New Migale website

The Migale bioinformatics facility website has been revamped: http://migale.inra.fr. We have made a great effort to make it as user-friendly, ergonomic and efficient as possible. You will find for example:

- fresh news,
- details of the services and resources we offer,
- a searchable list of tools and databases,
- a new FAQ with a focus on the Conda environment,
- access to tutorials on various subjects,
- real-time information on the computational resources.

Do not hesitate to tell us what you like, or not, on this site.

New Galaxy portal

A brand new Galaxy portal is now accessible at galaxy.migale.inra.fr with your Migale account.

We chose to install a new Galaxy instance to follow the best practices recommended by the Galaxy community. This mainly concerns the configuration of the services, the automatic installation of tools and their dependencies (via Bioconda). This should greatly improve the overall stability of Galaxy on Migale.

We have also refined our tool installation policy. In order to make a tool available on the portal, it must meet the following criteria: i) the tool must be available on the Galaxy Toolshed (https://toolshed.g2.bx.psu.edu) and ii) the dependencies must be satisfied in Bioconda (https://bioconda.github.io/search.html). This allows us to ensure that the tool will be easily installed and maintained on the instance. If you don’t know if a tool meets these criteria, don’t panic! You can request the installation and we will check it with you.

We have redefined the list of tools available on the instance and kept those used during our training sessions and those that have been the most used in the recent months. However, if you are missing a tool, you can request it via the dedicated form (http://migale.inra.fr/ask-tool).

By November 18 we will close the access to the old portal (http://migale.jouy.inra.fr/galaxy/). Practically, this means that we are asking all users to transfer their data to this new portal now and no longer use the old one. Below are the key steps for transferring your data:

- sort your data in order to keep only what is strictly necessary,
- extract the histories and workflows you want to keep. See here for a detailed procedure,
- upload your data to the new portal.

Feel free to contact us via help-migale@inra.fr if you have any questions or difficulties.

New Florilège release

Florilège is a database of habitats, phenotypes, and uses of food microbe flora. It aims to gather, in a unified representation, public information on food fermentation microbiota with a focus on positive flora (microorganisms involved in transformation, bioconservation or probiotics).

What’s new in the last Florilège release?

- an update of the data:
  - 673 869 Taxa - Habitat relations (588 752 extracted from PubMed, 64 584 extracted from GenBank, 620 from CIRM BIA, 19 913 from DSMZ),
  - 48 458 Taxa - Phenotype relations extracted from Pubmed,
  - 10 496 Taxa - Use relations,
  - an interface to browse the Ontobiotope ontology,
  - an advanced search allowing a multi-criteria search.

Mouhamadou Ba joined the team

Mouhamadou Ba has just been recruited as a permanent engineer in the Migale platform. He joined the team on October 2019 to develop text-mining services for bioinformatics.

A short self-introduction of Ba:
I did my graduate studies at the University Gaston Berger of Saint-Louis (Senegal) before completing my thesis in computer science at INSA/IRISA in Rennes as part of the SemLIS team in collaboration with the GenOuest platform. My thesis, which I defended in December 2015, focused on the guided composition of data analysis workflows with a bioinformatics application. After the thesis, I did 4 years of Post-Doc at INRA (MaAGE-Bibliome team) where I worked on methods and infrastructures for text and data mining. Since October 2019, I am Research Engineer at INRA to work on the construction of a text mining service within the Migale platform in collaboration with the MaAGE-Bibliome team.

Last publications


Research teams that have used Migale services must thank the Migale bioinformatics facility in the publications of their analyses with the following text:

« We are grateful to the INRA MIGALE bioinformatics facility (MIGALE, INRA, 2018. Migale bioinformatics Facility, doi: 10.15454/1.55723906555432393E12) for providing help and/or computing and/or storage resources. »