

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 available on 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 Florilege release

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

Last publications

- **Nguyen L**, Brun V, Combes F, **Loux V**, Vandenbrouck Y: Designing an In Silico Strategy to Select Tissue-Leakage Biomarkers Using the Galaxy Framework. *Methods Mol. Biol.* 2019, 1959:275–289.
- Vandenbrouck Y, **Christiany D**, Combes F, **Loux V**, Brun V: Bioinformatics Tools and Workflow to Select Blood Biomarkers for Early Cancer Diagnosis: An Application to Pancreatic Cancer. *Proteomics* 2019:1800489.
- Dugat-Bony E, Bonnarme P, Fraud S, Catellote J, Sarthou A-S, **Loux V**, **Rué O**, Bel N, Chuzeville S, Helinck S: Effect of sodium chloride reduction or partial substitution with potassium chloride on the microbiological, biochemical and sensory characteristics of semi-hard and soft cheeses. *Food Res. Int.* 2019, 125:108643.
- H. Falentin, L. Auer, **M. Mariadassou**, G. Pascal, **O. Rué**, E. Dugat-Bony, C. Delbès, A. Nicolas, E. Rifa, S. Mondy, M. Le Boulch, L. Cauquil, G. Hernandez-Raquet, S. Terrat, A.-L. Abraham (2019). Guide pratique à destination des biologistes, bioinformaticiens et statisticiens qui souhaitent s'initier aux analyses métabarcoding. Le cahier des techniques de l'Inra, vol 97.

Research teams that have used Migale services must thank the Migale bioinformatics facility in the publications of their analyses with the following sentence: « We are grateful to the INRA MIGALE bioinformatics facility (MIGALE, INRA, 2018. Migale bioinformatics Facility, doi: 10.15454/1.5572390655343293E12) for providing help and/or computing and/or storage resources ».

What's new in the last Florilege 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.



Paris Diderot university proposes in partnership with the Institut Français de Bioinformatique (IFB) the second edition of the Diplôme Universitaire en Bioinformatique intégrative (DU-Bii). This training is intended in priority to biologists looking for professional evolution or retraining, having already acquired some competences (short course, self-training, field experience) in computer science or bioinformatics/biostatistics (Unix environment, Python or R or another programming language).

The DU-Bii will bring a theoretical and practical training, followed by an immersion time in one of the IFB regional platforms which will mobilize, through a tutored project, the overall methods and tools learned during the courses to fulfill an integrative bioinformatics personal project. This project will combine data produced in the laboratory of each participant (BYOD : "bring your own data" principle) or collected from public databases.

Applications for the 2nd DU-Bii edition (courses: march 2020, tutored project: 4 weeks between april and middle-june 2020) are now over.

If you are interested for applying to the 3rd 2021 DU-Bii session, you can contact helene.chiapello@inra.fr and your local Inra center training service to ask for possibilities regarding financial support.

Complementary to its training offer, Migale is heavily involved in the DU-Bii as teachers in the Unix, Python, data production and data analyses modules, but also as a place where students can perform their tutored projects.

More information: [website](#)

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 (MaIAGE-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 MaIAGE-Bibliome team.