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ABRomics: A Galaxy-based one health antimicrobial resistance platform

Pierre Marin, Bérénice Batut, Kenzo-Hugo Hillion, Clea Siguret, Raphael Tackx, Lao Julie, Nadia Goué, Gildas Le Corguillé, Fabien Mareuil, Philippe Glaser, et al.

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A Galaxy-based One Health Antimicrobial Resistance Platform

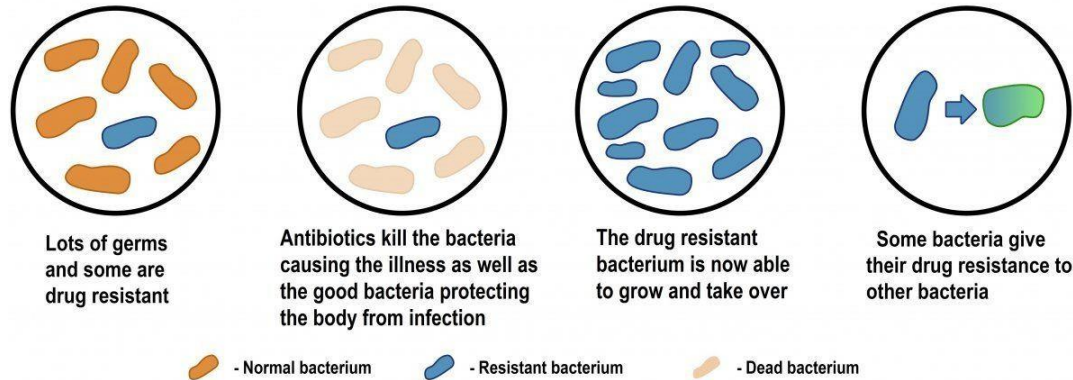
B er ence Batut on behalf of the ABRomics consortium

Galaxy Community Conference 2024

AntiMicrobial Resistance (AMR)

Bacteria, viruses, fungi and parasites no longer respond to antimicrobial medicines

How antibiotic resistance happens



One of the Top Global Public Health and Development Threats

THE COST IS
HIGH
IF WE DO NOT
ADDRESS
**ANTIMICROBIAL
RESISTANCE NOW**



1.27
MILLION DEATHS
DUE TO
ANTIMICROBIAL
RESISTANCE

**1 DEATH EVERY
25 SECONDS**

According to data from a 2019 study in The Lancet²

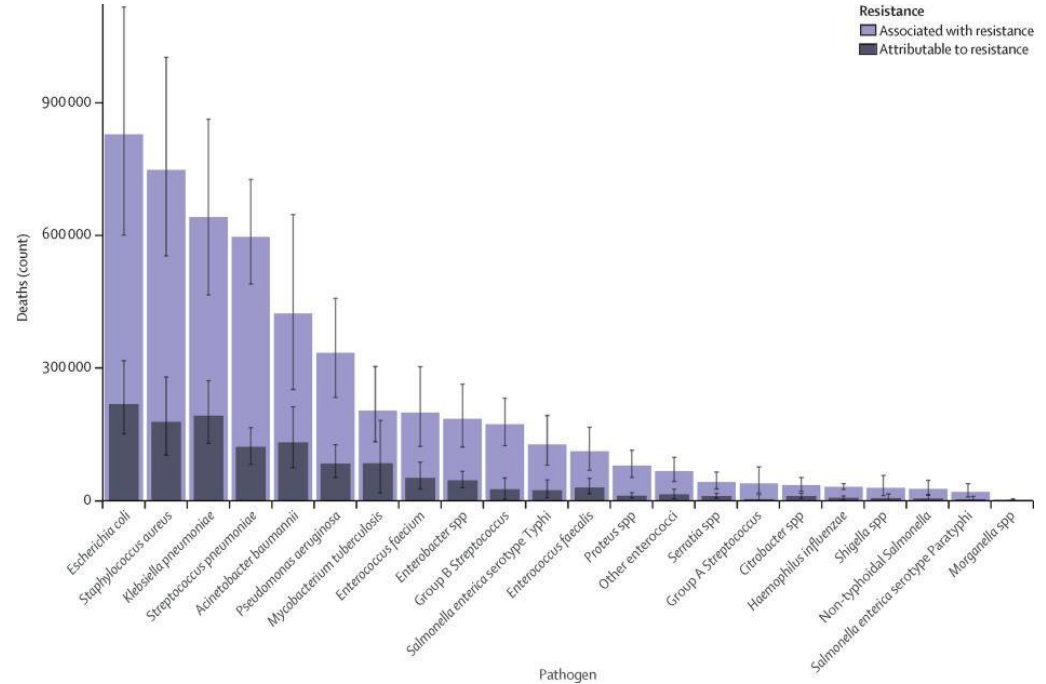


Figure 2 - Antimicrobial Resistance Collaborators et al, The Lancet, 2022.

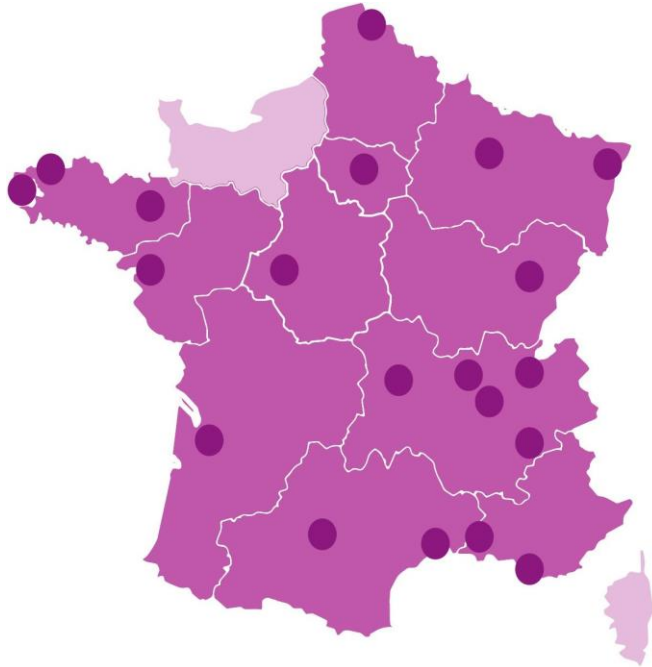
Rationale for ABRomics

1. Increasing access to **sequencing for clinical laboratories**, including outside university-teaching hospitals
2. Improvement thanks to **genomics** and **metagenomics** of our knowledge about the (complex) circulation of antibiotic-resistant bacteria, mobile genetic elements (MGE) and antibiotic resistance genes (ARG)
3. Mostly siloed investigations, while a **global picture** is needed

To address this gap in the French ecosystem:

ABRomics (2 M€ for 4 years): a multi-omics One Health platform for collaboration and data sharing between researchers and clinicians for AMR surveillance

ABRomics Consortium



National team effort

- 43 partners
- **Multidisciplinary consortium**
- **National reference centers for antibiotic resistance**

Coordination

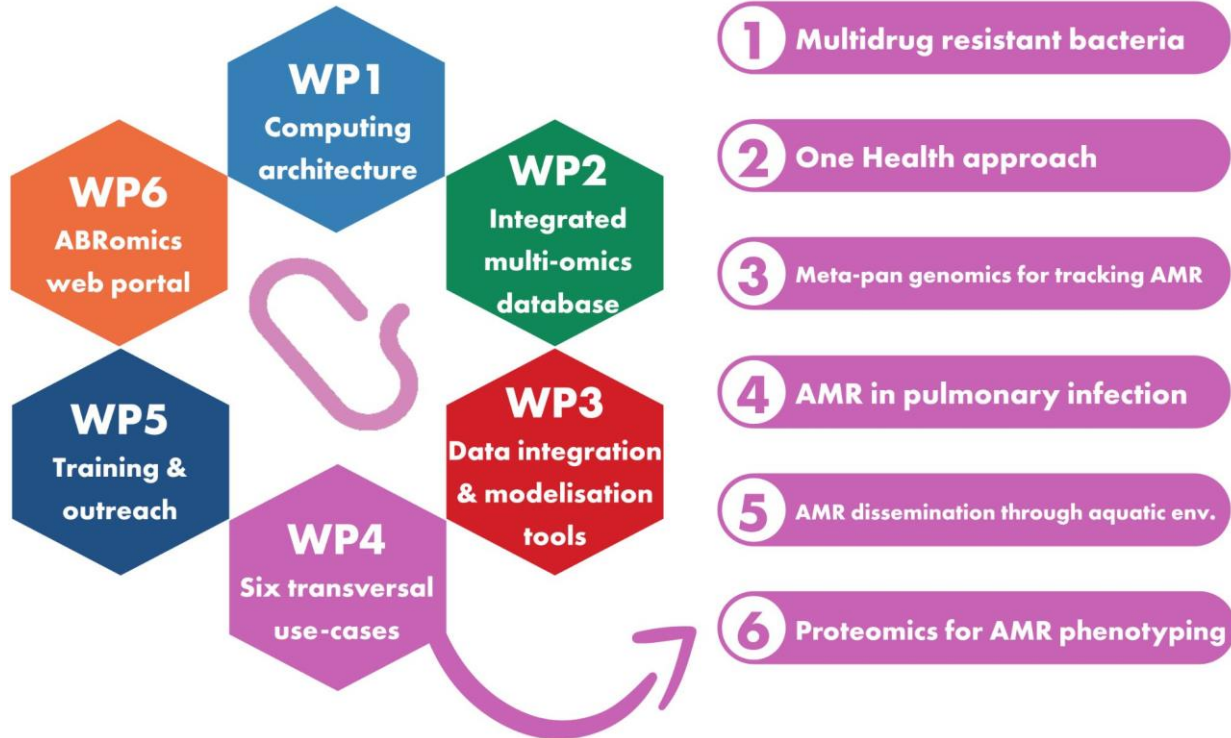
- Claudine Médigue (French Institute of Bioinformatics)
- Philippe Glaser (Institut Pasteur)

ABRomics Objectives

- Provide an open access to genomic and metagenomic analyses through **standardised and controlled pipelines** and an up-to-date set of **mathematical and bioinformatic tools**
- Build a repository of **structured, interoperable, standardized and well-annotated multi-omics microbiological data** from **human, animal and environmental origins**
- **Be easily usable** by non bio-informaticians and experts in AMR analysis
- Provide a **shared platform** to improve the **surveillance and research on antibiotic resistance across human, animal and environment sectors**

**Online One Health community-driven platform
to scale up and improve surveillance of antibiotic resistance**

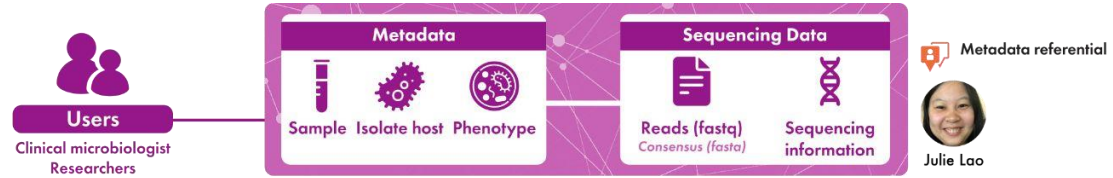
Work Packages of ABRomics



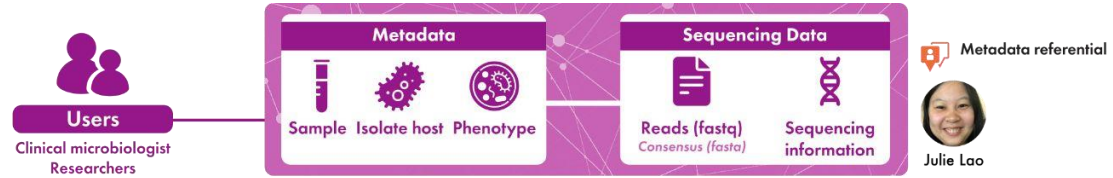
ABRomics Platform



ABRomics Platform

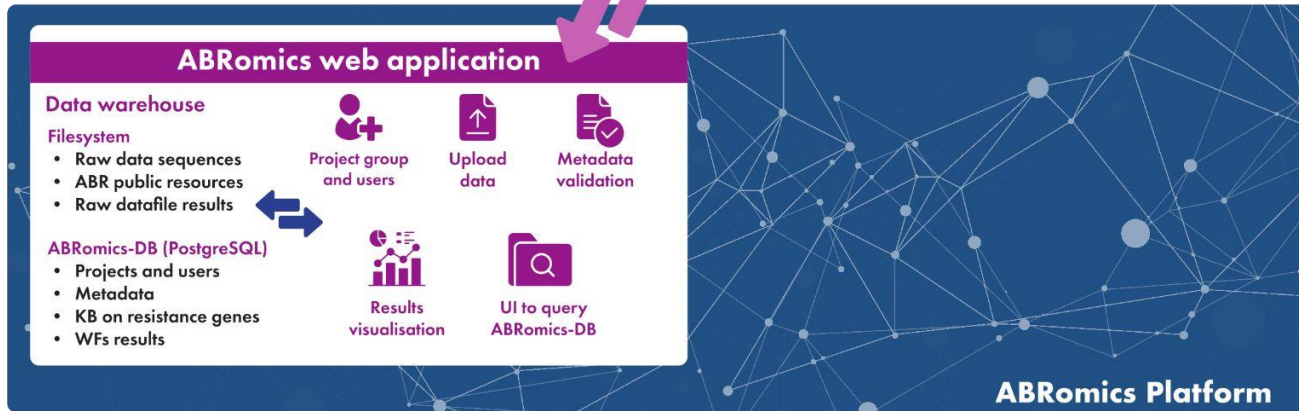


ABRomics Platform



Web application interface

-  Romain Dallet
-  Raphaël Tackx
-  Amanda Dieuaide
-  Thomas Mignon
-  Fabien Mareuil
- Database structure
-  Julie Lao



From Omics Workflows ...

Workflows here



To Analysis reports ...

Quality metrics

Analysis summary

Genomic result report

Antimicrobial resistance analyses - Acquired resistance genes

Sample metadata summary

The ABRomics Platform features ...

1 Project management

User list of Projects

CREATE PROJECT

- Add user to project
- Modify project
- Delete project

1 Projects > Etienne test ABRomics

2 IMPORT SAMPLES **3 CREATE ANALYSIS** **4 DOWNLOAD CSV** **5 DOWNLOAD XLSX** **6 PUBLISH SAMPLE(S)** **7 DELETE SAMPLE(S)**

Sample ID	Strain ID	Instrument model	Sample type	Host species	Microorganism scientific name	Country	Place	Sampling date format	Sampling date	Sample comment	Permission	Created on	Status	Actions
C_freundii_165	CT165	Illumina MiSeq	human	Blood	Homo sapiens	France		dd/mm/yyyy	2023-12-01			maedi 12 décembre 2023 à 18:08:30		

8 CREATE ANALYSIS FOR CITROBACTER FREUNDII

9 RESULTS

2 Upload data & metadata validation

3 Run analyses

4 Results visualisation

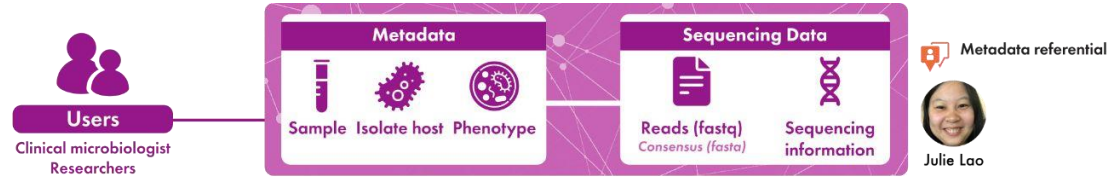
ABRomics database samples location (map visualization)

5 Explore results of the community using the ABRomics database

List of available analysis

- (fastq) AMR detection
- (fastq paired) Trimming, QC, Assembly, Taxonomy, Annotation, AMR detection
- (fastq paired) Trimming, QC, Assembly, Taxonomy, AMR detection
- (fastq paired) Trimming, QC

ABRomics Platform



Web application interface

Romain Dallet

Raphaël Tackx

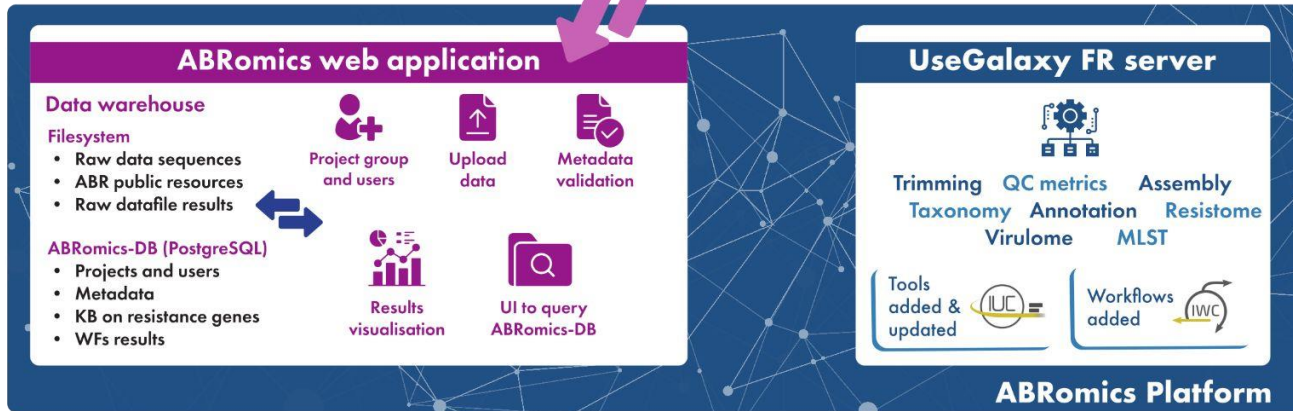
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Database structure

Julie Lao



Galaxy workflows

Pierre Marin

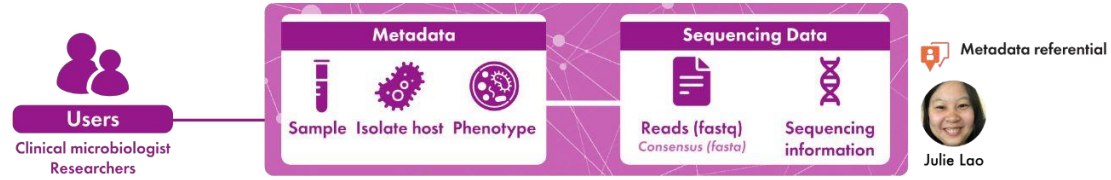
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Hugo Lefevre

ABRomics Platform



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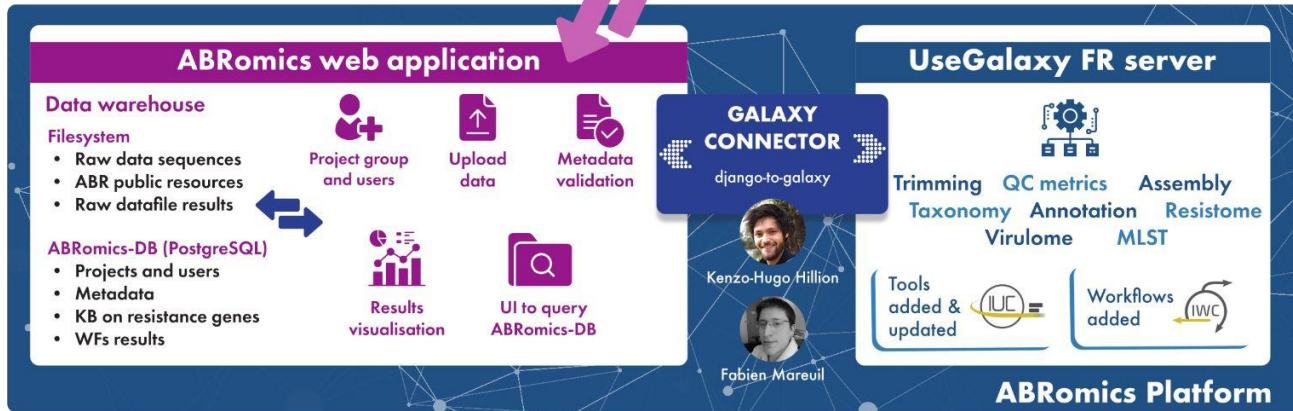
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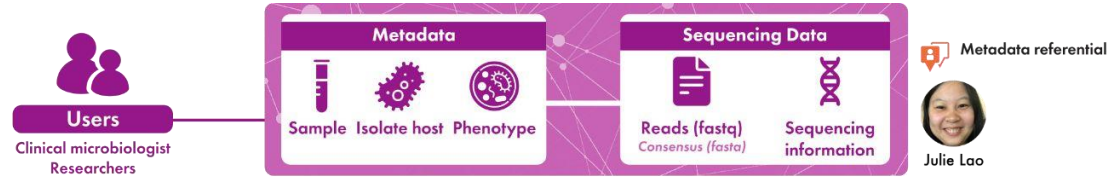
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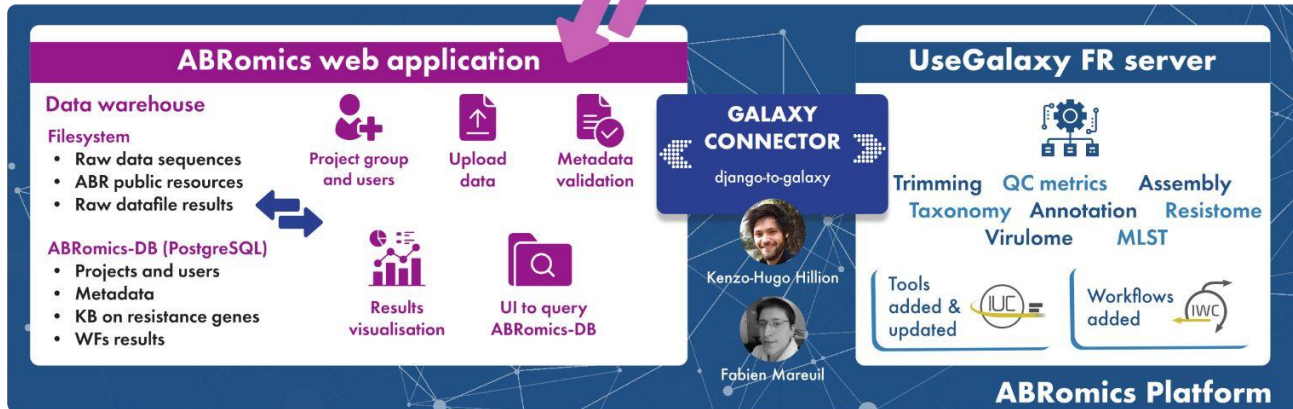
ABRomics Platform



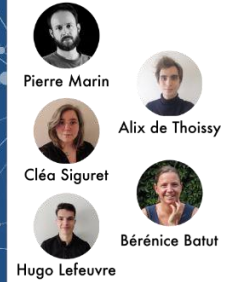
Web application interface



Database structure



Galaxy workflows

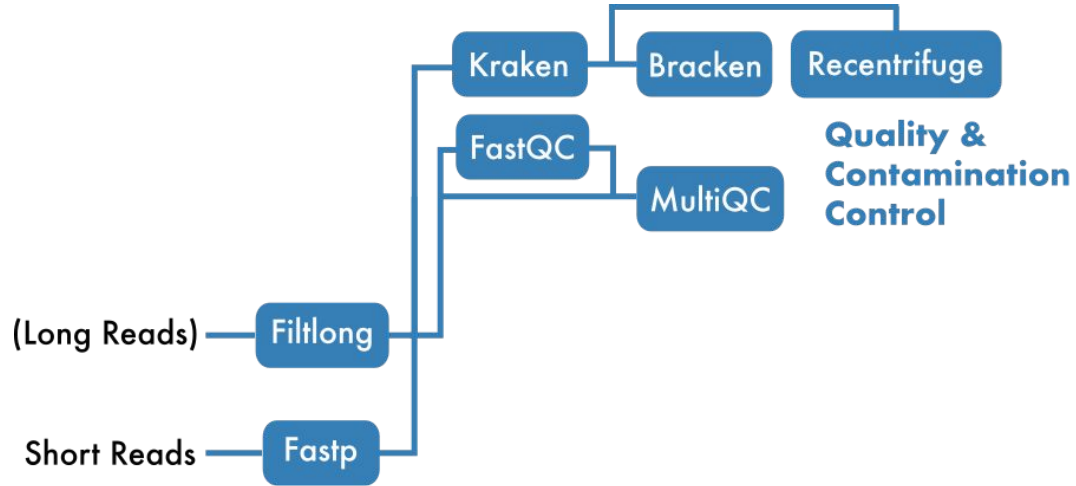


IFB core Cluster

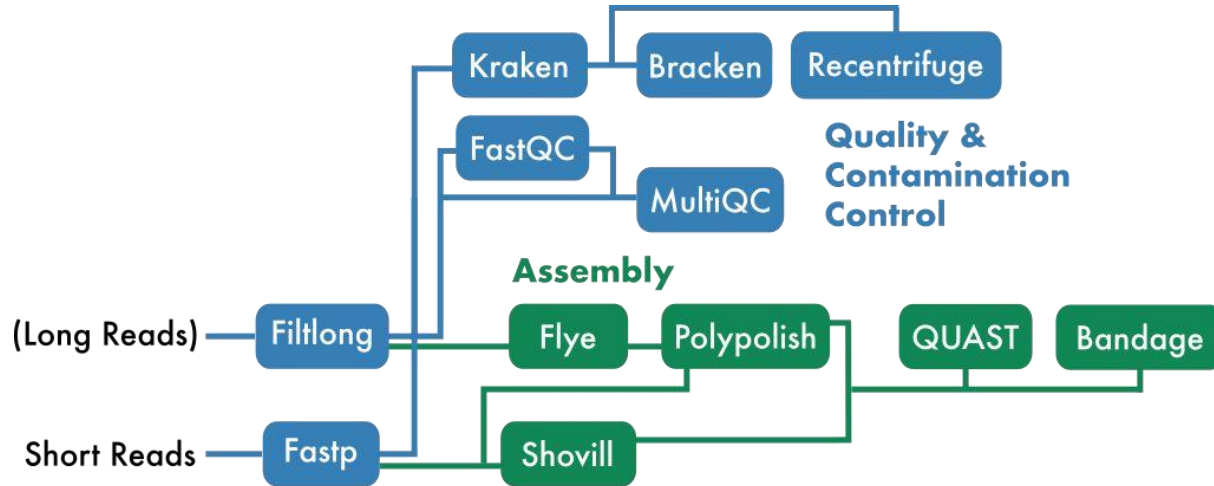


- Shared project space with right access
- Unix access to data/tools

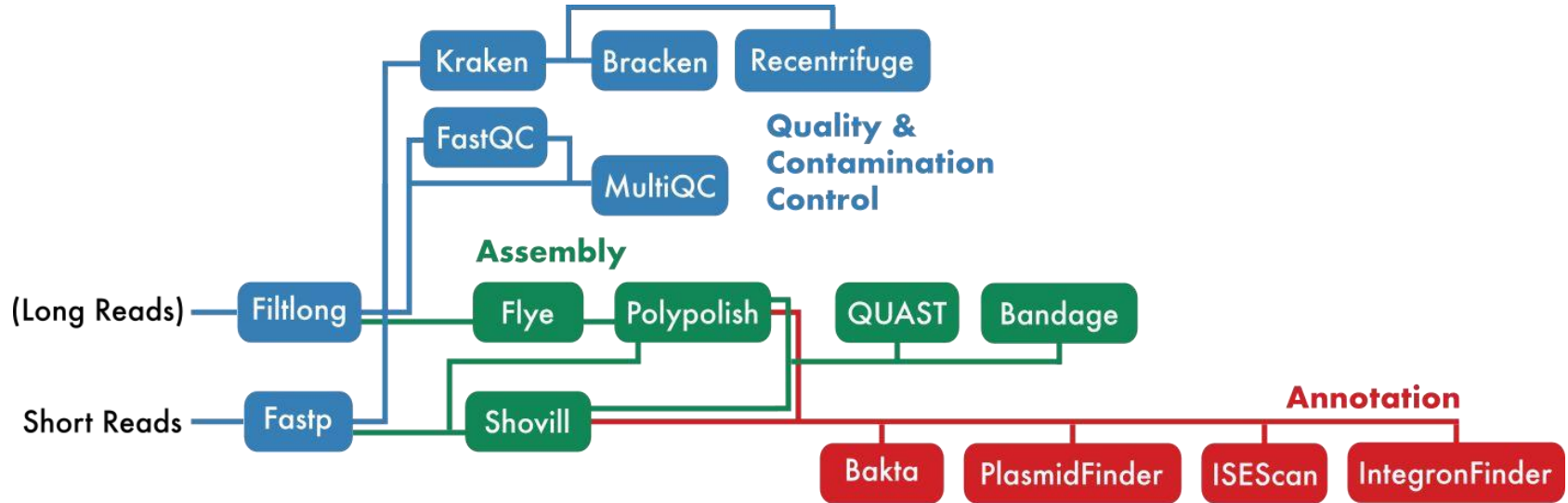
Genomics Workflows



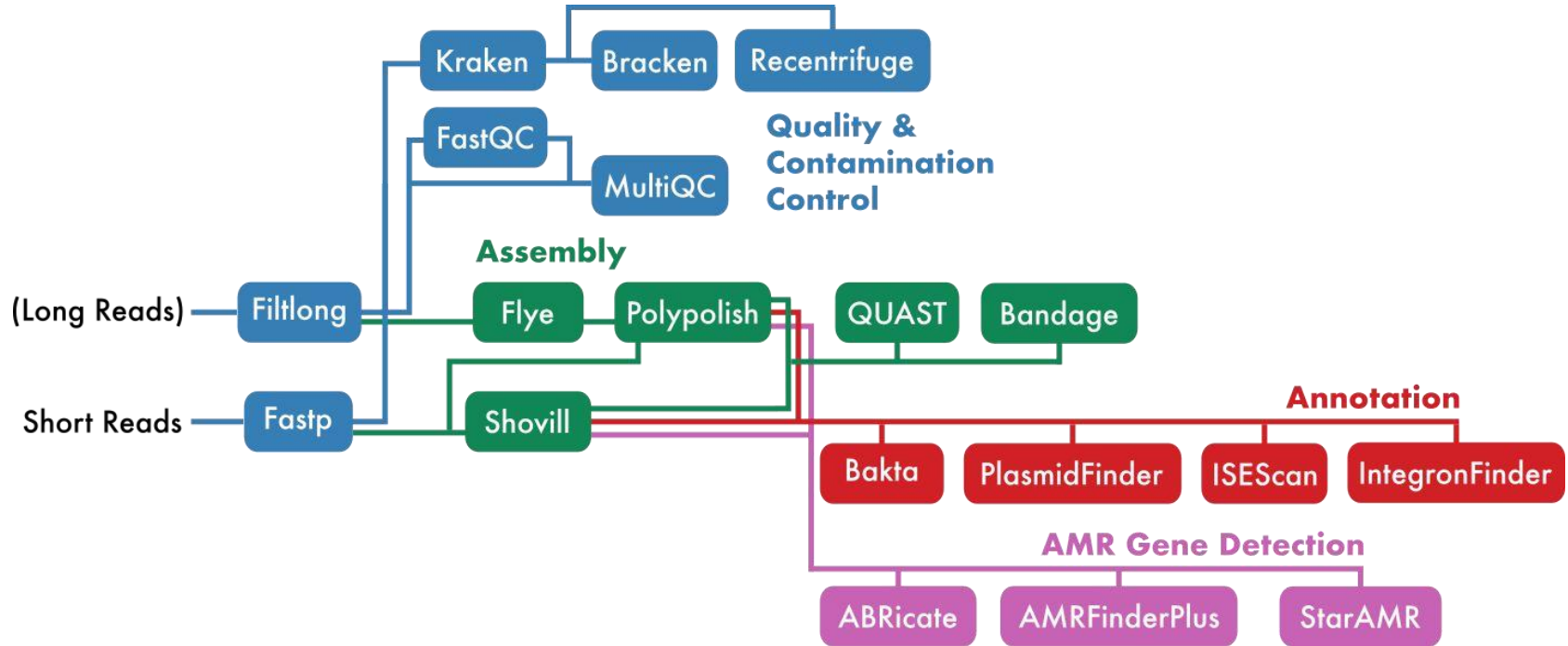
Genomics Workflows



Genomics Workflows



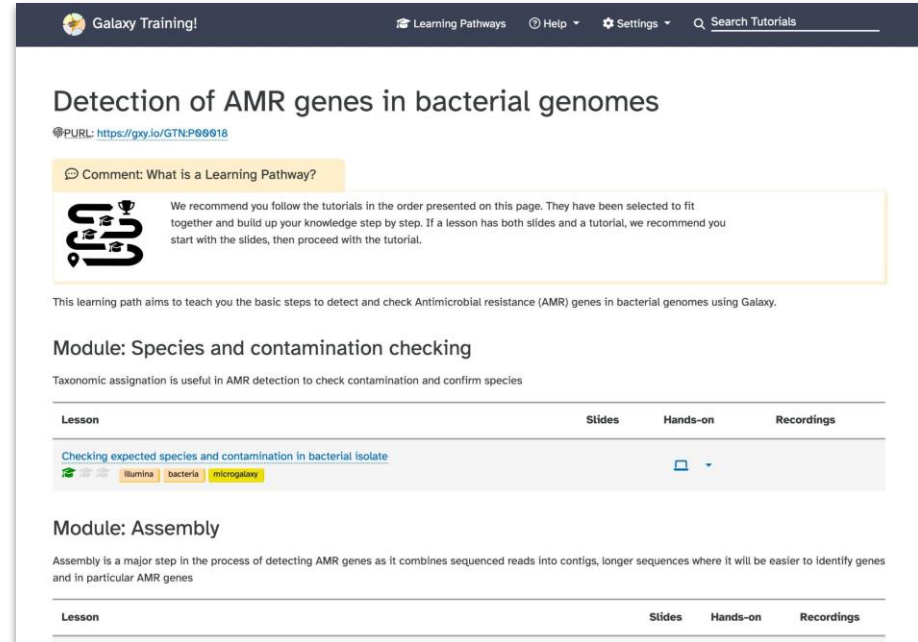
Genomics Workflows



Genomics Workflows

Subworkflows

- Available on WorkflowHub and Dockstore via IWC
- Documented as Learning Pathways on the GTN - <https://gxy.io/GTN:P00018>

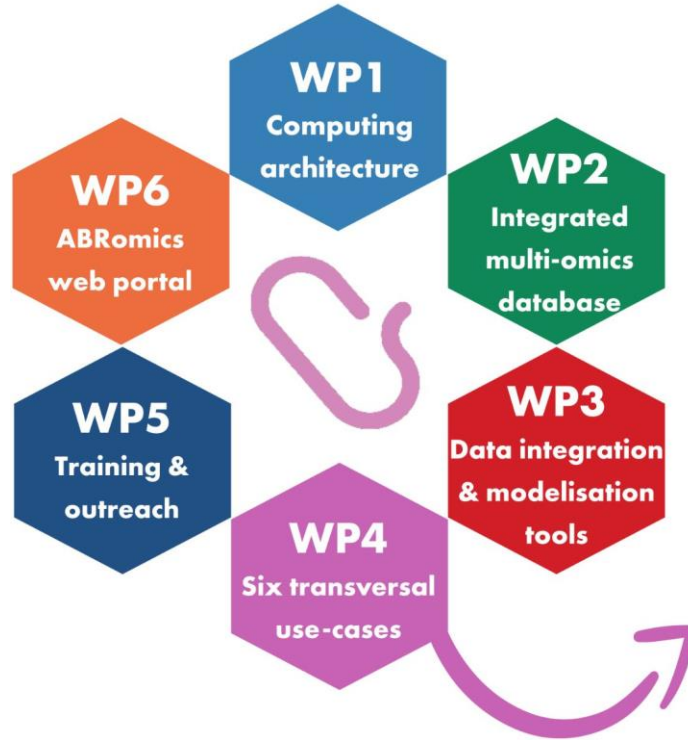


The screenshot displays the Galaxy Training! interface. At the top, there is a navigation bar with 'Galaxy Training!', 'Learning Pathways', 'Help', 'Settings', and a search bar for 'Search Tutorials'. The main content area is titled 'Detection of AMR genes in bacterial genomes' with a PURL: <https://gxy.io/GTN:P00018>. Below the title is a comment box asking 'What is a Learning Pathway?' with a response explaining that the tutorials are recommended to be followed in order. A paragraph below states: 'This learning path aims to teach you the basic steps to detect and check Antimicrobial resistance (AMR) genes in bacterial genomes using Galaxy.' The next section is 'Module: Species and contamination checking', with a sub-heading 'Taxonomic assignment is useful in AMR detection to check contamination and confirm species'. Below this is a table with columns 'Lesson', 'Slides', 'Hands-on', and 'Recordings'. The first row shows a lesson titled 'Checking expected species and contamination in bacterial isolate' with a 'Hands-on' icon. Below the lesson title are tags for 'illumina', 'bacteria', and 'microgalaxy'. The next section is 'Module: Assembly', with a sub-heading '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'. Below this is another table with columns 'Lesson', 'Slides', 'Hands-on', and 'Recordings', but it is mostly empty.

Next Steps

Workflows beyond genomics

- cgMLST
- Metagenomics
- Pangenomics
- Multi-OMICs



- 1** Multidrug resistant bacteria
- 2** One Health approach
- 3** Meta-pan genomics for tracking AMR
- 4** AMR in pulmonary infection
- 5** AMR dissemination through aquatic env.
- 6** Proteomics for AMR phenotyping

Thank You!



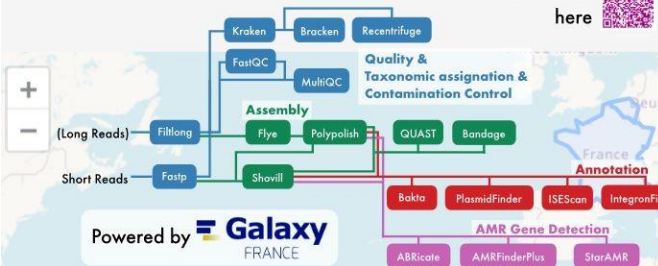
ABRomics
ANTIBIORESISTANCE

The logo for ABRomics, featuring a stylized white icon of a heart or a drop shape to the left of the text. The text "ABRomics" is in a bold, white, sans-serif font, and "ANTIBIORESISTANCE" is in a smaller, white, sans-serif font below it. The logo is centered within a dark blue circular background.

<https://www.abromics.fr/>

From Omics Workflows ...

Workflows here



To Analysis reports ...

The ABRomics Platform features ...

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2 Upload data & metadata validation

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4 Results visualisation

ABRomics database samples location (map visualization)

5 Explore results of the community using the ABRomics database