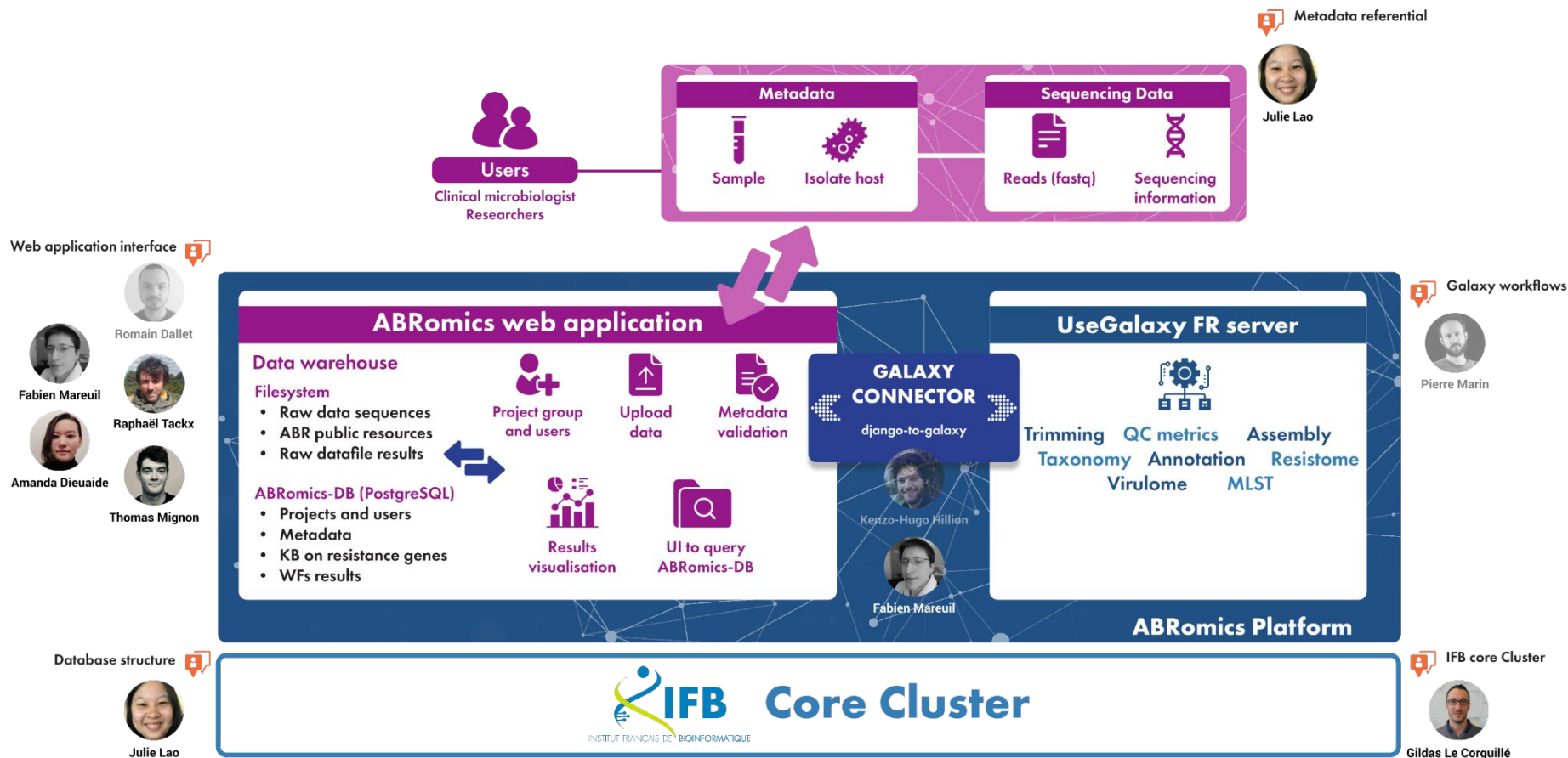
GitLab

28 novembre 2025 - Séminaire PEPI IBIS - Pôle Modélisation des connaissances - Plateforme d'analyse ABRomics

ABRomics
ANTIBIORESISTANCE

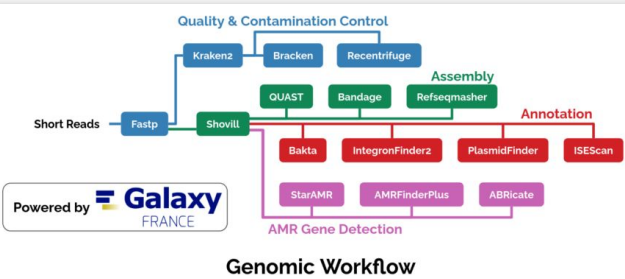








ABRomics Database De Workflows omics ...



à des rapports d'analyses ...

Contents

Sample Summary

Analysis Summary

Antimicrobial Resistance

Acquired resistance genes

Violence genes

Plasmid typing

Organism Identification

Quality Metrics

Quality Assembly

GENOMIC RESULT REPORT

Short paired-end read analysis to provide assembly, typing, gene

FILE RESULTS

28 files generated during analysis

SAMPLE SUMMARY

Original Sample ID

Strain ID

QUALITY METRICS

Trimming and quality control with Fastp v1.21.0

Strain ID

Strain ID

Strain ID

Strain ID

Strain ID

Strain ID

Strain ID

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Strain ID

Strain ID

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Strain ID

Strain ID

Strain ID

ANALYSIS SUMMARY

Self description missing

MLST Sequence Type (ST)

Number of genes with known resistance to target antibiotics

List of target antibiotics:

Amikacin, Gentamicin, and Tobramycin

Amikacin and Tobramycin

Ampicillin

Ampicillin, Amoxicillin/clavulanic acid, and Cefepime

MLST scheme

MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

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MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

ORGANISM IDENTIFICATION

Self description missing

Species name

NCBI ID

Proportion of reads

Escherichia coli

WGS...

Strain typing: mlst v2.2.0

Sequence Type (ST)

12

MLST scheme

mlst_coli_mecA_4

MLST Sequence name

EscherichiaShigella

MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

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MLST Sequence name

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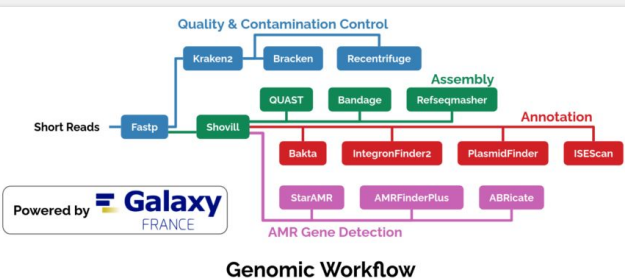
MLST Sequence name

MLST Sequence name

MLST Sequence name

MLST Sequence name

ABRomics Database De Workflows omics ...



à des rapports d'analyses ...

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GENOMIC RESULT REPORT

Short paired-end read analysis to provide assembly, typing, genome metrics, and quality metrics.

FILE RESULTS

28 files generated during analysis

SAMPLE SUMMARY

Original Sample ID

Strain ID

QUALITY METRICS

Trimming and quality control with Fastp v1.21.0

Strain ID

Strain ID

Strain ID

Strain ID

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Strain ID

ANALYSIS SUMMARY

Isolate identified as

HLST Sequence Type (ST)

Number of genes with known resistance to target antibiotics

List of target antibiotics:

Amikacin, Gentamicin, and Tobramycin

Amikacin and Tobramycin

Ampicillin

Ampicillin, Amoxicillin/clavulanic acid, and Cefepime

HLST scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

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HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

ORGANISM IDENTIFICATION

Self description missing

Species name

NCBI ID

Proportion of reads

Escherichia coli

WGS...

Strain typing: mlt v2.2.0

Sequence Type (ST)

HLST scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

HLST Specimen name

HLST Sequence Type (ST)

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HLST Scheme

HLST Specimen name

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HLST Scheme

HLST Specimen name

HLST Sequence Type (ST)

HLST Scheme

ANTIMICROBIAL RESISTANCE ANALYSES

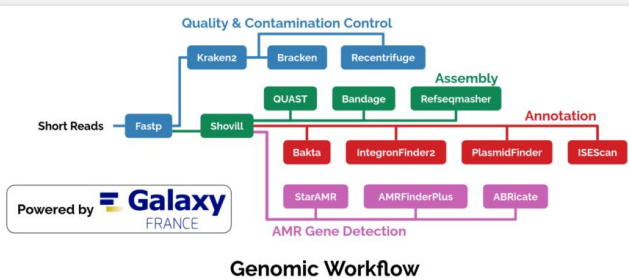
Acquired resistance genes

Acquired antimicrobial resistance genes annotation with StarAMR v1.10.0 using RefFinder 2.4.4 database (annotated v102102 - 2024 Sep 23) (parameters used: 70% identity and 40% coverage cutoff)

Resistance gene	Gene length	Identity (%)	Coverage (%)	Contig	Start in contig	End in contig	Strand	Antibiotic class
blaTEM-1B	861	100	100	contig0036	670	1530	+	Beta-lactam
blaTEM-1B	861	100	100	contig0036	670	1530	+	Beta-lactam
dhfr17	474	100	100	contig0062	8591	9064	-	Folate pathway antagonist

Les fonctionnalités de la plateforme ABRomics ...

ABRomics Database De Workflows omics ...



à des rapports d'analyses ...

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Quality Assembly

GENOMIC RESULT REPORT

Short paired-end read analysis to provide assembly, typing, and

FILE RESULTS

28 files generated during analysis

SAMPLE SUMMARY

Original Sample ID

Strain ID

QUALITY METRICS

Trimming and quality control with Fastp v0.23.0

Strain ID

Sequencing type

Cycle average

Reads before filtering

Reads after filtering

Quality

Quantity

ANALYSIS SUMMARY

Isolate identified as

HLST Sequence Type (ST)

Number of genes with known resistance to target antibiotic

List of target antibiotics:

Amikacin, Gentamicin, and Tobramycin

Amikacin and Tobramycin

Ampicillin

Ampicillin, Amoxicillin/Ticarcliclavate, and

HLST scheme

HLST Specimen name

Escherichia coli

Sequence Type (ST)

HLST scheme

HLST Specimen name

Escherichia coli

Sequence Type (ST)

HLST scheme

HLST Specimen name

Escherichia coli

Sequence Type (ST)

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HLST Specimen name

Escherichia coli

Sequence Type (ST)

HLST scheme

HLST Specimen name

Escherichia coli

Sequence Type (ST)

HLST scheme

HLST Specimen name

Escherichia coli

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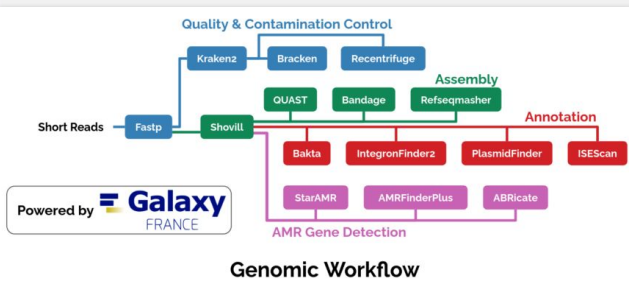
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Sequence Type (ST)

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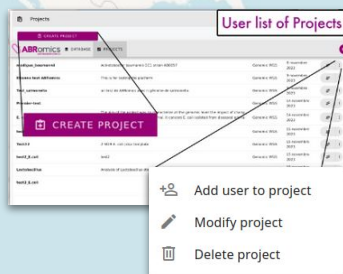
ABRomics Database De Workflows omics ...



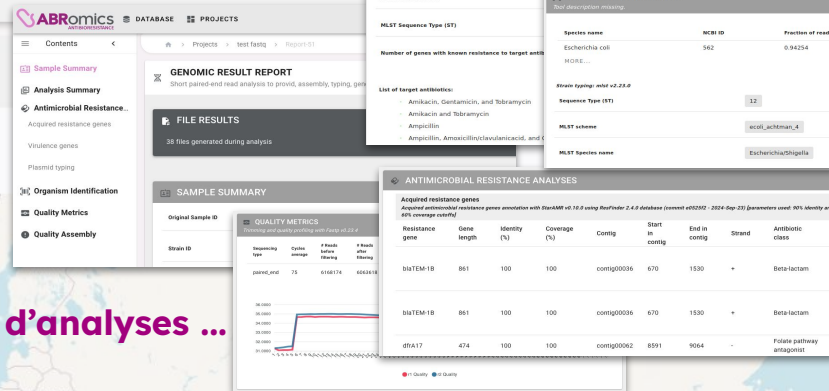
à des rapports d'analyses ...

Les fonctionnalités de la plateforme ABRomics ...

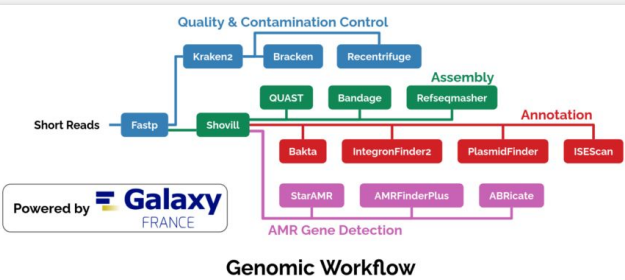
1 Gestion de projets



2 Upload de données & validation des métadonnées



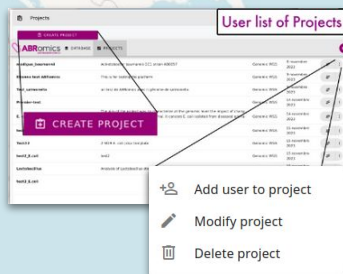
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à des rapports d'analyses ...

Les fonctionnalités de la plateforme ABRomics ...

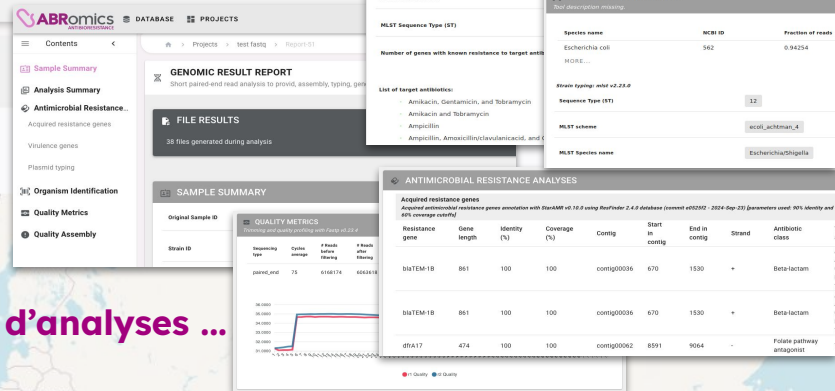
1 Gestion de projets



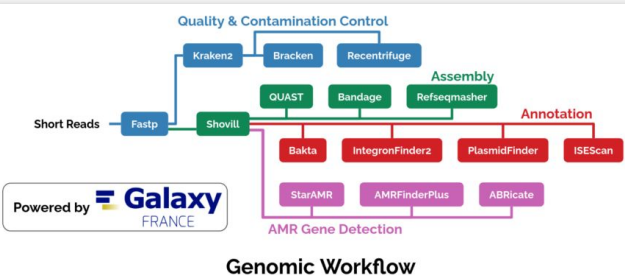
2 Upload de données & validation des métadonnées



3 Lancement d'analyses



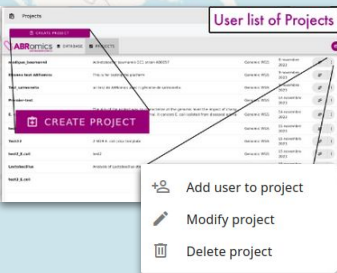
ABRomics Database De Workflows omics ...



à des rapports d'analyses ...

Les fonctionnalités de la plateforme ABRomics ...

1 Gestion de projets

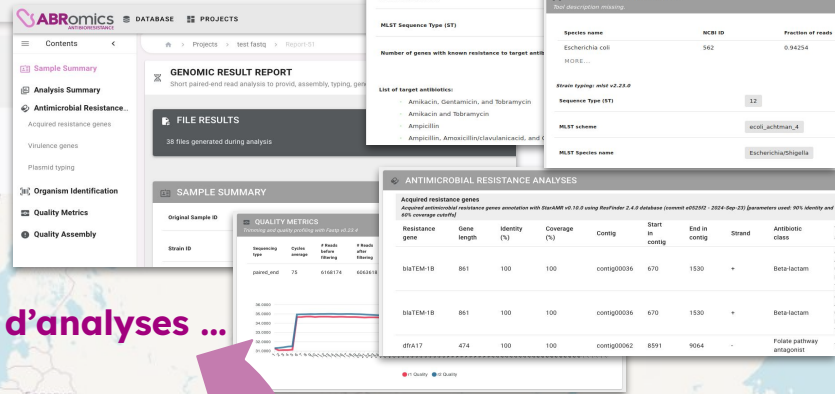


2 Upload de données & validation des métadonnées

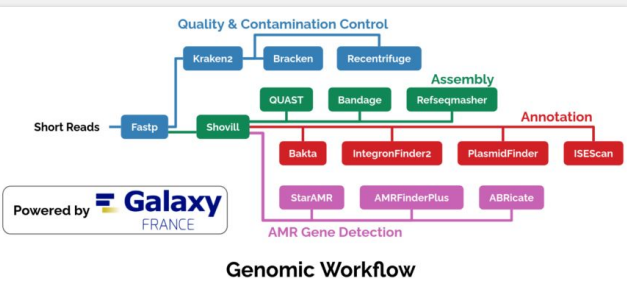


Visualisation des résultats

3 Lancement d'analyses



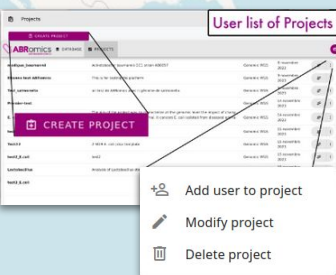
ABRomics Database De Workflows omics ...



à des rapports d'analyses ...

Les fonctionnalités de la plateforme ABRomics ...

1 Gestion de projets



2

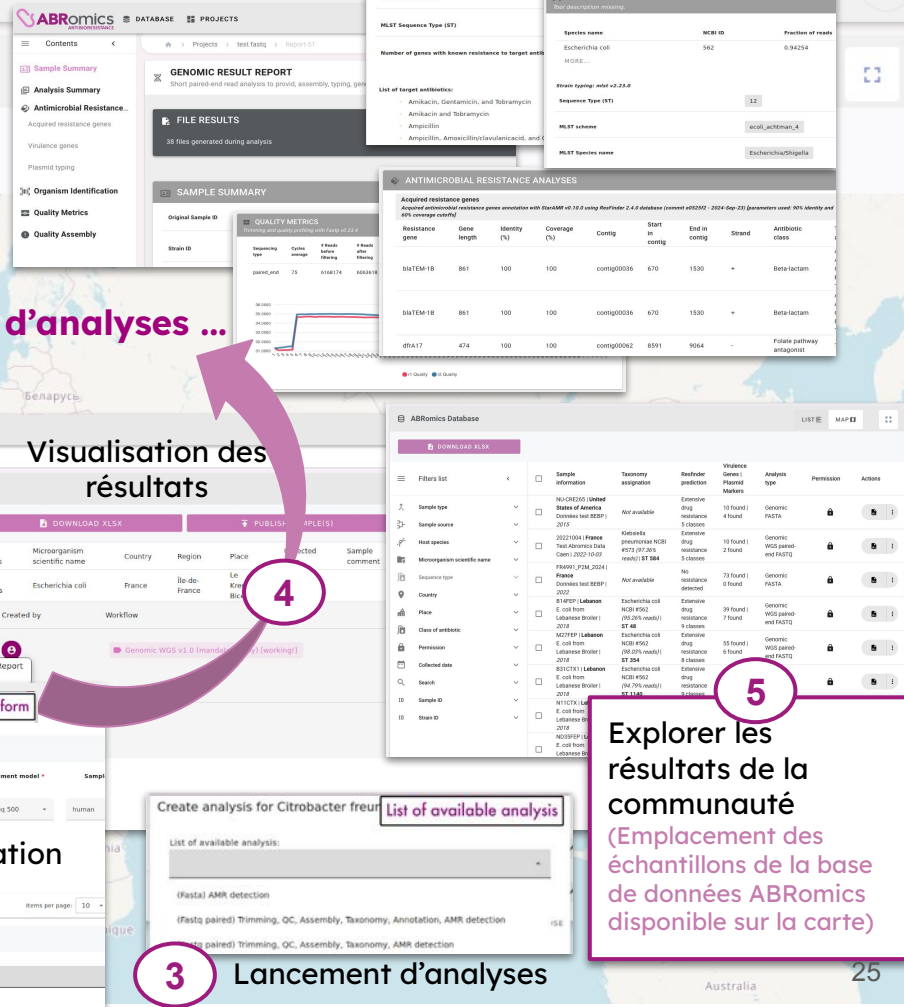
Upload de données & validation des métadonnées



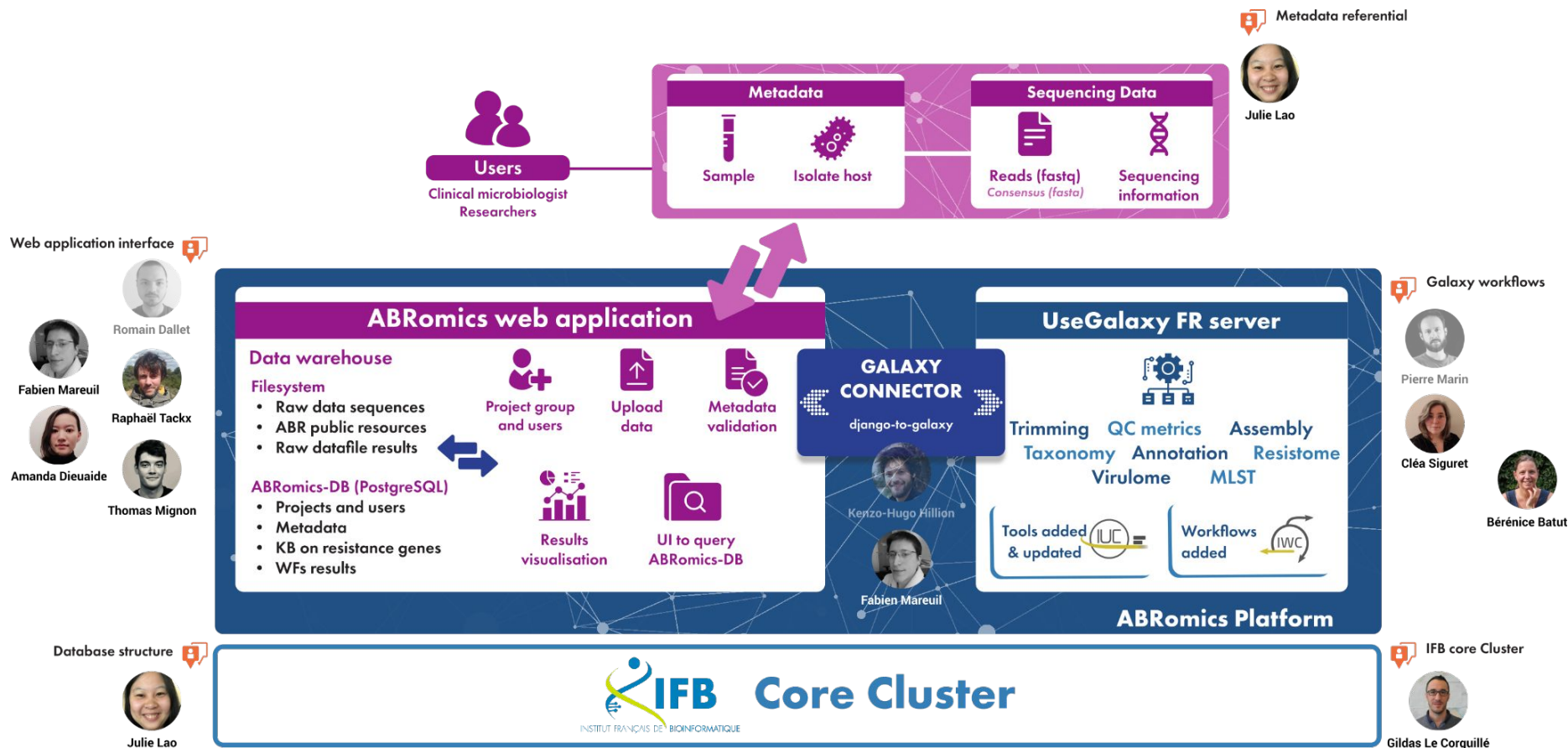
Visualisation des résultats

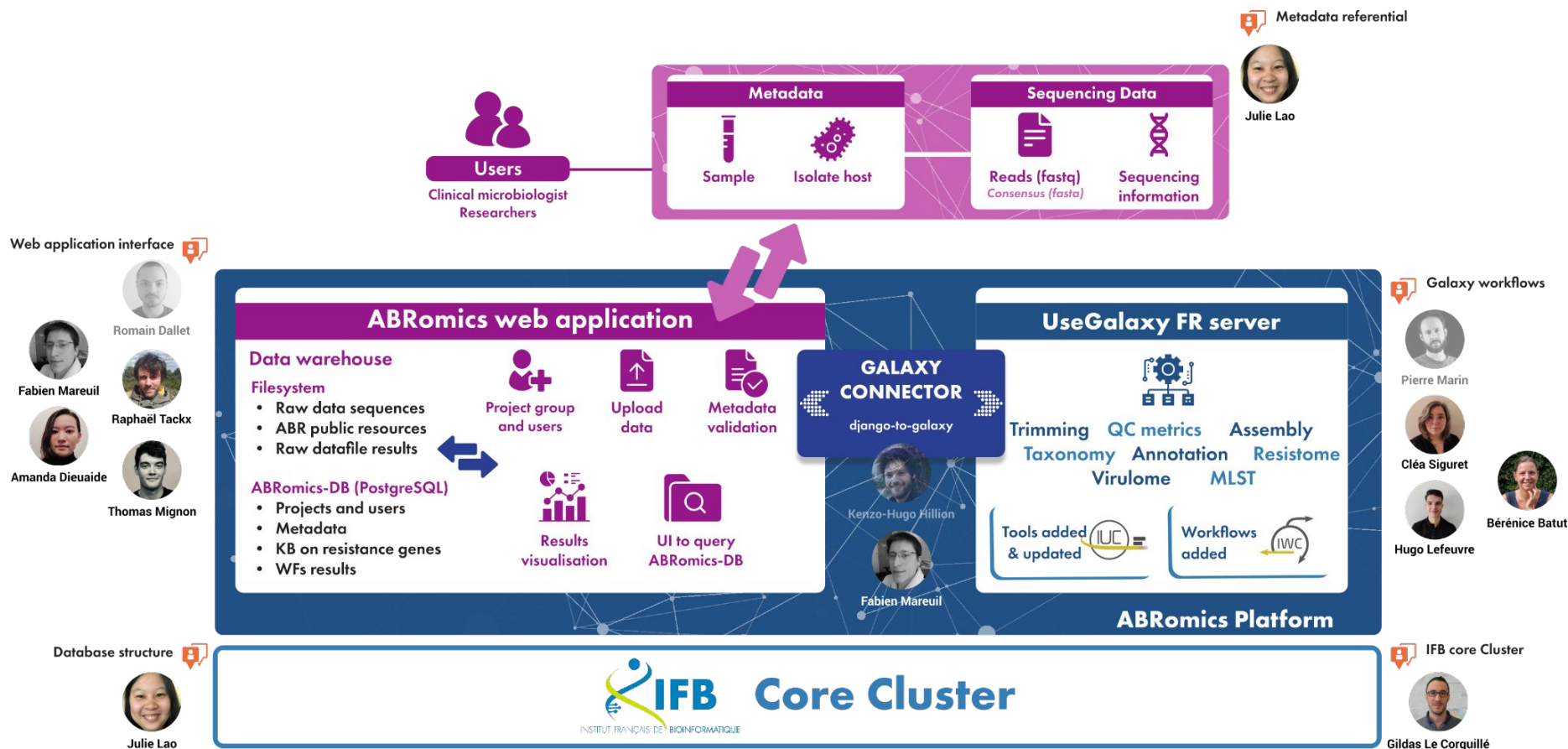
3

Lancement d'analyses



5 Explorer les résultats de la communauté (Emplacement des échantillons de la base de données ABRomics disponible sur la carte)





Sous-workflows *short reads*

- Disponible sur des registres de workflows : **WorkflowHub** et **Dockstore** via Galaxy IWC



- Documenté comme **Learning Pathways** sur le Galaxy Training Network
<https://gxy.io/GTN:P00018>



Galaxy Training! Learning Pathways Help Settings Search Tutorials

Detection of AMR genes in bacterial genomes

@PURL: <https://gxy.io/GTN:P00018>

Comment: What is a Learning Pathway?

We recommend you follow the tutorials in the order presented on this page. They have been selected to fit together and build up your knowledge step by step. If a lesson has both slides and a tutorial, we recommend you start with the slides, then proceed with the tutorial.

This learning path aims to teach you the basic steps to detect and check Antimicrobial resistance (AMR) genes in bacterial genomes using Galaxy.

Module: Species and contamination checking

Taxonomic assignment is useful in AMR detection to check contamination and confirm species

Lesson	Slides	Hands-on	Recordings
Checking expected species and contamination in bacterial isolate			

Module: Assembly

Assembly is a major step in the process of detecting AMR genes as it combines sequenced reads into contigs, longer sequences where it will be easier to identify genes and in particular AMR genes

Lesson	Slides	Hands-on	Recordings
--------	--------	----------	------------

Tutoriel : Annoter, préparer, tester et publier ses workflows Galaxy dans les registres de workflows

A purple rectangular graphic with a white geometric pattern. In the top left is the GTN logo (a multi-colored star) and the text 'GTN USING GALAXY AND MANAGING YOUR DATA'. Below this is the text 'Annotate, prepare tests and publish Galaxy workflows in workflow registries'. On the left, a vertical white bar contains the names 'Clea Siguret', 'Nadia Goué', and 'Bérénice Batut'. In the center, there is an illustration of a person sitting at a desk with a laptop, with a small plant on the desk and a box of books. Above the person is the text 'E-Learning Material'. At the bottom, there is a link icon followed by 'gxy.io/GTN:T00533'.

Author(s)   Clea Siguret   Nadia Goué   Bérénice Batut

Reviewers   

<https://gxy.io/GTN:T00533>

Atelier(s) : Promotion du partage et de la réutilisation des données de recherche autour des workflows Galaxy



<https://hal.inrae.fr/hal-05095680v1>

Réutilisation dans la formation
Galaxy Avancée en 2026

- **Recherche d'éléments sur un contig contre 3 bases de données**
 - ResFinder (gènes de résistance)
 - PointFinder (mutations ponctuelles confèrent une résistance)
 - PlasmidFinder (marqueurs plasmidiques)
- **Limitations FAIR**
 - Versions des bases de données sont dépendantes de la version de l'outil
 - Comment mettre à jour les bases de données dans usegalaxy ?
 - Pull request, mettre à jour l'outil, mettre à jour le wrapper Galaxy
 - Ou montée de version manuelle par l'administrateur Galaxy
- **Amélioration réalisée**
 - Data Manager : *Bonne pratiques* pour la gestion des données Galaxy



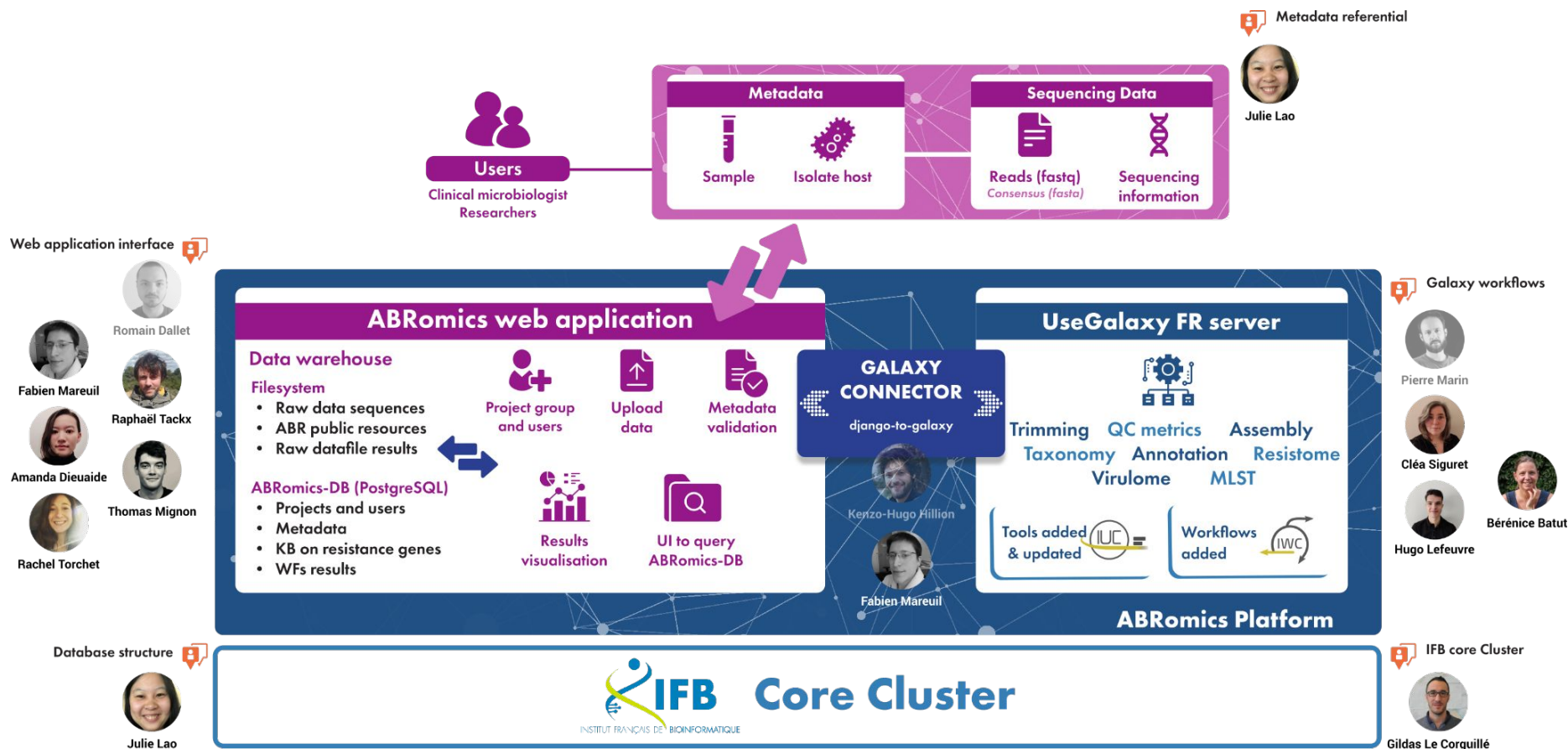
Cléa Siguret



Bérénice Batut



Hugo Lefeuvre



 DATABASE PROJECTS AA

ABRomics - The French national multiomics platform For antibiotic Resistance research and surveillance

A collaborative digital platform to improve Antimicrobial Resistance surveillance and research from a *One Health* approach.

Know more about the ABRomics project on the [ABRomics portal](#)

 New to ABRomics? Please read our **User Manual**

GET THE **DEMO FILES**

Main features



Upload

Upload bacterial genome sequencing data and metadata

Sequencing data and metadata are required

Accepted sequencing data formats: **fastq.gz, fasta**

Direct validation of metadata upon upload

38 bacterial species

About the **metadata**



Analysis

Automated detection of AMR genes in bacterial genomes

From  **Sequencing data ...**

- Quality control
- Species and contamination checking
- Genome assembly
- Genome annotation
- AMR gene detection

To  **All-in-one analysis report**



Collaborate

Share and compare with other genomes in ABRomics

- Based on AMR genes content
- Based on species identification
- Based on any metadata criteria

Publish your analysis

For more information, **please log in**

ABRomics
ANTIBIORESISTANCE

ABOUTSERVICESTEAMSCONTACT

LOG IN

Welcome to the ABRomics platform

ABRomics is an online community-driven platform to scale up and improve surveillance and research on antibiotic resistance from a One Health perspective. The platform is open to all users, and allows them to upload their data and analyze it with the ABRomics pipeline.

The platform is currently in active development, and new features are added regularly.

Learn more

Get started

Standardized data

AMR gene detection

One Health approach

ABRomics
ANTIBIORESISTANCE

Create an Account

Join our community today and unlock all features of the ABRomics platform.

Sign Up

Pratique mais on se rend dépendant d'une ressource qu'on maîtrise pas

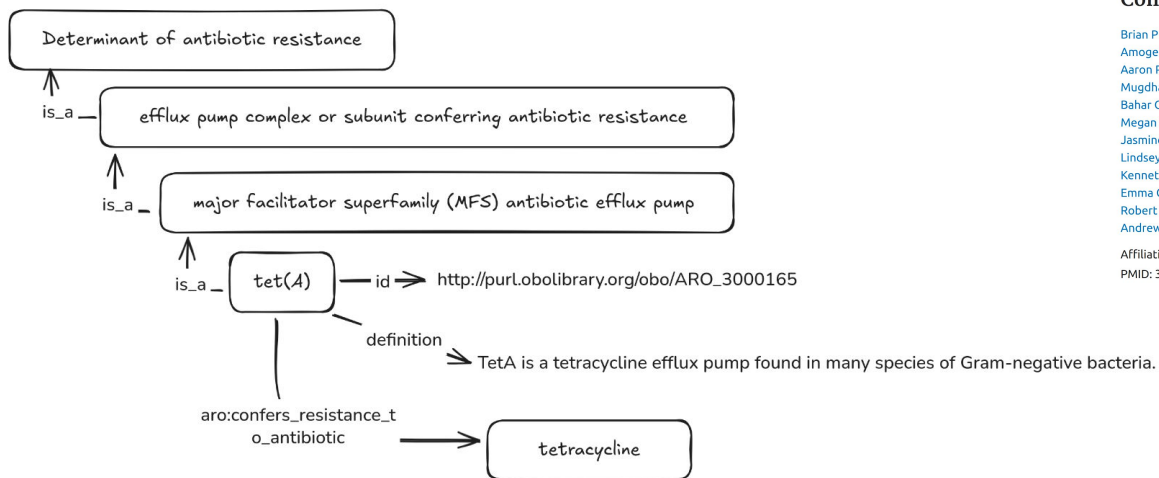
Données	Source des données	Récupération automatique ?
Institution	ROR	API
Technologies de séquençages	?	?
Hôtes	?	?
Source	?	?
Taxonomie	NCBI Taxonomy	API
Taille de génome	NCBI Genome Size	API
Gènes de Resfinder	Resfinder DB	Repository Bitbucket
Schémas MLST	pubMLST, BigsDB, ...	API, FTP, ...

Pratique mais on se rend dépendant d'une ressource qu'on maîtrise pas

Données	Source des données	Récupération automatique ?
Institution	ROR	API
Technologies de séquençages	?	?
Hôtes	Problème de sémantique Solution envisagée : Utilisation d'ontologies	
Source		
Taxonomie	NCBI Taxonomy	API
Taille de génome	NCBI Genome Size	API
Gènes de Resfinder	Resfinder DB	Repository Bitbucket
Schémas MLST	pubMLST, BigsDB, ...	API, FTP, ...

“A **formal specification** of a **shared conceptualization**” - Borst 1997

Antibiotic Resistance Ontology (ARO)



CARD 2023: expanded curation, support for machine learning, and resistome prediction at the Comprehensive Antibiotic Resistance Database

Brian P Alcock^{1 2 3}, William Huynh^{1 2 3}, Romeo Chalil^{1 2 3}, Keaton W Smith^{1 2 3}, Amogelang R Raphenya^{1 2 3}, Mateusz A Wlodarski^{1 2 3}, Arman Edalatmand^{1 2 3}, Aaron Petkau^{4 5}, Sohaib A Syed^{1 2 3}, Kara K Tsang^{1 2 3}, Sheridan J C Baker^{1 2 3}, Mugdha Dave^{1 2 3}, Madeline C McCarthy^{1 2 3}, Karyn M Mukiri^{1 2 3}, Jalees A Nasir^{1 2 3}, Bahar Golbon^{1 2 3}, Hamna Imtiaz^{1 2 3}, Xingjian Jiang^{1 2 3}, Komal Kaur^{1 2 3}, Megan Kwong^{1 2 3}, Zi Cheng Liang^{1 2 3}, Keyu C Niu^{1 2 3}, Prabakar Shan^{1 2 3}, Jasmine Y J Yang^{1 2 3}, Kristen L Gray⁶, Gemma R Hoad⁷, Baofeng Jia⁶, Timsy Bhandu^{1 2 3}, Lindsey A Carfrae^{1 2 3}, Maysa A Farha^{1 2 3}, Shawn French^{1 2 3}, Rodion Gordzevich^{1 2 3}, Kenneth Rachwalski^{1 2 3}, Megan M Tu^{1 2 3}, Emily Bordeleau^{1 2 3}, Damion Dooley⁸, Emma Griffiths⁸, Haley L Zubyk^{1 2 3}, Eric D Brown^{1 2 3}, Finlay Maguire^{9 10 11}, Robert G Beiko^{9 10}, William W L Hsiao^{6 8}, Fiona S L Brinkman⁶, Gary Van Domselaar^{5 12}, Andrew G McArthur^{1 2 3}

Affiliations + expand

PMID: 36263822 PMCID: PMC9825576 DOI: 10.1093/nar/gkac920

Import samples for Genomic WGS

DOWNLOAD TEMPLATE

IMPORT TEMPLATE

Metadata (* required fields)

R1 fastq filename *	R2 fastq filename *	Instrument model *	Sample type *	Sample source *	Host species *	Microorganism scientific name *	Country *	Region	Place
			human						
				Alveolar sac Anterior Nares Anus Blood Bone and joint Breast Milk					

Items per page: 10 1-1 of 1

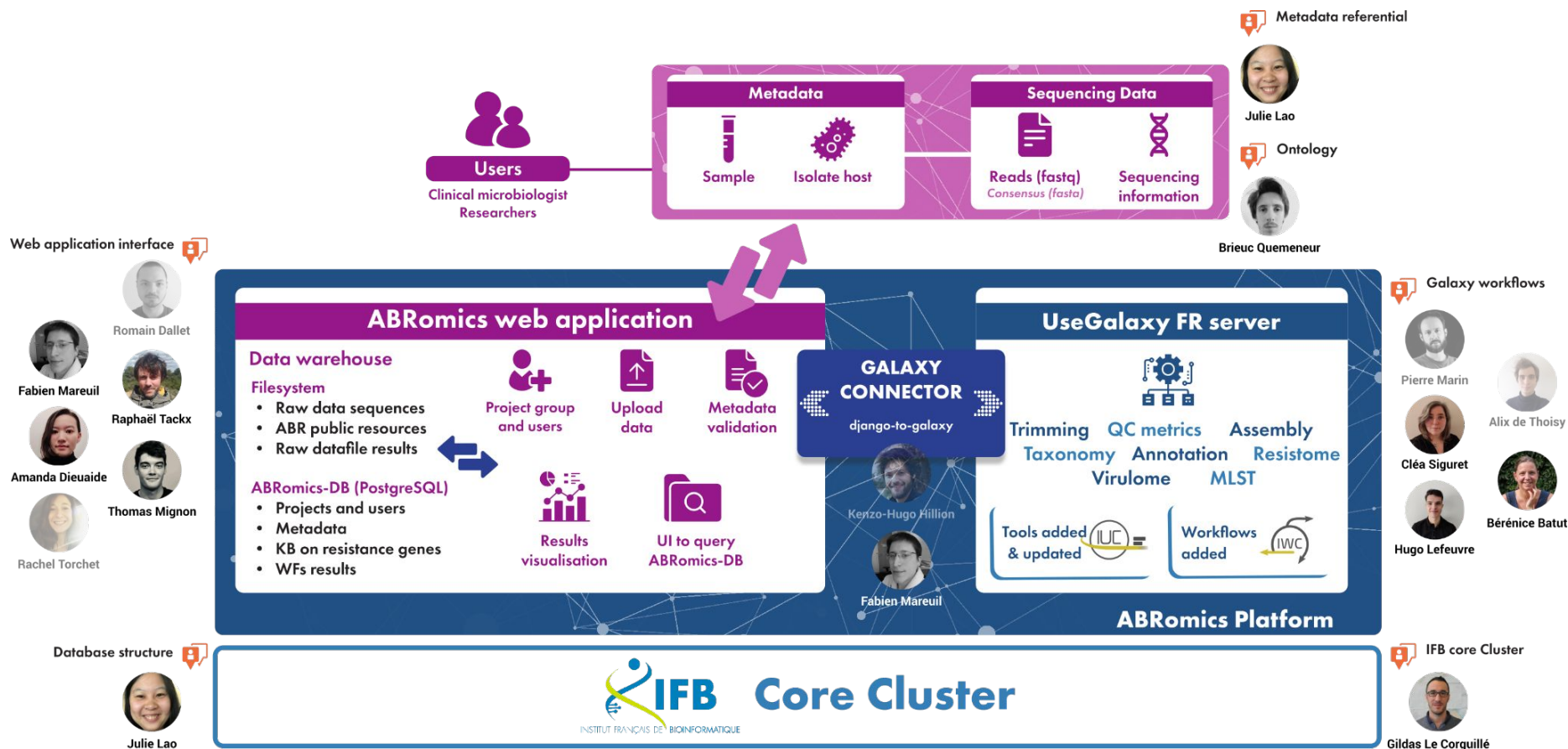
Files

Select the data file(s) to upload and complete your import. Please ensure that they match exactly the filename(s) given in your metadata.

Browse your data files

Prochaines étapes (*déjà en cours*) :

- cgMLST
- Librairie ABRomics pour les CNR
- La métagénomique



Merci pour votre attention !