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The Genotoul-Bioinfo platform

Florent Blaise, Philippe Bordron, Patrice Dehais, Vincent Dominguez, Christine Gaspin, Fabien Graziani, Claire Hoede, Christophe Klopp, Didier Laborie, Céline Noirot, et al.

► To cite this version:

Florent Blaise, Philippe Bordron, Patrice Dehais, Vincent Dominguez, Christine Gaspin, et al.. The Genotoul-Bioinfo platform. JOBIM2025, Jul 2025, Bordeaux, France. ⟨hal-05163782⟩

HAL Id: hal-05163782

<https://hal.science/hal-05163782v1>

Submitted on 15 Jul 2025

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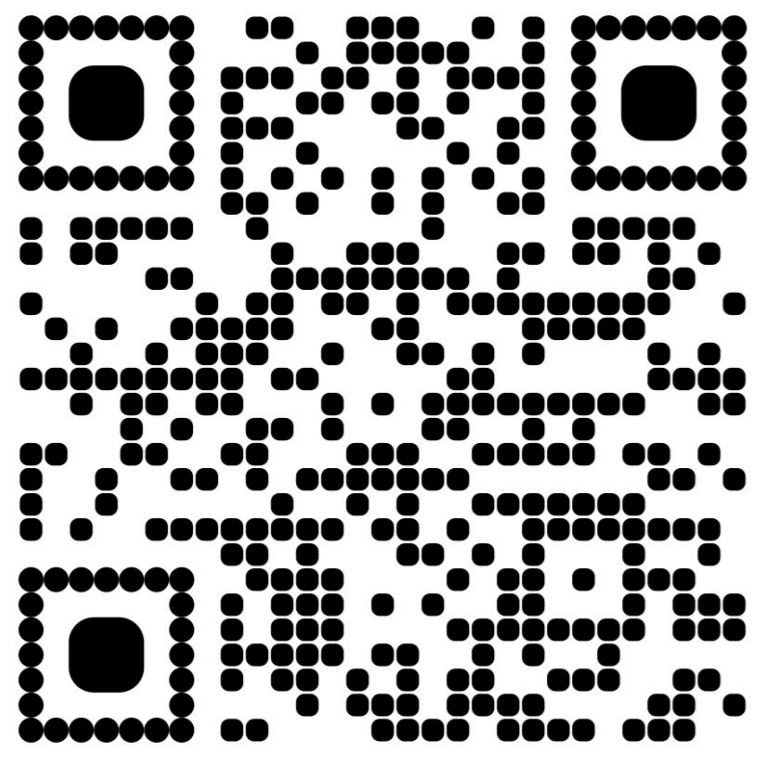


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Corresponding author : matthias.zytnicki@inrae.fr

The Genotoul-Bioinfo platform offers several services in sequencing analysis. The team gathers 17 people with expertise in system administration, bioinformatics, and biostatistics. It is a team of the MIAT lab (INRAE-Toulouse). It is an IBiSA labelled platform, and a strategic platform for INRAE. It is certified ISO 9001 and NF-X 50-900. It belongs to Genotoul, the Research Infrastructure BioinfOmics, and the Institut Français de Bioinformatique.



Website: <https://bioinfo.genotoul.fr/>

Contact: anim.bioinfo-Occitanie-Toulouse@inrae.fr

Check out our other poster!



Our missions

Provide an infrastructure

- 4.5 PB performant storage
- 1.5 PB replicated storage
- 5000 CPUs
- 4 Nvidia A100 80GB GPUs
- > 800 installed software
- ~ 150 data banks
- > 2000 tickets / year

Host GUI tools

- Rstudio
- Jupyter
- Linux desktop

Conduct analyses

- ~ 20 projects, mainly on
- assembly/annotation
- metagenomics
- pangenomics
- transcriptomics
- omics integration

Offer training

- Linux/cluster/Nextflow
- RNA-Seq/variant discovery
- metagenomics
- omics integration
- Awk/Perl/Python
- also at Master level

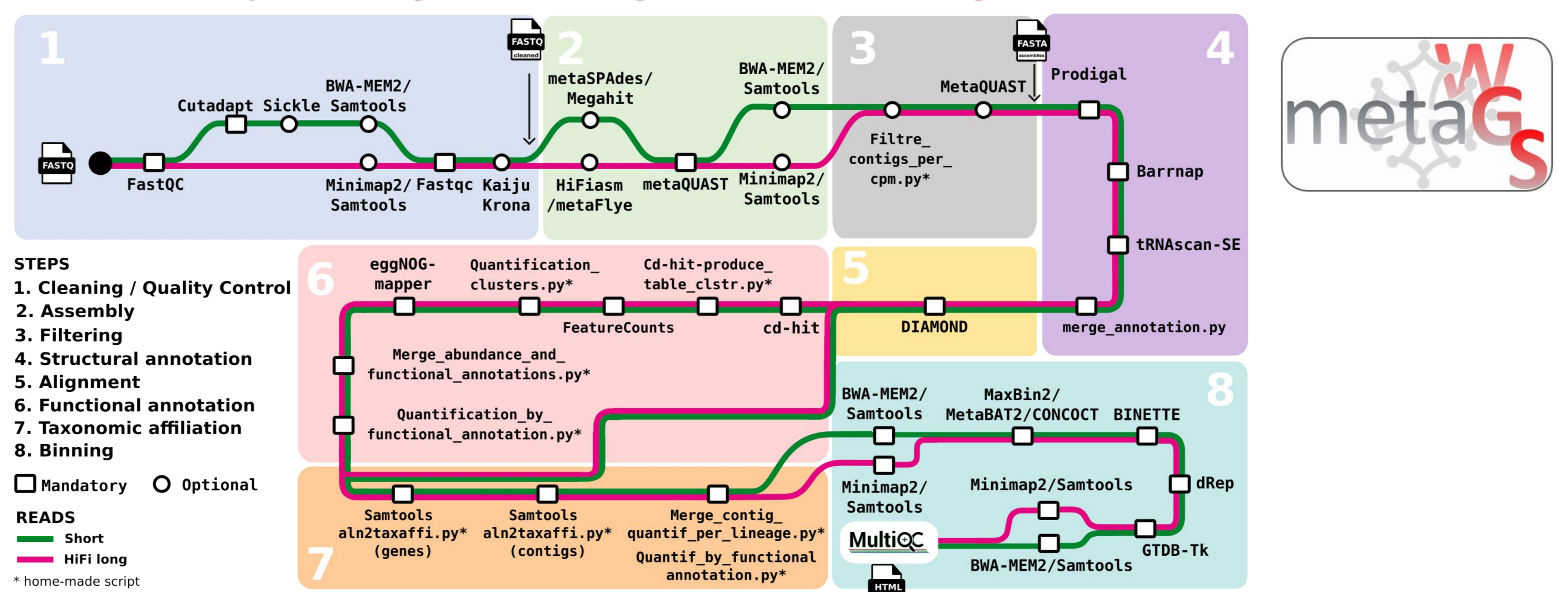
Serve our users

- > 1200 users
- ~50% INRAE, ~50% Region
- > 80 mentions in articles

Drive projects

- Co-leading PEPR
- Co-supervising PhDs
- ~10 articles / year

Analyzing shotgun metagenomics with



<https://forge.inrae.fr/genotoul-bioinfo/metagwgs>

asterics
A tool for the exploration and integration of omics data

ASTERICS is an online tool designed to help you to perform your statistical and integrative analyses in an interactive and easy-to-use way.

<https://asterics.miat.inrae.fr/>

Carbon footprint per CPU.hour

1.98 g CO₂e per CPU.hour

11 g CO₂e per GB per year

