

2025 Activity Report

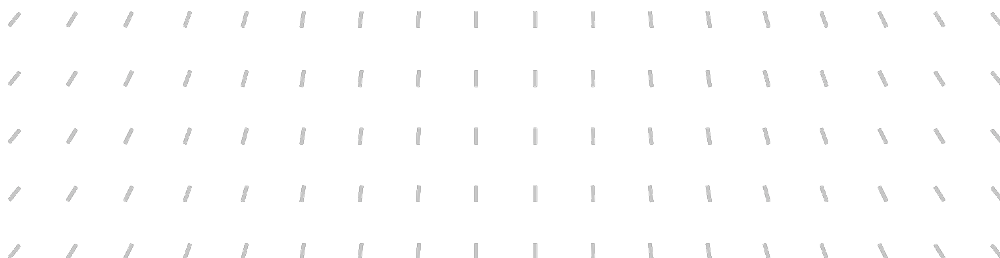
RESEARCH CENTRE: Inria Centre at the University of Bordeaux
IN PARTNERSHIP WITH: CNRS, INRAE

Project-Team

PLEIADE

Patterns of diversity and networks of function

In collaboration with Laboratoire Bordelais de Recherche en Informatique (LaBRI),
Biodiversité, Gènes & Communautés (BioGeCo)



Project-Team PLEIADE

Creation of the Project-Team: 2019 March 01

Each year, Inria research teams publish an Activity Report presenting their work and results over the reporting period. These reports follow a common structure, with some optional sections depending on the specific team. They typically begin by outlining the overall objectives and research programme, including the main research themes, goals, and methodological approaches. They also describe the application domains targeted by the team, highlighting the scientific or societal contexts in which their work is situated. The reports then present the highlights of the year, covering major scientific achievements, software developments, or teaching contributions. When relevant, they include sections on software, platforms, and open data, detailing the tools developed and how they are shared. A substantial part is dedicated to new results, where scientific contributions are described in detail, often with subsections specifying participants and associated keywords. Finally, the Activity Report addresses funding, contracts, partnerships, and collaborations at various levels, from industrial agreements to international cooperations. It also covers dissemination and teaching activities, such as participation in scientific events, outreach, and supervision. The document concludes with a presentation of scientific production, including major publications and those produced during the year.

Keywords

Computer sciences and digital sciences

- A3.1. – Data
 - A3.1.1. – Modeling, representation
- A3.2. – Knowledge
 - A3.3.2. – Data mining
 - A3.3.3. – Big data analysis
- A3.4. – Machine learning and statistics
- A6.1. – Methods in mathematical modeling
 - A6.2.3. – Probabilistic methods
- A8.2. – Optimization
- A9.8. – Reasoning

Other research topics and application domains

- B1.1.4. – Genetics and genomics
- B1.1.7. – Bioinformatics
- B1.1.10. – Systems and synthetic biology
- B2. – Digital health
- B3. – Environment and planet
 - B3.6. – Ecology
 - B3.6.1. – Biodiversity

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1 Team members, visitors, external collaborators

Research Scientists

- David Sherman [Team leader, INRIA, Senior Researcher, HDR]
- Olivia Bulka [INRIA, Starting Research Position, from Oct 2025]
- Clemence Frioux [INRIA, Researcher]
- Pritam Kundu [INRIA, Starting Research Position, from Nov 2025]
- Simon Labarthe [INRAE, Senior Researcher]
- Guilhem Sommeria-Klein [INRIA, Researcher]

Post-Doctoral Fellows

- Paola Fournier [INRAE, Post-Doctoral Fellow]
- Felix Roy [INRAE, Post-Doctoral Fellow, from Mar 2025]
- Camille Saint-Martin [INRIA, Post-Doctoral Fellow, from Oct 2025]

PhD Students

- Chabname Ghassemi Nadjad [UNIV BORDEAUX]
- Coralie Muller [INRIA]
- Mathilde Sola [INRAE]
- Emna Stambouli [INRIA, from May 2025]
- Sthyve Tatho [INRAE]

Technical Staff

- Leonard Brindel [INRIA, Engineer, until Sep 2025]
- Alioune Badara Diouf [INRIA, Engineer, from Nov 2025]
- Jean-Marc Frigerio [INRAE, Engineer]
- Isabelle Kupin [INRIA, Engineer, from Sep 2025]
- Franck Salin [INRAE, Engineer]

Interns and Apprentices

- Juliette Audemard [INRIA, Apprentice, until Sep 2025]
- Eliot Bois [Collège Saint Selve, Intern]
- Alioune Badara Diouf [INRAE, Intern, from Mar 2025 until Aug 2025]
- Killian Dugueperoux [ENS de Lyon, Intern, from Jun 2025 until Jul 2025]
- Youssef Ikrou [Collège Henri Brisson, Intern]

Administrative Assistants

- Flavie Blondel [INRIA]
- Anne-Laure Gautier [INRIA]

Visiting Scientist

- Chandler Ross [Univ Turku, from Apr 2025 until Jun 2025]

External Collaborators

- Alain Franc [INRAE, from May 2025, HDR]
- Alain Franc [INRAE, until Apr 2025, HDR]

2 Overall objectives

Digital microbial ecology studies communities of microorganisms in delimited ecosystems, who interact notably through the production and consumption of metabolic goods. These interactions define *complex behaviors* that are much more than the sum of the individual behaviors of the community members, and arise from cooperation and competition between a diversity of organisms providing a diversity of beneficial and harmful functions.

Pleiade is an interdisciplinary Inria-INRAE research team that combines computer science, mathematical modelling, bioinformatics and ecological theory to address microbial ecology questions and challenges. Our research is motivated by the need for computational and numerical models that integrate large-scale biological data and provide hypotheses about the organisation, dynamics and function of microbial communities. Pleiade builds high-fidelity and high-performance methodological tools for digital microbial ecology.

We are interested in **microbial communities** of all sizes, from small-scale experimentally controlled consortia to the large-scale microbiomes found in the environment. Our application fields include host-associated microbiomes, found in the mammalian gut or the plant phyllosphere; and environmental microbial ecosystems, found in soil and the ocean. We ask:

- How can we obtain **simplified representations** of microbial communities that are robust, interpretable and actionable?
- How can we **reconcile the variability** of microbiome composition with their **functional stability**?
- How can we **decipher microbial interactions** and link them to the **community structure and function**?
- What are the **spatial and temporal dynamics** of microbial communities and how are they affected by microbe dispersal?

Pleiade maintains strong collaborative relations with experimental biologists and field ecologists, and is committed to facilitating their adoption of our research, through development of reusable software, reproducible workflows that run on distributed computing platforms, and FAIR open data sets.

3 Research program

Our research program tackles methodological developments that seek to characterize functional and taxonomic diversity in microbial communities.

3.1 Metabolic models of microbial communities

Metabolic models are computational abstractions of an organism's metabolic activity, related to the transformation of molecules, or metabolites, through biochemical reactions. Some reactions are performed spontaneously, but the most are induced by enzymes associated with gene sequences embedded in microorganisms genomes. The collection of all reactions associated with an organism is called a *genome-scale metabolic network* (GSMN). The first step of metabolic modelling is to obtain such a GSMN, for instance *de novo* by relying on gene annotations [6]. Then we design, develop, and apply computational and mathematical models whose simulations predict the behaviour of (micro)organisms under defined conditions. Metabolic models can predict the growth of organisms, interactions within a community, nutritional needs, and more. Pleiade uses two main families of models as described below.

Numerical models of metabolism: We use constraint-based modelling, such as *flux balance analysis* to decipher the roles of microbes and the interactions between them, and model their dynamics [12, 81].

Knowledge representation and reasoning: We abstract metabolism using discrete models and solve combinatorial problems in order to propose mechanistic hypotheses about large scale microbial communities. [21] [4]

3.2 Statistical learning of microbial community structure and function

Natural microbial communities, associated with a host or an environment, are called *microbiotas* [76]. They consist of populations of hundreds or thousands of microbes. We use the word *microbiome* to define these populations, their genomes and their theatre of activity (environment, abiotic conditions...). Considering such a large microbial populations and the inherent interindividual variability observed between samples, the task of identifying common patterns in large cohorts (typically 10^2 to 10^4 samples) is both a theoretical and a computational challenge. There is thus a huge interest in reducing the dimension of data in order to highlight the main compositional signatures in the taxonomic diversity, or the important functional signatures when considering the whole collection of genes in microbiomes, referred to as the *metagenome*. Pleiade uses statistical learning to perform this task. We also use statistical learning to alleviate the computational cost of simulation when building complex numerical models of microbial community metabolism.

Dimensionality reduction: We identify microbial guilds and functional groups as latent structures in the composition of microbiomes. [8] [79] [16]

Surrogate models of metabolism: We learn the behaviour of microbes from constraint-based models in order to reduce the computational cost of complex simulations. [10]

3.3 Probabilistic modeling of microbial communities in space and time

High-throughput sequencing offers considerable potential for a better understanding of how and why naturally-occurring microbial communities vary in space and time, yet this potential is still largely untapped due to a lack of models based on **ecological processes** and amenable to **quantitative statistical inference**. Such a modelling framework can be built by bringing together models from different fields thanks to probabilistic modelling and Bayesian inference. We apply this approach to spatial, time-series and tree-structured data from different microbial ecosystems, namely soil, gut microbiota, and ocean plankton. Through these different applications, we strive to address three general questions: 1) At what scales do communities vary in space and time; 2) What ecological processes shape community assembly, and in particular what is the relative role of *dispersal limitation* and *local selection*; and 3) What is the link between community composition and function?

Dynamics across timescales: We model the dynamics of microbial communities from ecological to evolutionary timescales. [51] [14] [78]

Modeling spatial distribution: We model the spatial distribution of microbial communities and how it is jointly shaped by environment and dispersal. [16] [82] [17] [24]

3.4 Metagenomic bioinformatics for microbiomes

The *metagenome* refers to the collection of genetic sequences associated with a microbial community. It is detected using DNA sequencing, which produces 10^6 – 10^9 small DNA sequences called *reads* that must be assembled to reconstruct the original microorganism genomes. Most metagenomic data is made of short reads (150 base pairs), but more recent technologies tend to provide reads of larger lengths, which facilitates the subsequent assembly process.

We explore metagenomic data to try to improve the characterisation of complex microbiomes. We survey the wealth of metagenomes sequenced on biomes of interest to compare individual ecosystems, and we also develop methods and algorithms to enhance the reconstruction of *metagenome-assembled genomes* (MAGs). [23] [18] [47]

3.5 Towards digital twins of microbial communities

Microbial systems are a very suitable model for developing digital twins: 1) defined simplified communities (known as SynCom) can be easily assembled and studied in controlled experimental setups; 2) a large variety of -omics data can be produced to screen their dynamics; 3) advanced bioinformatic, machine learning or statistical analysis tools can be deployed to extract informative features from the data; 4) several methodological frameworks can be leveraged to build digital models and fit them; 5) control engineering methods can be applied to articulate model predictions and actionable commands; 6) microbial engineering techniques can be used to implement these commands into the microbial systems to steer the microbial community.

While all of these six bricks muster dedicated research communities, whose intensive research effort continuously enhances their accuracy and speed, an interdisciplinary challenge persists: effectively articulating these modules to close the feedback loop that defines digital twins.

Building digital twins of microbial communities. In the *Artemis Consortium*, an interdisciplinary network gathering experimentalists, bioinformaticians and mathematicians, we work on conceptualising the methodological gaps to fill in order to build digital twins of microbial systems.

4 Application domains

4.1 Plant microbiome

Objectives Microorganisms are associated with all tissues of plants: the *rhizosphere* is the microbiome associated to roots, the *phyllosphere* associates to leaves, and there are also microbes inside the plants [84]. Plant-associated microbiomes provide fitness advantages to their plant host, provide key steps of carbon and potassium cycles, and can promote plant health through direct barrier effect against pathogens or modulations of plant immunity. Understanding these mechanisms is of the utmost interest in agriculture and agro-ecology, particularly with the global objectives of reducing the use of pesticides and other harmful chemical inputs in cultures.

Strategy We partner with experimental biologists to study and model the microbiome of plants in order to understand the taxonomic structure and functional diversity of plant microbiomes. We are particularly interested in plant health and microbial-derived protection of crop plants against harmful pathogens, such as mildew in vine and tomato, or seed pests. We develop data-driven research by gathering large datasets of plant microbiomes to detect specific microbial signatures of health and disease. These signatures can be used for epidemiosurveillance of crops as an early biomarker of disease to provide a management tool in a precision agriculture context. We also develop advanced modeling tools to identify microbial interactions involved in barrier effects against pathogen or in plant immune system elicitation.

Partners Our main historical partner is the team of *Corinne Vacher* and other members of the *INRAE SAVE lab* in Bordeaux (France): collaborations with SAVE has been launched in the PPR CPA project VITae, and are now continued in the PARSADA GetUP project, the INRAE SPE MicroSentry and the ANR

“Grand Défi Biocontrôle” Durabics project. Another structuring project for plant microbiome is the PEPR “Agroécologie Numérique” Mystic project, uniting the Pleiade, Genscale and Maches Inria teams, and the ISA, BioGeCo, SAVE, BFP, and Agroécologie labs at INRAE. Mystic helped us develop new collaborations with INRAE labs: IGEEP (Rennes), IRHS (Angers), Pathologie Végétale (Avignon), and EABX (Bordeaux).

4.2 Soil microbiome

Objectives Microbial communities found in soils are the most diverse of naturally-occurring microbial communities and are key to the productivity of terrestrial ecosystems through the recycling of plant organic matter. Their activity also controls the storage of carbon in the ground, and thus needs to be accounted for in climate modelling. Because of their diversity and heterogeneity, soil microbial communities are among the least understood. In particular, the links between their taxonomic composition, the molecular functions they perform, and soil physical and chemical characteristics remain poorly understood and difficult to model and predict. It also remains unclear at what spatial scales these communities vary, and to what extent processes other than local environmental selection, such as limits to dispersal, play a role in their formation.

Strategy We develop a spatially explicit Bayesian modeling framework capable of integrating large volumes of metagenomic data and based on previous work on dimensionality reduction approaches. We aim ultimately at predicting soil functional potential at the European or global scale, based on the relative abundance of a limited number of functional profiles, with the longer-term perspective of contributing to the modelling of the microbial compartment in climate models.

Partners Microflora Danica consortium, University of Aalborg (Mads Albertsen, Prof.). Laboratoire de Sciences du Climat et de l’Environnement (LSCE, Saclay), ERC GAMEChange (Elsa Abs, CNRS).

4.3 Human gut microbiome

Objectives Human intestines host hundreds to thousands of microbial populations. The human gut microbiome is established at birth and reaches a stable but dynamic equilibrium in adulthood. Microorganisms provide many services to the human host, ranging from providing important nutrients to supporting the immune system. Perturbations of gut microbiome have been associated with disease [77]. Mechanisms of association between the gut microbiome, diet, health, disease and lifestyle are not yet understood, inspiring research in this area.

Strategy A non-invasive means of studying the human gut microbiome is through the DNA sequencing of fecal metagenomic samples. In the team, we rely on publicly-available metagenomes but we are also associated with large consortia that generate data for large cohorts of individuals.

Partners We work with the [Quadram Institute](#) and [Earlham Institute](#) in Norwich (UK), especially the teams of Falk Hildebrand and Christopher Quince. We also work closely with INRAE partners of the [MetaGenoPolis](#) lab in Jouy-en-Josas (France), notably on [Le French Gut](#) project. Finally, we collaborate with members of the [FINRISK](#) project consortium, such as [Leo Lahti’s lab](#) in Turku (Finland) and [Katariina Pärnänen](#) in Helsinki (Finland).

4.4 Animal rumen

Objectives The rumen microbiome of cattle plays an important role in the digestion of feed and the well-being of animals, and has been associated with their emission of the greenhouse gas **methane** [80, 83]. Understanding the role of microbes in this organ is therefore of interest for agricultural practices but also for agro-ecology perspectives.

Strategy The rumen microbiome of cattle has been deeply sequenced over the past decade, generating large collections of metagenomes and MAGs than can be studied through a metabolic lens to understand methane production mechanisms and suggest mitigation strategies.

Partners Pleiade works with INRAE partners in Saclay (France) - [MOSAR UMR](#) with Rafael Muñoz-Tamayo lab - and Clermont-Ferrand (France) - [UMRH](#) Milka Popova’s team - who build models and perform wet lab experimentations. Together, we combine microbiology and models in a systems biology strategy.

4.5 Microbial bioprocesses in agrifood chain

Objectives Microbial community functions have long been used in product transformation processes in agrifood chain. Dedicated microbial communities are used in food production to transform raw materials into improved components: microbial bioprocesses can be used to enhance food preservation, improve organoleptic quality or to provide health benefit in milk (yogurt, cheese, kefir...), vegetables (alcoholic beverages, pickles, kefir, kombucha...) or meat-derived foods (ham, sausages...). At the other side of the agrifood chain, microbial communities are used to digest organic waste and unused biomass into high value compounds (e.g. methane or amino-acids) or to depollute waters and soils. Microbial communities are consequently central to environmental challenges such as reducing food spoilage, enhancing biomass value or improving waste treatment.

Strategy We partner with several INRAE teams specialized in food or bioprocesses microbiology. In food microbiology, accurate models of microbial metabolism are key to deciphering microbial interactions involved in biotransformation of raw materials into fermented food. In environmental microbiology, we couple community-scale kinetic models of large metabolic pathways with genome-scale metabolic models of microbial individuals involved in key steps of the bioprocess, placing a particular emphasis on coupling thermodynamics with metabolic models.

Partners We developed different partnerships with INRAE labs involved in food microbiology: in the TANGO project, funded by the CNIEL, we collaborated with the STLO unit (Rennes). In the Holovini project (funded by INRAE Holoflux metaprogram), we partner with the SPO unit (Montpellier) and the ISVV (Bordeaux) to focus on the fate of fermentative yeasts in the field and the cellar. For environmental microbiology, a PhD project is co-supervised with the LBE unit (Narbonne), funded by INRAE.

5 Social and environmental responsibility

5.1 Promoting equality and diversity in science

Promoting inclusion and diversity in science is essential at all levels: when planning science during project conception, when executing science and publishing its results, and also within the community of scientists itself. Members of Pleiade are involved in promoting the place of women in science through the participation in outreach activities, but also by committing to working groups and committees on the subject at the local and national level.

- Clémence Frioux – member of the Inria national committee for equality and inclusion
- Clémence Frioux, Coralie Muller – members of the gender equality and diversity working group in the Inria Centre at the University of Bordeaux
- Clémence Frioux – participation as a teacher to “MIMM, moi informaticienne, moi mathématicienne” 2025, a free internship at the University of Bordeaux for young girls in 9th and 10th grade in order to encourage them to choose mathematics and computer science, allowing them to discover training, research and jobs in these two disciplines.

5.2 Impact of research results

Many of Pleiade’s projects are specifically designed to have a positive impact on the environment:

- Olympus §10.3.11 aims at reducing atmospheric carbon by improving permanent underground carbon storage.
- H2Rumen §10.3.4 aims at reducing greenhouse gases by reducing methane production by ruminants.
- MISTIC §10.3.1 aims at helping agriculture adapt crops to global warming. Both MISTIC and GETUP §10.3.10 promote *biocontrol* as an alternative to pesticides for crop health with a smaller impact on the environment.

6 Highlights of the year

Defenses

In December 2025, **Chabname Ghassemi Nedjad defended her PhD** entitled “Modelling and solving combinatorial optimisation problems for reverse ecology” [44]. In September, **Clémence Frioux defended her HDR** entitled “Machine reasoning, dimensionality reduction, and numerical modelling for exploring microbial community metabolism” [43].

New arrivals in the team and human resources

2025 was a prolific year for scientific recruitment in Pleiade. **Emna Stambouli was hired as a PhD student**, working on modelling soil bacterial community functions at large spatial scale using dimensionality reduction. **Five postdoctoral fellows and starting researchers** were also recruited. **Olivia Bulka** was hired as part of the INRAE EXPLORAE-funded project TARGET and is working on metabolic modelling to facilitate the growth of uncultivable phytopathogens. **Paola Fournier** was hired as part of the Nouvelle Aquitaine region funded MicroMod project, and is working on dimensionality reduction of metabarcoding data. **Pritam Kundu** was hired as part of the ANR-funded project H2Rumen, and is working on metabolic modelling of the rumen microbiome for methane production reduction. **Felix Roy** was hired as part of the VITAE project and is working on inferring ecological interactions from time series of microbial population dynamics. **Camille Saint-Martin** was hired as part of a public partnership between Inria and IFPEN and is working on numerical and metabolic modelling of microbial communities for geological CO₂ storage. In addition, two engineers were hired: **Isabelle Kupin** hired as part of the MISTIC project, and **Alioune Badara Diouf** as part of the GET-UP project. Finally, **Simon Labarthe** promoted to research director at INRAE since January 2025.

Scientific highlights

The recruitment of Guilhem Sommeria-Klein in 2024 sparked growth towards **microbial ecology** within the team, with Emna Stambouli’s PhD in the environmental sciences doctoral school (École Doctorale Sciences et Environnement, EDSE) and Guilhem’s participation in a sampling campaign in Finland on the islands of the Turku archipelago.

Another notable highlight is the involvement of Inria, initiated by the Pleiade team, in the scientific consortium of the **Le French Gut** project. This initiative aims to study the relationships between diet, lifestyle, and health and the gut microbiome in the French population, with an expected recruitment of 100,000 participants in this citizen science endeavour.

Alain Franc, former member of the team published his book “Linear Dimensionality Reduction” [42] in Springer Nature’s Lecture Notes in Statistics (LNS, volume 228) .

Significant journal article publications include the work of Constanza Andreani et al. in *Environmental Microbiome* as part of the Inria Associated Team SymBioDiversity that ended in 2024 [18]. A large part of Chabname Ghassemi Nedjad’s work was published in *Bioinformatics* [21]. Finally, several members of the team participated to the work of Beliaro et al., published as a preprint and providing metagenomic sequencing and assembly recommendations for complex microbiome samples [47].

Several members of the team organised the French Bioinformatics conference, **JOBIM 2025**. Clémence Frioux and Simon Labarthe were co-leads of the organisation committee.

Finally, several major scientific projects for the team started this year. Among them, *INRAE EXPLORAE’s funded project TARGET* aims at combining systems biology, computational biology, genetic engineering, culturomics and microfluidics to facilitate the culture of uncultivable bacteria, particularly targeting a phytoplasma impacting grapevine culture. *GET-UP project, funded by PARSADA*, aims to develop alternative strategies to combat grapevine downy mildew, drawing on both biocontrol approaches and conservation-based methods.

Awards

Juliette Audemard obtained the best talk award at the French Bioinformatics conference, JOBIM 2025, for her work entitled “Metagenome-scale metabolic modelling for the characterization of cross-feeding interactions in freshwater cyanobacteria-associated microbial communities” [28]

7 Latest software developments, platforms, open data

7.1 Latest software developments

7.1.1 Metage2Metabo

Keywords: Metabolic networks, Microbiota, Metagenomics, Workflow

Scientific Description: Flexible pipeline for the metabolic screening of large scale microbial communities described by reference genomes or metagenome-assembled genomes. The pipeline comprises several main steps. (1) Automatic and parallel reconstruction of metabolic networks. (2) Computation of individual metabolic potentials (3) Computation of collective metabolic potential (4) Calculation of the cooperation potential described as the set of metabolites producible by species only in a cooperative context (5) Computation of minimal-sized communities satisfying a metabolic objective (6) Extraction of key species (essential and alternative symbionts) associated to a metabolic function

Functional Description: Metabolic networks are graphs which nodes are compounds and edges are biochemical reactions. To study the metabolic capabilities of microbiota, Metage2Metabo uses multiprocessing to reconstruct metabolic networks at large-scale. The individual and collective metabolic capabilities (number of compounds producible) are computed and compared. From these comparisons, a set of compounds only producible by the community is created. These newly producible compounds are used to find minimal communities that can produce them. From these communities, the keystone species in the production of these compounds are identified.

URL: <https://github.com/AuReMe/metage2metabo>

Publication: hal-02395024

Contact: Clemence Frioux

Participants: Clemence Frioux, Arnaud Belcour, Anne Siegel

7.1.2 MiSCoTo

Name: Microbiota Screening and COmmunity Selection with TOpology

Keywords: Metabolic networks, ASP - Answer Set Programming, Logic programming

Scientific Description: MiSCoTo solves combinatorial problems using Answer Set Programming. It aims at minimizing either the number of selected species or both the number of selected species and the cost of the interaction between them, characterized by the number of metabolic exchanges. In the first case, the level of modeling is called lumped or mixed-bag, in the latter, it is compartmentalized.

Functional Description: Metabolic networks are composed of biochemical reactions and gather the expected metabolic capabilities of species. For organisms that live in interaction altogether (microbiotas), complementarity between these networks can be exploited to predict cooperation events. This software takes as inputs metabolic networks for various species (host, symbionts of the microbiota), components of the growth medium and a metabolic objective (metabolites to be produced), and aims at selecting a minimal set of symbionts to ensure the metabolic objective can be achieved. The software can use two types of modelings: a simplified one and another that takes into account the cost of metabolic exchanges and aims at minimizing it.

Release Contributions: Memory usage optimization. Fix issues with input file formats.

URL: <https://github.com/cfrioux/miscoto>

Publication: hal-01871600

Contact: Clemence Frioux

Participants: Clemence Frioux, Anne Siegel, Arnaud Belcour, 2 anonymous participants

7.1.3 MeneTools

Name: Metabolic networks Topological tools

Keywords: Metabolic networks, Graph, Topology, Bioinformatics, Systems Biology, ASP - Answer Set Programming

Scientific Description: MeneTools are a set of tools for the exploration of the producibility potential in a metabolic network using the network expansion algorithm. The MeneTools can: - assess whether targets are producible starting from nutrients (Menecheck) - get all compounds that are producible starting from nutrients (Menescope) - get all reactions that are activable from nutrients (Meneacti) - get production paths of specific compounds (Menepath) - obtain compounds that if added to the nutrients, would ensure the producibility of targets (Menecof) - identify metabolic deadends, i.e. metabolites that act as reactants of reactions but never as products, or metabolites that act as products of reactions but never as reactants. This is a purely structural analysis. All MeneTools using modelling follow the producibility in metabolic networks as defined by the network expansion algorithm.

Functional Description: MeneTools consist in four topological tool to analyze metabolic models in a graph-based perspective. Menecheck verifies the producibility of target compounds from available substrates (growth medium) of the metabolic network. Menescope gives the whole range of accessible compounds in the metabolic network starting from substrates. Menepath give the production paths of given compounds in the model. Menecof proposes compounds that need to be produced or added as substrate for ensuring the producibility of targets.

URL: <https://github.com/cfrioux/MeneTools>

Publications: hal-01819150, hal-02395024

Contact: Clemence Frioux

Participants: Clemence Frioux, Anne Siegel, Arnaud Belcour

7.1.4 Emapper2GBK

Keywords: Bioinformatics, Metabolic networks, Functional annotation

Functional Description: Starting from FASTA and EggNog-mapper annotation files, Emapper2GBK builds a GBK file that is suitable for metabolic network reconstruction with Pathway Tools, and adds the GO terms and EC numbers annotations in the GenBank file.

Release Contributions: Replace a dependency that has been deprecated by their authors (replace ete3 by ete4).

URL: <https://github.com/AuReMe/emapper2gbk>

Publication: hal-02395024

Contact: Clemence Frioux

Participants: Clemence Frioux, Arnaud Belcour, Anne Siegel

7.1.5 TANGO

Keywords: Computational biology, Systems Biology, Metabolic networks, Bacterial strains

Functional Description: The organoleptic properties that provide the added value of fermented dairy products result from specific metabolites that are produced by metabolic processes performed in concert by consortia of microbial species. TANGO enable a deeper understanding of the molecular and cooperative mechanisms underlying the production of organoleptic compounds. Tango uses a combination of whole-genome metabolic modeling and dynamic numerical simulation to assemble a complete, precise model of cheese production using lactic acid and propionic acid bacteria. The results of this modeling reveal interactions between the members of the bacterial community, follow dynamically organoleptic compounds and fit with experimental data.

Contact: Simon Labarthe

Participants: Julie Aubert, H el ene Falentin, Clemence Frioux, Simon Labarthe, Maxime Lecomte, David Sherman

7.1.6 Mapler

Name: Metagenome Assembly and Evaluation Pipeline for Long Reads

Keywords: Metagenomics, Genome assembly, Benchmarking, Bioinformatics

Functional Description: Mapler is a pipeline to compare the performances of long-read metagenomic assemblers. The pipeline is focused on assemblers for high fidelity long read sequencing data (e.g. pacBio HiFi), but it supports also assemblers for low-fidelity long reads (ONT, PacBio CLR) and hybrid assemblers. It currently compares metaMDBG, metaflye, Hifiasm-meta, opera-ms and miniasm as assembly tools, and uses reference-based, reference-free and binning-based evaluation metrics. It is implemented in Snakemake.

URL: <https://gitlab.inria.fr/mistic/mapler>

Publication: [hal-04142837](https://hal.archives-ouvertes.fr/hal-04142837)

Contact: Nicolas Maurice

Participants: Nicolas Maurice, Claire Lemaitre, Riccardo Vicedomini, Clemence Frioux

7.1.7 seed2lp

Keywords: ASP - Answer Set Programming, Metabolic networks, Logic programming, Linear programming

Scientific Description: Seed2LP is a formal framework for metabolic seed inference, based on logical and combinatorial modelling of metabolic networks, and extended to a hybrid approach combining logical reasoning and flow analysis. The objective is to identify the minimal sets of metabolites necessary for the functional activation of a metabolic network, while integrating constraints from stoichiometry and flow feasibility.

In its basic formulation, Seed2LP represents a metabolic network as a system of logical rules derived from the reaction structure: a reaction is activatable if all of its substrates are available, and its activation makes its products available. This logical abstraction makes it possible to define metabolic accessibility independently of any kinetic dynamics or objective function, and to formulate the seed inference problem as an optimisation problem in constraint-based logical programming (Answer Set Programming). This formalisation guarantees the completeness of the solutions, allows the enumeration of alternative minimal sets, and makes the network's implicit environmental dependencies explicit.

In order to overcome the limitations inherent in a purely topological approach, Seed2LP proposes a hybridisation with flux analysis (FBA). Logically inferred seed sets can be filtered, validated or refined using stoichiometric constraints, imposing the feasibility of steady-state fluxes compatible with the

production of target metabolites or growth. This articulation makes it possible to distinguish structurally sufficient seeds from those that are stoichiometrically unfeasible, and to identify dependencies induced by thermodynamically or quantitatively constrained cycles. The hybrid approach thus provides a compromise between logical completeness and biochemical realism, while maintaining formal interpretability of the solutions.

The framework has been extended to the analysis of microbial communities, considering each organism as a distinct metabolic network, interconnected by exchangeable metabolites representing inter-species transfers. Seeds can then be defined at different levels: individual (environmental dependencies specific to each taxon), community (minimum resources for the entire system). Metabolic transfers are explicitly modelled as production/consumption relationships between networks, allowing the inference of trophic complementarities, cross-dependencies and syntrophy scenarios.

By providing a unified framework for reasoning about seeds and transfers, as well as fluxes, Seed2LP is a tool for critical analysis of metabolic models, capable of linking network structure, ecological assumptions, and observable functional capacities.

Functional Description: Seed2lp is a computer tool, coded in Python and using Answer Set Programming (ASP), which identifies the minimum resources required for a microorganism or group of microorganisms to function. Based on the description of their metabolic reactions, it determines which compounds must be provided by the environment for the system to produce molecules of interest or ensure its growth.

Unlike traditional approaches, which rely on numerous quantitative assumptions, Seed2lp uses logical reasoning to explore all possible solutions, highlighting several alternative scenarios for functioning. The tool can also take into account metabolite exchanges between organisms in order to analyse microbial communities and identify mechanisms of cooperation or dependence.

Seed2lp is used to better understand the nutritional needs of microorganisms, compare their metabolic capacities, and analyse interactions within communities

Release Contributions: Extension of seed search to bacterial communities, with a search for transfers between species. Several algorithms for optimising seed sets and transfers are proposed in order to minimise or approximate a minimisation of seed sets.

News of the Year: Extension of seed search to bacterial communities, with a search for transfers between species. Several algorithms for optimising seed sets and transfers are proposed in order to minimise or approximate a minimisation of seed sets.

Publications: [hal-05230510](#), [hal-04713829](#)

Contact: Clemence Frioux

Participants: Chabname Ghassemi Nedjad, Loic Paulevé, Clemence Frioux

7.1.8 GeMeNet

Name: Genomes to Metabolic Networks

Keywords: Bioinformatics, HPC, Metabolic networks, Genomics

Scientific Description: GeMeNet is a pipeline for generating multiple metabolic networks essentially from their genomes but from other data (gbk, ect...).

Functional Description: GeMeNet is a pipeline for generating multiple metabolic networks essentially from their genomes but from other data (gbk, ect...).

URL: <https://gitlab.inria.fr/slimmest/gemenet>

Contact: Coralie Muller

Participants: Clemence Frioux, Coralie Muller

7.1.9 CoCoMiCo

Name: Cooperation and competition potentials in large microbial communities

Keywords: Automated Reasoning, Metabolic networks, Answer Set Programming, Microbiota, Systems Biology

Scientific Description: By discretely modelling metabolic cross-feeding and dependency on limiting metabolites between organisms, CoCoMiCo defines novel optimisation criteria that can be used at scale for screening microbial communities using combinatorial methods. The criteria can be used for evaluation of large sets of naturally-occurring communities, or of large sets of generated candidate communities screened to identify species of interest for health or ecology applications.

Functional Description: Metabolic cross-feeding and dependency on limiting metabolites between organisms are logically modeled using an ad hoc knowledge base derived from whole genome metabolic models in SBML format, and analyzed by logical inference rules defined using the answer set programming paradigm.

URL: <https://gitlab.inria.fr/CCMC/CoCoMiCo>

Contact: David James Sherman

Participants: Maxime Lecomte, David Sherman, Chabname Ghassemi Nedjad, Clemence Frioux, an anonymous participant

7.1.10 pherosensor-toolbox

Keywords: Data assimilation, Computational biology

Scientific Description: Insect pests are a major threat to agricultural systems, leading to intensive use of pesticides for crop protection with unsustainable drawbacks on the environment, biodiversity, and human health. Most insects produce pheromones for conspecific communication, making pheromone sensors an effective tool for early specific detection of pests, in order to reduce pesticide use within the context of precision agriculture.

‘Pherosensor-toolbox’ is a Python package containing numerical tools for pheromone sensor data assimilation to infer the position of emitting pest insects. It contains specific tools to model pheromone propagation and solve the corresponding inverse problem to determine emitters’ position taking into account the environmental context (wind, landscape, vegetation...). A specific focus is put on the integration of biological knowledge of pest behavior during inference.

Functional Description: This toolbox brings together numerical methods for solving a data assimilation problem for a reaction-convection-diffusion PDE describing pheromone propagation in an agricultural landscape using variational methods penalised by biology-informed regularisation terms (population dynamics of the emitting insect, preferred habitat, exclusion zones).

News of the Year: publication dans JOSS

URL: <https://forgemia.inra.fr/pherosensor/pherosensor-toolbox>

Publications: [hal-04669546](https://hal.archives-ouvertes.fr/hal-04669546), [hal-04572831](https://hal.archives-ouvertes.fr/hal-04572831)

Contact: Simon Labarthe

Participant: Simon Labarthe

7.1.11 MetaNetMap

Name: MetaNetMap: automatic mapping of metabolomic data onto metabolic networks

Keywords: Metabolomic data, Metabolic networks, Systems Biology, Metabolic modelling, Mapping

Functional Description: MetaNetMap is a Python package designed to automatise the process of mapping metabolomic data onto metabolic networks. It includes several layers of identifier matching, the use of customisable databases, and molecular ontology integration to suggest the most matches between experimentally-identified metabolites and molecules defined in the network.

URL: <https://github.com/coralie-muller/metanetmap>

Publication: [hal-05419350](https://hal.archives-ouvertes.fr/hal-05419350)

Contact: Coralie Muller

Participants: Coralie Muller, Clemence Frioux, Sylvain Prigent

Partner: INRAE

7.1.12 Metage2Metabo-postAViz

Name: Metage2Metabo-postAViz

Keywords: Metabolic modelling, Metabolism, Metabolic networks, GUI (Graphical User Interface)

Functional Description: Metage2Metabo-PostaViz (M2M-PostAViz) is a Python package that performs analyses on the predictions generated by the metabolic-modelling tool Metage2Metabo (M2M). M2M screens the metabolic potential of a microbial community represented as a collection of genome-scale metabolic networks. When working with cohorts of hundreds or thousands of samples, one has to run the tool as many times as there are samples, then analyse the results of the model. The tool's outputs are, for each community, several data frames describing the role of each microorganism with respect to the whole community's functions. Properly comparing all samples requires combining all the outputs, and taking into account sample metadata describing individuals lifestyle or clinical information for instance.

M2M-PostaViz integrates all such data and provides a visualisation interface that permits exploration through custom plot generation and statistical tests. The underlying data treatment was optimised in order to deal with large numbers of samples without impeding user experience. M2M-PostaViz notably permits a pre-treatment and storage of the data such that future exploration can be launched in a computationally efficient manner. Exploration is performed at several levels: molecules (metabolites) that may or may not be producible across samples, microorganisms that may have different behaviours across samples depending on interactions with other community members, or more general overviews of the community functions. The tool works as a local web-based application.

News of the Year: First release of the tool

URL: <https://github.com/AuReMe/metage2metabo-postaviz/tree/main>

Contact: Clemence Frioux

Participants: Clemence Frioux, an anonymous participant

7.1.13 LUCIA

Name: LUCIA - mobile robot firmware

Keywords: Artificial intelligence, Robotics, Science outreach

Scientific Description: The LUCIA robot combined a Thymio-II educational robot with a Raspberry Pi and a wide-angle camera, mounted on a custom support made from folded acrylic plastic. The firmware has two parts. The low-level "autonomous nervous system" brain for the Thymio-II robot is responsible for movement and feeling the close environment. The high-level "prefrontal and visual cortex" brain for the Raspberry Pi is responsible for vision and object recognition, strategizing, and decision making.

Functional Description: LUCIA is the firmware of the mobile robot used for the robotics lesson of UCIA (Usages et Connaissances de l'Intelligence Artificielle), developed by the Ligue de l'Enseignement, Inria, and Poppy Station. It implements different AI-based strategies. A web interface allows users to choose objectives, and observe how the robot uses its perception of the environment to make decisions that achieve those objectives.

Release Contributions: Final version submitted to the Région Nouvelle Aquitaine for acceptance, and deployed in the 32 kits distributed to educational structures.

News of the Year: Final version submitted to the Région Nouvelle Aquitaine for acceptance, and deployed in the 32 kits distributed to educational structures.

Contact: David Sherman

Participant: David Sherman

Partners: Ligue de l'Enseignement, Poppy Station

7.1.14 AsebaHub

Name: Turn-key bridging of Aseba mobile robots to wifi networks

Keywords: Robotics, Education

Scientific Description: The Thymio-II educational robot teaches robotics programming to 8-18 year old children. Since 2014 Inria has contributed to the Thymio ecosystem. Thymio-II robots only communicate through USB connections from a host computer, so until now it has been necessary to install Aseba software on that computer. This is not always possible in schools, which increasingly use tablets.

This software provides an OpenWRT-based firmware image for a wifi Access Point that takes responsibility for communication with each robot, advertising it on the local network to learner programming environments running on tablets. It provides device manager and web-based configuration services, out of the box.

Functional Description: AsebaHub is the firmware for the Thymio-2-plus smart wifi access point for Thymio educational robots connected by LR-WPAN. Every robot is made available as a network target on the wifi and wired local-area networks, where they can be discovered using mDNS-sd (Zeroconf/Bonjour). No network or user configuration is necessary.

The device works out of the box with Thymio programming environments on tablets and computers: VPL3, Scratch, Python, and Aseba Studio.

It can function as an independent Access Point, to which user may connect, or as a Bridge to an existing local network. Either configuration may be chosen by flipping a switch.

Release Contributions: Release v1.0.0 provides a complete firmware image based on OpenWRT, for compatible mini-routers including GL.iNET and Raspberry Pi.

News of the Year: An updated version compiled for ramips-mt76x8 is deployed as the firmware for Mobsya's Thymio 2-plus mini-router (<https://www.thymio.org/products/thymio-2plus>). More than 600 are currently installed in schools.

Contact: David Sherman

Participant: David Sherman

7.2 New platforms

Participants: David Sherman, , Lamine Cissé (DSI), , Jean-François Scariot (DSI), , Ahmed Kallel (DSI), .

As a founding principle, Pleiade supports reproducible scientific analyses and promotes a declarative approach using reusable software modules, rigorous documentation of data provenance, and systematic recording of electronic lab notebooks. Pleiade automates the deployment of environments that support these goals for non-technical end users. We built a Kubernetes platform *Pleiadès* that is since 2023 integrated into Inria's national IT Management (DSI-SP).

Use cases were identified by the project-team and from the [MISTIC data management plan](#):

- Fast deployment of **containerized user environments**, combining biological data and databases, software modules specified by version, a CWL executor, and interactive tools including web front ends, notebooks, or Galaxy. A user environment will provide at least one specific HTTPS endpoint, created dynamically. A single researcher may deploy several different environments in the course of one day.
- Support for **development and testing of workflows**, as above but configured for team members who are developing software modules or interfaces, and who must often deploy several different environments simultaneously.
- Dynamically allocated **containerized compute tasks**, including both individual analysis steps in workflows and GitLab runner containers used for continuous integration. These tasks arrive in bursts that often cannot be planned in advance.
- Long-running **stream preprocessing**, a low-priority background task that watches external databases for changes, chooses pertinent data, precomputes representations and ingests them into local data bases.

The following requirements were derived from these use cases:

- Tasks must run in OCI containers. A typical environment will be constructed from ten to one hundred containers, grouped in Kubernetes Pods of co-localized containers that share a private network.
- Containers run unprivileged and must rely on role-based access control (RBAC), secrets, and service accounts.
- Different storage classes must be available for dynamic volume allocation: ReadWriteSingle, ReadWriteMany, Object (S3) Bucket.
- An application must be able to allocate a route with wildcard DNS in order to offer an endpoint, internally to the Inria network.
- A collection of Kubernetes custom resource definitions and RBAC definitions, specific to Pleiade's applications, is needed.
- A collection of OpenShift Operators for deployment of applications, is needed. These include database services, workflow execution, and container building using source-to-image (S2I).
- A management interface through the OKD console that allows inspection and management of app topologies, pods, volumes, and Kubernetes objects.

We support community best practices for reproducible computing in bioinformatics, using [biocontainers](#) generated by [bioconda](#), in [CWL](#) or [Galaxy](#) workflows. For internal use we provide [model serving](#) endpoints and host [JupyterHub](#) environments.

The Pleiadès platform is built on [OKD 4](#), the community distribution of [Kubernetes](#) developed alongside of [RedHat OpenShift](#). OKD4 uses the [CRI-O](#) runtime, not Docker, and containers run unprivileged. Software-defined storage and S3 endpoints are provided by Ceph. Pleiadès follows the *gitops* pattern and all management and implementation use Git repositories as the single source of truth.

Continuous integration for software development is supported for Inria's Gitlab instance. Two dozen project-specific CI runners are currently hosted on Pleiades.

To support our scientific users, Pleiades hosts an instance of *Open Data Hub* (ODH), an AI platform for the hybrid cloud. Each project in ODH can host Jupyter workbenches, shared cluster storage and data connections to S3 buckets, pipelines, and AI model serving runtimes including Kserve and OpenVINO.

This platform is also central in data management plan of the Parsada GETUP project.

8 New results

8.1 Metabolic models of microbial communities

8.1.1 Numerical models of metabolism

Participants: Sthyyve Tatho, Simon Labarthe, Sahak Yeghiazaryan, David Sheman, Clémence Frioux, Coralie Muller, Chabname Ghassemi Nedjad, Isabelle Kupin, Franck Salin.

Building up on metabolic models of microbial strains to derive dynamical models of microbial communities is still a major scientific challenge that Pleiade is addressing. At the **interface between bioinformatics and applied mathematics**, the objective is to solve numerical issues in order to couple large-scale accurate metabolic models of microorganisms with ordinary or partial differential equations describing the population dynamics, in order to integrate multi-omic data.

Coupling metabolic models and dynamic systems is the topic of **Sahak Yeghiazaryan's PhD**, started in dec. 2023. This project is a collaborative work with the LBE INRAE Laboratory (Narbonne), and is co-supervised by Nicolas Bernet, Elie Le Quemener and Simon Labarthe. The aim of the project is to study a syntrophy articulated around hydrogen metabolism in anaerobic digestion in a bioprocess context. Sahak Yeghiazaryan will **couple metabolic models to thermodynamics-based kinetic models** of microbial growth to integrate omic data acquired in slow-growing community obtained in a waste water treatment context.

In **Sthyyve Tatho's PhD project**, the goal is to use metabolic models to integrate multi-omic time series. The metabolic models are used to code microbial metabolism as a prior biological knowledge into statistical learning problems. The goal is to find an optimal distribution of metabolic fluxes within a microbial community by solving an optimization problem minimizing discrepancies with observed data (import/export rates of metabolic compounds and microbial growth curves) while complying with metabolic constraints (metabolic models) and expression data through a metatranscriptomic-based logistic penalty. The framework is called cMFA, for **community Metabolic Flux Analysis (cMFA)** (Fig 1).

Numerical modeling of metabolism relies on genome-scale metabolic models: a key issue is then efficient pipelines and **engineering support** to go from microbial genomes to metabolic models. Coralie Muller (during an engineer position before her PhD contract), Isabelle Kupin and Franck Salin are in charge of developing, maintaining and executing efficient pipelines to provide rule-of-the-art metabolic models to support research.

The **Artemis project** is a research network founded by the INRAE metaprogram Digitbio. It gathers about 40 researchers from INRAE and Inria, either modelers developing models of microbial systems or experimentalists with strong interest in mathematical models and digital twins. The different microbial systems represented in the network covers the whole set of applications of microbiology at INRAE: environmental, bioprocesses, plant, animal, food and human microbiology. The network gathers different Inria teams, in particular Macbes, Musca and Pleiade. The final goal of the network is to produce an opinion paper about the concept of digital twins applied to microbial systems. Artemis is led by Simon Labarthe and involves numerous researchers of Pleiade: Clémence Frioux, Isabelle Kupin, Franck Salin and David Sherman strongly contributed to the opinion paper, while Sthyyve Tatho, Coralie Muller and Chabname Ghassemi Nedjad have been involved in the organization of a research training on the modeling of microbial consortia.

The PhD project of **Coralie Muller** addresses the challenge of **integrating metabolomic data into metabolic models** and improve their quality through a better integration of secondary (specialised) metabolism information. In 2025, she developed a tool facilitating and automatising the mapping of metabolomic data

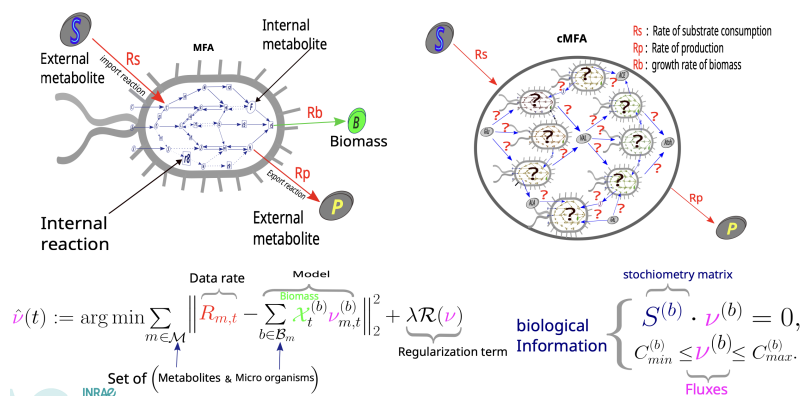


Figure 1: Extending metabolic flux analysis to microbial communities with complex interactions, from [39].

onto metabolic networks (7.1.11, [75]). The associated work was published as a preprint [50]. Coralie presented her work as posters during several events including JOBIM 2025 conference [60, 62, 61, 63].

8.1.2 Knowledge representation and reasoning applied to metabolic modelling

Participants: Juliette Audemard, Leonard Brindel, Clémence Frioux, Chabname Ghassemi Nedjad, Coralie Muller, Camille Saint-Martin, David Sherman.

As a part of her PhD, defended in December 2025 [44], **Chabname Ghassemi Nedjad** developed an approach for the **identification of seed metabolites in metabolic networks**, i.e. inputs, proxy of microorganisms growth medium. We take advantage of the possibility to reconstruct metabolic networks from genomic information, thereby obtaining a blueprint of the metabolic potential of species. We apply to this metabolic network a set of rules and constraints under the reasoning paradigm of Answer Set Programming (ASP) to provide sets of metabolites that would enable the activation - modelled through network expansion and/or flux balance analysis - of functions of interest in the corresponding species. Chabname’s work is implemented in a tool Seed2LP (7.1.7). The work has been published in the journal *Bioinformatics* [21] and as a *Computational Methods in Systems Biology* conference paper [27]. She also presented a poster during JOBIM 2025 conference [57].

A key development of the team over the past few years is Metage2Metabo (M2M) (7.1.1), a computational framework for the **reasoning-based modelling of metabolic potential in microbial communities** [4]. This work has been central to several projects this year. **Leonard Brindel** has been working as an engineer to develop Metage2Metabo-postaviz which is a graphical interface for the interactive analysis of multiple M2M runs accounting for metadata (7.1.12). He presented a poster at JOBIM 2025 [55]. **Constanza Andreani**, a visitor of the team in 2024 as part of the Inria Associated Team SymBioDiversity (2020-2024) published with her coauthors a work in *Environmental Microbiome* that integrates M2M in a systems biology framework from metagenomic data of Atacama Desert soils. She demonstrated the importance of considering not only the metabolic potential of metagenome-assembled genomes (MAGs) but also the one of the entire metagenome to characterise the soil functions [18].

Juliette Audemard worked as a Masters student on the **metabolic characterisation of freshwater phycospheres** composed of cyanobacteria and associated heterotrophic bacteria, as part of the COMIC project. She analysed metagenomic and metabolomic data and built metabolic models to simulate the functional complementarity between microorganisms. She presented her work at the JOBIM 2025 conference and earned the best presentation award [28].

Post-doc **Camille Saint-Martin**, with David Sherman of Inria and Arnaud Pujol of IFPEN has developed a framework §10.3.11, for reasoning about the composition and functional roles of microbial communities implicated in deep (>1 km) geological storage for carbon capture. The approach links microbial species in

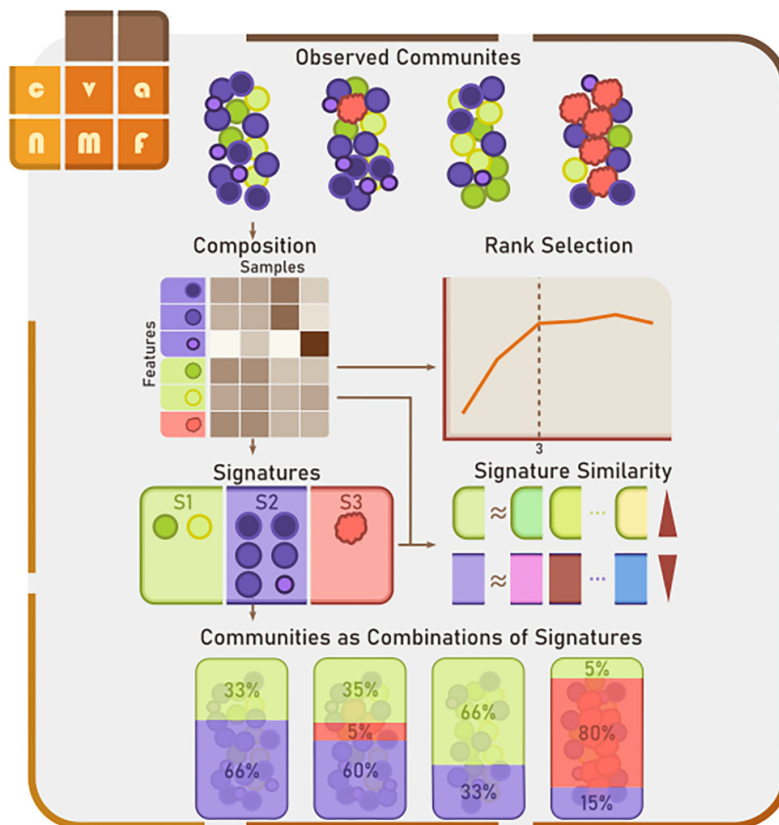


Figure 2: Non-negative matrix factorization to identify human gut microbial enterosignatures, from [19].

chimiolithotrophy and their potential for beneficial functions, such as the formation of impermeabilizing biofilms, or detrimental functions, such as well corrosion.

8.2 Modelling structures in microbial communities' taxonomic and functional composition

Participants: Clémence Frioux, Simon Labarthe, Guilhem Sommeria-Klein, Alioune Badara Diouf, Jean-Marc Frigerio, Paola Fournier, Mathilde Sola.

Building on previous work detecting **latent structures in gut microbiome taxonomic composition** (Enterosignatures [8]), we collaborated with the Earlham Institute and the Quadram Institute to develop a tool for non-negative matrix factorisation (NMF) and to facilitate cross-validation [19] (Fig 2). Whereas enterosignatures were developed to reduce the dimensionality of gut microbiome taxonomic composition, a taller order is to reduce the dimensionality of microbiome functional composition. Indeed, there are thousands of bacterial species in the gut, but they harbour millions of genes. With L3 intern **Killian Dugueperoux** from ENS de Lyon, we explored and benchmarked NMF-based dimensionality reduction approaches applied to collections of bacterial genomes at the protein cluster level.

Prior to starting her PhD **Mathilde Sola** developed a new method for **network inference from microbiome compositional data**. In 2025, she submitted a preprint describing NeighborFinder, the associated tool [52].

Another central application field in the team of **statistical learning of microbial communities is plant microbiome**. Given the profound impact of plant microbiota on host health, understanding the invariant ecological rules that govern protection against pathogens or infection susceptibility is of particular interest. In the framework of VITAE and Micromod projects, building on large datasets of microbial screening of parcels

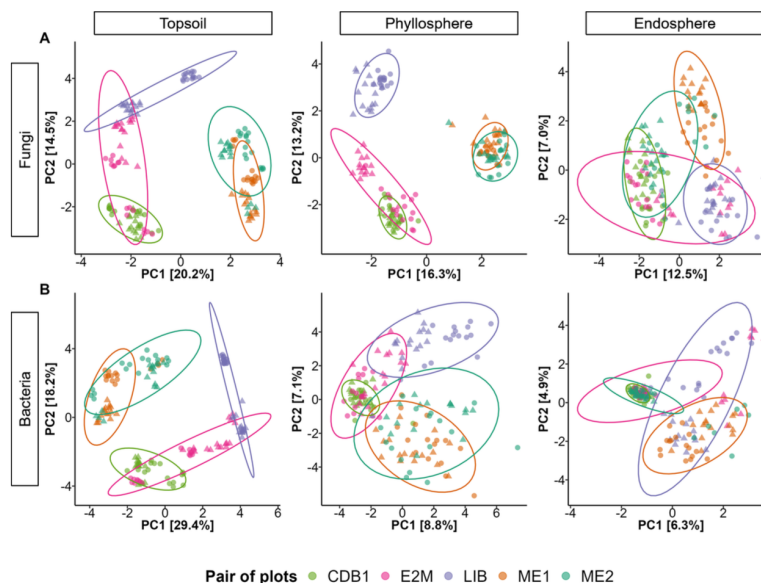


Figure 3: Microbial taxa characteristic of protection from or susceptibility to infection by downy mildew, from [20].

with an history of high or low pathogenic pressure, **Paola Fournier** identified key microbial taxa characteristic of protection or infection susceptibility [20, 26] (Fig 3). This work has been followed up with the Microsentry project (funded by INRAE SPE department), a project focusing on the use of microbiome data for early detection of pathogen infection for epidemiosurveillance. In Microsentry, **Alioune Badara Diouf** has been hired for a M2 internship in order to develop a method coupling dimension reduction, classification and variable selection to detect **reduced microbial signatures of infection**. During this M2, the development of the extendedNMF package has been started, with the **support of Jean-Marc Frigerio for software engineering**. This research will be followed up in the GETUP project (PARSADA), started in march 2025.

8.3 Statistical models of microbial communities in space and time

Participants: Guilhem Sommeria-Klein, Emna Stambouli, Chandler Ross, Felix Roy, Simon Labarthe.

Understanding the **dynamics of microbial communities, including their spatial dynamics through dispersal**, is key in quantifying and predicting their impact on ecosystems. In his PhD project co-supervised with the University of Turku in Finland, Chandler Ross develops models of human gut microbiome dynamics that can be applied to short time-series data typical of large population cohorts. He has focused in particular on the statistical characterisation of bistable dynamics [51]. In another collaboration with the University of Helsinki and the University of Turku in Finland, we explored the drivers of antibiotic resistance gene prevalence in the gut microbiome across a large Finnish cohort and its impact on public health [24].

In applications to soil microbiome, spatial aspects are particularly important to account for. In her PhD started in May 2025, Emna Stambouli seeks to model the **spatial distribution of soil bacterial communities as a function of environmental parameters**, buiding on dimensionnality reduction approaches and on data obtained through a collaboration with the University of Aalborg, Denmark. In August 2025, we also organised with collaborators from the University of Oxford a fieldwork campaign to **sample bacterial communities from island soils** in the Finnish archipelago. Island soils indeed represent a unique opportunity to better understand the processes of spatial dispersal and diversity accumulation through time that shape soil

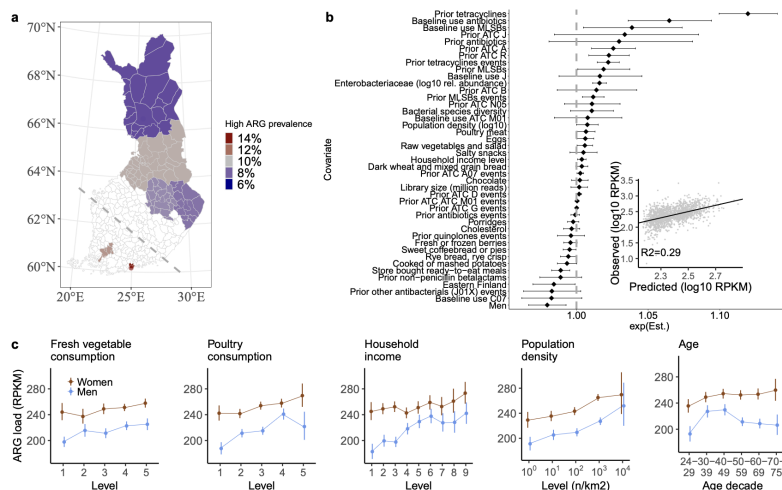


Figure 4: Antibiotic resistance gene (ARG) prevalence in Finnish gut microbiomes, across spatial and lifestyle variables, from [24].

communities.

Another topic is the study of the **dynamics of barrier effect against pathogen in plant microbiota after pathogen infection**, driven by microbial interactions. In the context of downy mildew in vineyard studied in VITAE (PPR CPA, ANR) and Micromod (Région Nouvelle-Aquitaine) projects, **Felix Roy**'s postdoc project focuses in identifying **interaction patterns during infection dynamics** by fitting dynamical models from theoretical ecology with time series of microbial counts. He is both developing theoretical work by benchmarking different methods on synthetic data, and he applies them on real data obtained in controlled experiments of microbial dynamics in leaves (with SAVE, INRAE, Bordeaux) and seeds (with IRHS, INRAE, Angers)

8.4 Metagenomic bioinformatics for microbiomes

Participants: Nicolas Maurice, Mathilde Sola, Franck Salin, David Sherman, Jean-Marc Frigerio, Clémence Frioux.

The interest of Pleiade for the treatment of DNA sequences has renewed over the past few years with the MISTIC project aiming at developing models for complex microbial communities in an Agroecology context.

The PhD project of **Nicolas Maurice** (hosted in Inria Genscale team) targets the difficult task of **assembling genomes in high-diversity microbiomes such as soil**. He developed MAPLER (7.1.6, Fig 5) for the assessment of metagenomic assembly quality. The associated work was published in 2025 in *Bioinformatics* [23], and Nicolas presented his work as a poster during JOBIM 2025 conference [59]. This year's developments focused on assessing the relevance of pre-assembly clustering for complex metagenomes; Nicolas presented it as an oral presentation during the SeqBim working group workshop organised by GDR BIMMM [37].

The work of Carole Belliardo, Nicolas Maurice and colleagues in the MISTIC project assesses the relevance of combining short read and HiFi long read metagenomics to reconstruct the most genomes in complex ecosystems such as soil. In 2025, they published a preprint discussing the added value of using short reads as a proxy of long-read assembled contig abundance during binning [47]. Carole also presented a poster [54].

As part of her PhD project, **Mathilde Sola** works on Le French Gut project, that aims at **studying the gut microbiome of the French population** through a large-scale citizen science initiative that targets 100,000 volunteers. In 2025, Mathilde explored the first 5,000 metagenomic samples by combining the identification

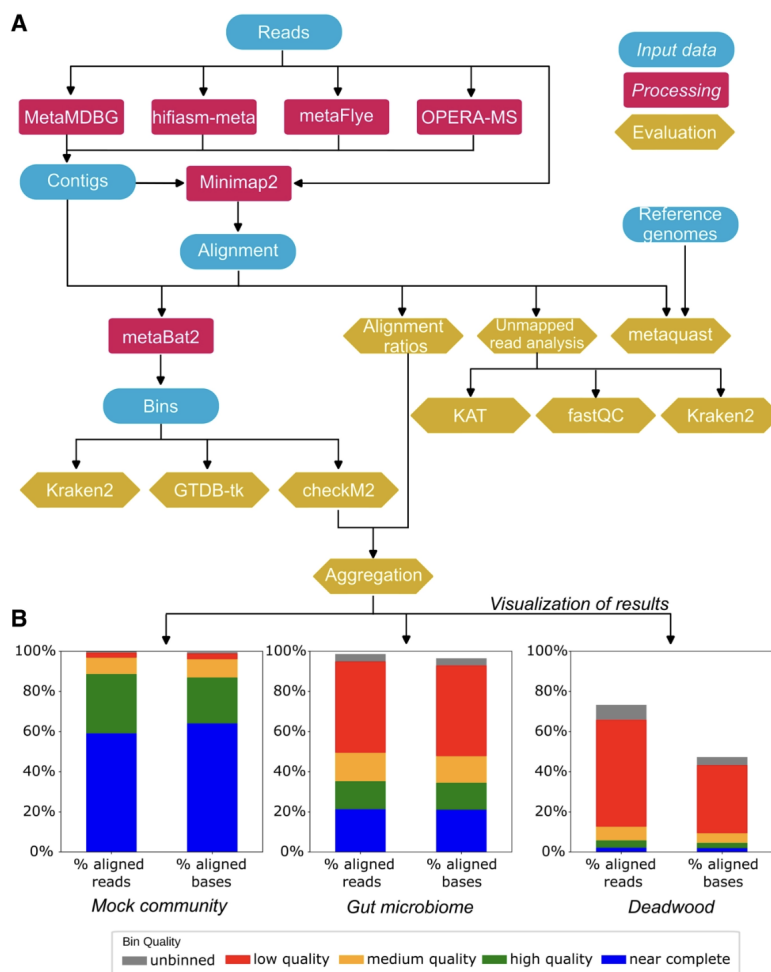


Figure 5: Assessing metagenomic assembly quality with MAPLER, from maurice:hal-05288241.

of latent structures in the gut microbiome composition with enterosignatures [8] and the analysis of the cohorts metadata on diet, lifestyle and health. She presented her work as a poster during the JOBIM 2025 conference [64].

8.5 Other systems biology results

Participants: Simon Labarthe.

Apart from microbial ecology, we are also peripherally involved in the Pherosensor project, which is an epidemiosurveillance project founded by the ANR-PPR CPA program dedicated to the development of pheromone sensor to track insect pests in a precision agriculture framework, in order to reduce pesticide use. Pleiade's involvement is to develop mathematical models to solve the inverse problem of pheromone propagation: from time-series obtained from a spatial network of sensors, the goal is to track back pheromone plumes towards the emission source, i.e. the targeted pest insect. To this end, we specifically focus on integrating biological prior knowledge about pest in the inverse problem, by developing a biology-informed data assimilation method (BI-DA) published in early 2025 [22]. New developments were published in a preprint [48] (Fig 6).

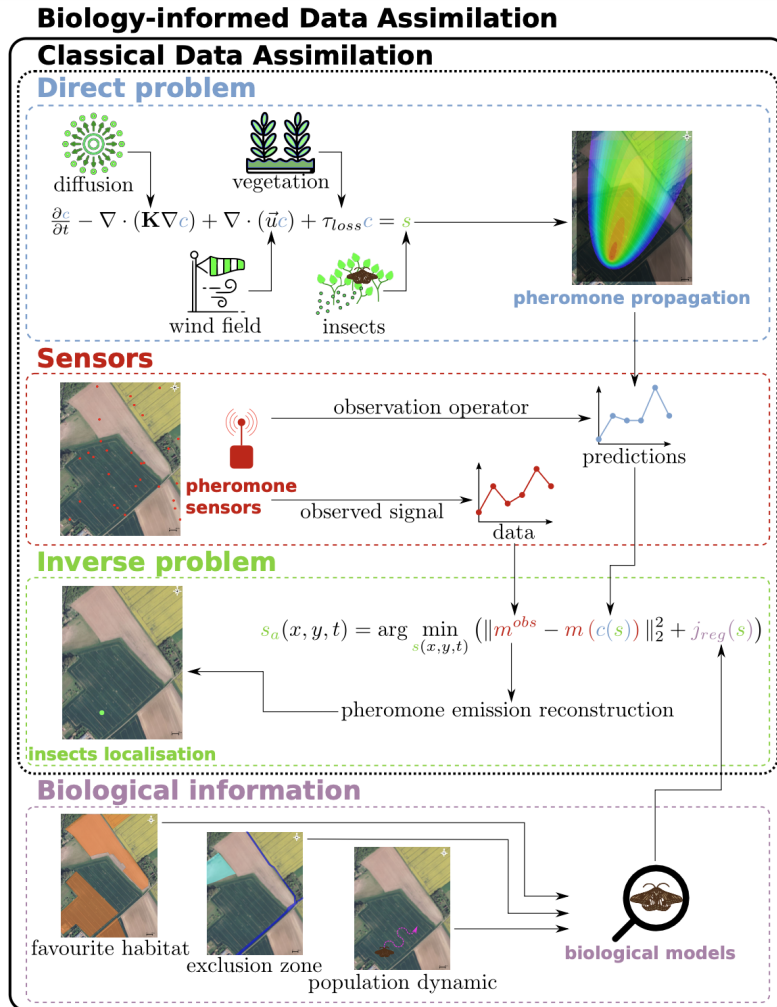


Figure 6: Detection of insect populations in crop fields by data assimilation of detected pheremone plumes, from malou:hal-05340937.

9 Bilateral contracts and grants with industry

Participants: Simon Labarthe, Clémence Frioux, Franck Salin, David Sherman, Paola Fournier, Isabelle Kupin, Felix Roy.

Pleiade's impact on industry is channeled through agroecological project MISTIC (§10.3.1). In 2025, additional interactions were added through the GETUP project grant, which involve industrial entities (Moët and Hennessy groups).

PLEIADE also collaborates with Starfish Bioscience.

10 Partnerships and cooperations

10.1 International initiatives

10.1.1 Associate Teams in the framework of an Inria International Lab or in the framework of an Inria International Program

Pleiade members (Clemence Frioux, Guilhem Sommeria-Klein, Simon Labarthe) are involved in the associated team Valpo, led by Marta Avalos Fernandez, partnering with Chilean laboratories.

10.2 International research visitors

10.2.1 Visits of international scientists

Other international visits to the team

Matti Ruuskanen

Status Lecturer

Institution of origin: University of Turku

Country: Finland

Dates: April 24th to 25th

Context of the visit: Collaboration with the University of Turku

Mobility program/type of mobility: Research stay

Connor Tiffany

Status Post-doc

Institution of origin: Children's Hospital of Philadelphia

Country: USA

Dates: September 5th to 9th

Context of the visit: Collaboration with the Children's Hospital of Philadelphia

Mobility program/type of mobility: Research stay

Christopher Quince**Status** Group leader**Institution of origin:** Earlham Institute**Country:** United Kingdom**Dates:** September 18th to 19th**Context of the visit:** HDR Clémence Frioux**Mobility program/type of mobility:** Clémence Frioux's HDR jury and research stay**Pirta Palola****Status** Post-doc**Institution of origin:** University of Oxford**Country:** United Kingdom**Dates:** September 24th to 26th**Context of the visit:** Collaboration with the University of Oxford**Mobility program/type of mobility:** Research stay**10.2.2 Visits to international teams****Research stays abroad****Clémence Frioux****Visited institution:** Centro de Modelamiento Matemático, Universidad de Chile**Country:** Chile**Dates:** January 8th to 18th**Context of the visit:** Inria Associated Team SymBiodiversity that ended in 2024**Mobility program/type of mobility:** Research stay**Guilhem Sommeria-Klein****Visited institution:** University of Turku & University of Helsinki**Country:** Finland**Dates:** January 7th to 10th, August 11th to 15th, November 27th to 28th.**Context of the visit:** Co-supervision of doctoral students Chandler Ross and Moein Khalighi (University of Turku; Moein's defense on November 28th), collaboration with Matti Ruuskanen (University of Turku) and Katariina Pärnänen (University of Helsinki), invited talk to microbial ecology symposium at the University of Turku on November 27th.**Mobility program/type of mobility:** Research stay

Guilhem Sommeria-Klein**Visited institution:** University of Oxford**Country:** United Kingdom**Dates:** June 9th to 13th**Context of the visit:** Collaboration with Aura Raulo (Queen's College, Oxford) and Christopher Quince (Earlham Institute)**Mobility program/type of mobility:** Research stay**Guilhem Sommeria-Klein****Visited institution:** Tvärminne research station**Country:** Finland**Dates:** August 3th to 9th.**Context of the visit:** Fieldwork to collect soil samples from Finnish archipelago islands**Mobility program/type of mobility:** Research stay**Guilhem Sommeria-Klein, Emna Stambouli****Visited institution:** University of Aalborg**Country:** Denmark**Dates:** November 24th to 26th.**Context of the visit:** Invited seminar and collaboration around Microflora Danica project**Mobility program/type of mobility:** Research stay**10.3 National initiatives****10.3.1 MISTIC (PEPR Agroecology and ICT)**

Participants: David Sherman, Clémence Frioux, Simon Labarthe, Guilhem Sommeria-Klein, Franck Salin, Alain Franc, Jean-Marc Frigerio, Nicolas Maurice, Coralie Muller, Sthyve Tatho, Isabelle Kupin.

MISTIC, *Microbial communities and ICT*, has been selected as a five-year flagship project in the PEPR Agroecology and ICT program of the French Government. MISTIC will develop methodological tools for defining spatio-temporal models of microbial community dynamics in the phyllosphere and rhizosphere of crop plants, with the goal of creating new understanding of the role of these communities in plant adaptation to environmental stresses, including climate change. MISTIC is a partnership between seven Inria and INRAE teams in Bordeaux, Rennes, and Sophia Antipolis. The project formally began in November 2022.

10.3.2 CULTISSIMO (PEPR Food Systems, Microbiome, and Health)

Participants: Clémence Frioux, Simon Labarthe.

The Cultissimo project, funded by the PEPR Food Systems, Microbiome and Health (SAMS), is dedicated to the development of culturomics approaches to study the human gut. The Pleiade team is involved, together with MaIAGE (INRAE) and Musca team, in the development of modeling approaches to predict culture media to cultivate microbial defined communities.

10.3.3 TARGET (INRAE EXPLORAE Transformation)

Participants: Clémence Frioux, Olivia Bulka, Coralie Muller, Franck Salin.

The TARGET project combines computational modelling, culturomics and genetic engineering to tackle the challenge of cultivating a phytoplasma, a small bacterium responsible for the grapevine disease Flavescence Dorée. The underlying objective is to develop strategies that could be applied to broader applications in the field of non-culturable microorganisms.

10.3.4 H2Rumen (ANR)

Participants: Clémence Frioux, David Sherman, Simon Labarthe, Pritam Kundu.

The H2Rumen project aims to decipher the interactions and dynamics of the rumen microbiota, the microbial communities of the ruminant gastrointestinal track involved in the digestion of vegetable fibres. Rumen microbiota has a key role in the health and well being of the animals, but is also responsible of methane production, one of the main negative externalities of cattles. The project articulates kinetic and metabolic modeling with experimental approaches on complex and defined communities, to focus on H2 turn over and methane production. The overall goal is to better understand microbial interactions to propose solutions to mitigate methane production while preserving other microbial functions.

10.3.5 VITAE, Pherosensor (PPR Cultiver et protéger autrement)

Participants: Simon Labarthe, Paola Fournier, Felix Roy.

Pleïade participates to two projects of the PPR CPA, dedicated to research towards an agriculture without pesticide. Pléïade co-leads a work package of the VITAE project, taking in charge modeling tasks to analyse culturomics data in order to identify antagonist micro-organisms against powdery mildew in grapevine. Pléïade leads a work package of the Pherosensor project, dedicated to the design of new sensors of pheromone. The main task of the team is to solve an inverse problem on a PDE model of pheromone propagation to track back the pheromone emitters.

10.3.6 Holovini (Holoflux INRAE metaprogram)

Participants: Simon Labarthe, Clémence Frioux.

Pleïade is involved in the Holovini flagship project of the **Holoflux metaprogram**. Holovini studies the berry microbiome of grapevine, focusing on the microbial flux involved in the assembly of the berry microbiome. Pléïade takes in charge the analysis of metagenomics data and the co-lead of a modeling workpackage.

10.3.7 REBON (ANR)

Participants: Clémence Frioux.

REBON, piloted by Joachim Niehren, abstracts reaction networks to boolean networks with the goal of improving inference and control in systems biology.

10.3.8 Artemis (Digit-bio INRAE metaprogram)

Participants: Simon Labarthe, Clémence Frioux, David Sherman, Coralie Muller, Chabname Ghassemi Nedjad, Sthyye Tatho, Franck Salin, Isabelle Kupin.

Pleiaide pilots the Artemis pre-project funded by the **Digit-bio** metaprogram, aimed at developing methodologies for defining digital twins in microbial ecology.

10.3.9 Microsentry (SPE and MATHnum INRAE departments)

Participants: Simon Labarthe, Clémence Frioux, Alioune Badara Diouf.

In collaboration with SAVE unit (INRAE), this project aims to explore the use of q-PCR screening of sentry microorganisms to get early detection of powdery mildew infection in environmental samples. The Pleiaide team is involved in methodological developments to select a small set of sentry microorganisms.

10.3.10 GETUP (PARSADA project)

Participants: Simon Labarthe, Clémence Frioux, Franck Salin, David Sherman, Paola Fournier, Isabelle Kupin, Felix Roy.

Led by C.Vacher (SAVE unit, INRAE Bordeaux), the GETUP project aims to provide micro-organism based solutions for crop protection in viticulture. Gathering a large consortium of academic (INRAE, U.Bourgogne, U.Rennes, U.Bordeaux, ISVV, MNHN, Inria) and private (Möet-Hennessy, IFV) research laboratories, the GETUP project explores microbial determinant of pathogen infection at the plant or the parcel levels, together with providing practical devices to screen grapevine microbiota and developing collections of micro-organisms with biocontrol effect.

10.3.11 Olympus (Inria-IFPEN joint laboratory)

Participants: Camille Saint-Martin, David Sherman.

In the framework of the **Inria-IFPEN joint laboratory** we are working together to study the interaction between microbial communities, lithic media, and carbon dioxide in deep carbon storage sites. These interactions produce biological phenomena that are both beneficial and deleterious, and can play a key role in the efficiency and reliability of carbon capture storage (CCS).

In the Olympus project we develop a common framework for simulating these phenomena, by coupling two existing codes developed at the IFPEN and Inria. The IFPEN provides codes for phenomenological modeling of chemolithotrophy, in the form of coupled autonomous non-linear dynamic systems, that predict biological effects and transformations. Inria provides codes for mechanistic modeling of metabolic exchanges of very large communities, that predict the potential for biofilm formation and the activation of biological functions.

10.4 Regional initiatives

10.4.1 Micromod (Région Nouvelle Aquitaine)

Participants: Simon Labarthe, Clémence Frioux, Paola Fournier, Felix Roy, Coralie Muller.

The micromod project build on other research projects in the team (VITAE and Mistic) by co-funding postdoc and Phd projects in order to articulate different research efforts for microbiology-based solutions for the biocontrol of plant pathogens. In particular, Micromod makes a continuum between 1) data-based modeling of plant microbiota, obtained during *in planta* sampling in crops, 2) mathematical methods to select small microbial consortia presenting collective bio-control effect against pathogen, 3) high-accuracy metabolic models of these micro-organisms to detect interactions driven by secondary metabolism.

11 Dissemination

11.1 Promoting scientific activities

11.1.1 Scientific events: organisation

Member of the organizing committees

- Clémence Frioux, Simon Labarthe - Co-head of the 2025 edition of the French Bioinformatics Conference, [JOBIM](#) - July 8th to 11th
- Guilhem Sommeria-Klein - One of the three co-organisers of the annual meeting of the TheoMoDive (Theory and Modelling in Biodiversity science) national research network - 1st to 3rd December in Bordeaux.

11.1.2 Scientific events: selection

Member of the conference program committees

- Clémence Frioux - Proceedings Program Committee of International Conference on Intelligent Systems for Molecular Biology European Conference on Computational Biology, [ISMB/ECCB 2025](#)

Reviewer

- Clémence Frioux - Proceedings Program Committee of International Conference on Intelligent Systems for Molecular Biology European Conference on Computational Biology, [ISMB/ECCB 2025](#)

11.1.3 Journal

Member of the editorial boards

- [BMC Microbiome](#) - Clémence Frioux, associate editor

Reviewer - reviewing activities

- [Nature Communications](#) - Clémence Frioux
- [NPJ Biofilms and Microbiomes](#) - Clémence Frioux
- [NPJ Systems Biology and Applications](#) - Clémence Frioux
- [Genome Biology](#) - Simon Labarthe
- [Mathematical Modelling of Natural Phenomena](#) - Simon Labarthe
- [Communications Earth & Environment](#) - Guilhem Sommeria-Klein
- [PCI Forest and Wood Sciences](#) - Guilhem Sommeria-Klein

11.1.4 Invited talks

- Clémence Frioux - IRISA, Inria Rennes, France, Data Knowledge Management department - *Machine reasoning, Statistical learning, and numerical modelling for exploring microbial community metabolism*
- Clémence Frioux - GT BioSS (CNRS GDR BIMMM) Monthly Seminar, online - *Machine reasoning, dimensionality reduction, and numerical modelling for exploring microbial community metabolism*
- Clémence Frioux - Symposium H2Rumen, Saclay, France - *Discrete models of metabolism for the exploration of microbial communities*
- Clémence Frioux - Inria Chile, Santiago de Chile - *Exploration of microbial communities: from compositional patterns to metabolic models*
- Clémence Frioux - Universidad O'Higgins, Chile - *Discrete models of metabolism for the exploration of microbial communities*
- Simon Labarthe - Symposium H2Rumen, Saclay, France - *Modeling the metabolism of microbial communities with numerical models*
- Simon Labarthe - Microbes 2025 (SFM), Bordeaux, France - *Modeling Microbial Communities: Toward Digital Twins.* [25]
- Simon Labarthe - ISI WSC, The Hague, Netherlands - *Four functional profiles for fibre and mucin metabolism in the human gut microbiome.* [36]
- Simon Labarthe - institut CENTURI seminar, Marseille, France - *Coupling microbial communities models with data.* [58]
- Guilhem Sommeria-Klein - University of Aalborg, Denmark - Microflora Danica lecture series: *Modelling microbial communities in space and time across ecosystems*
- Emna Stambouli - University of Aalborg, Denmark - *Modelling and predicting soil microbial communities at large spatial scale based on metagenomic dimensionality reduction*
- Guilhem Sommeria-Klein - University of Turku, Finland - Symposium "Diversity and dynamics of microbial communities through a quantitative lens": *Modelling microbial communities in space and time across ecosystems*
- David Sherman - Dijon, France - Annual PEPR Agroecology and ICT workshop - "Computational models of crop plant microbial biodiversity"

11.1.5 Leadership within the scientific community

- David Sherman was selected as a delegate representing the PEPR Agroecology and ICT during its mid-term evaluation by the CSTP

11.1.6 Scientific expertise

Recruitment committees

- Clémence Frioux - Junior researcher selection committee of the Plant Health Department (SPE) of INRAe
- Clémence Frioux - Junior researcher selection committee of the Inria Centre at the University of Bordeaux

Grant reviewing

- Clémence Frioux - Grant reviewing UC Louvain, Belgium
- Clémence Frioux - PhD grant reviewing MASTIC Doctoral School, Nantes, France
- Clémence Frioux - Grant reviewing - Human Frontier Science Programme
- Simon Labarthe - PhD grant reviewing ABIES Doctoral School, Saclay, France

Research evaluation

- Simon Labarthe - Evaluation of the agregation application of Elsa Rousseau (U.Laval)
- Simon Labarthe - Member of the CSS (commission scientifique spécialisée) MISTI in charge of the evaluation of mathematics and informatics researchers at INRAE.

11.1.7 Research administration

National responsibilities

- Clémence Frioux - Member of the Inria national committee for equality and inclusion
- Simon Labarthe - Member of the Conseil Scientifique de departement (CSD) of the SPE (santé des plantes et de l'environnement) departement at INRAE
- Simon Labarthe - Member of the steering commity (comité de pilotage) of the metaprogram Holoflux at INRAE
- David Sherman - Member of the steering committee of **Biosena**, a regional research network of the New Aquitaine region dedicated to Biodiversity and Ecosystemic Services.

Local responsibilities

- Clémence Frioux - Member of the gender equality and diversity working group in the Inria Centre at the University of Bordeaux
- Clémence Frioux - Member of the *Commission des Emplois de la Recherche* (CER) the Inria Centre at the University of Bordeaux

11.2 Teaching - Supervision - Juries - Educational and pedagogical outreach

11.2.1 Teaching

University

- Clémence Frioux - Master – ENSTBB Bordeaux INP - Bioinformatics (24 hours)
- Clémence Frioux - Master – ENSEIRB Bordeaux INP - Research algorithms (10 hours)

Scientific workshops

- Clémence Frioux - young researcher school **AI for microbiome**

11.2.2 Supervision

PhD defended this year

- Chabname Ghassemi Nedjad (2022-2025) - *Modelling and solving combinatorial optimisation problems for reverse ecology* - co-directed by Clémence Frioux and Loïc Paulevé (CNRS, LaBRI, Univ. Bordeaux)
- Moein Khalighi (2021-2025) - *Impact of memory on complex dynamics* - co-supervised by Leo Lahti (PhD director, University of Turku, Finland) and Guilhem Sommeria-Klein.

Ongoing PhD supervision

- Nicolas Maurice (2023-2026) - *Sequence algorithmics for genome reconstruction from complex metagenomic data* - Supervision: Clémence Frioux (co-advisor), Claire Lemaitre (Inria, Univ. Rennes - director) and Riccardo Vicedomini (Inria, Univ. Rennes, co-advisor)
- Coralie Muller (2024-2027) - *Generation of metabolomic-informed models of metabolism in complex microbial communities* - Supervision: Clémence Frioux (co-director) and Sylvain Prigent (INRAE BFP, Bordeaux - co-director)
- Mathilde Sola (2024-2027) - *Characterization of large-scale "gut microbiota-diet-health" links in humans using combined approaches of digital microbial ecology, metabolic modeling, and artificial intelligence* - Supervision: Clémence Frioux (co-advisor), Magali Berland (INRAE MGPS, Jouy-en-Josas - co-director) and Patrick Veiga (INRAE MGPS, Jouy-en-Josas - co-director)
- Sthyyve Tatho (2024-2027) - *Intégration de données multi-omiques pour l'analyse de la dynamique de communautés microbiennes en santé des plantes* - Supervision: Simon Labarthe (co-director), Valentina Baldazzi (co-director, INRAE ISA, Inria Macbes, Sophia-Antipolis).
- Sahak Yeghiazarian (2023-2026) - *Modèles métaboliques sous contraintes thermodynamiques pour la modélisation de l'oxydation syntrophique des acides organiques dans la digestion anaérobie* - Supervision: Simon Labarthe (co-director), Nicolas Bernet (co-director, INRAE LBE, Narbonne), Elie Le Quemener (co-director, INRAE LBE, Narbonne).
- Emna Stambouli (2025-2028) - *Modelling and predicting soil microbial communities at large spatial scale through metagenomic dimensionality reduction* - Supervision: Guilhem Sommeria-Klein.
- Chandler Ross (2022-2026) - *Bayesian modelling of stochastic gut microbiome dynamics in large population cohorts* - Supervision: Guilhem Sommeria-Klein, Leo Lahti (PhD director, University of Turku, Finland).

Master's students and apprentices

- Juliette Audemard (Univ. Paris Cité, France) - Apprentice (Master 2) supervised by Clémence Frioux
- Alioune Badara Diouf (Univ. Orléans, France) - Apprentice (Master 2) supervised by Simon Labarthe, Paola Fournier et Jean-Marc Frigerio

Bachelor students

- Killian Duguépérroux (ENS de Lyon, France) - Intern 7 weeks supervised by Clémence Frioux and Guilhem Sommeria-Klein

11.2.3 Juries

PhD defense juries

- Martin Garic, U.Paris Cité. *Multi-scale modeling of transport in the gastro-intestinal tract.* — Simon Labarthe (reviewer).

PhD thesis advisor committees (CSI)

- Charles Goedefroit (Univ. Bordeaux) - Clémence Frioux
- Emma Crisci (Univ. Lyon) - Clémence Frioux
- Bastien Morel (Univ. Bordeaux) - Simon Labarthe
- Koloina Rabemanantsoa (INP Toulouse) - Simon Labarthe
- Céline Hosteins (Univ. Bordeaux) - Simon Labarthe

11.3 Popularization

- Clémence Frioux taught 6 workshops during the "**MIMM, moi informaticienne, moi mathématicienne**" 2025 week, a free internship at the University of Bordeaux for young girls in 9th and 10th grade in order to encourage them to choose mathematics and computer science, allows them to discover training, research and jobs in these two disciplines.
- Clémence Frioux taught a workshop during an event gathering high-school computer science teachers at the Inria Centre of the University of Bordeaux
- **Chiche ! Un ou une scientifique, une classe** — Clémence Frioux (2 classes)
- David Sherman participated in several UCIA demonstration sessions and trainer teachers in using the Poppy Rosa.
- David Sherman participated in a recorded conference-debate on the role of AI in teaching, organized by the Ligue de l'Enseignement

11.3.1 Specific official responsibilities in science outreach structures

- David Sherman is member of the board (membre du Conseil d'administration) and secretary of the Mobsya Association, Lausanne. Mobsya develops and commercializes the Thymio educational robot, geared towards K-12.
- David Sherman is member of the board (membre du Conseil d'Administration) and lead advisor for software of the Poppy Station Association. Poppy Station develops open-hardware open-source humanoid robots for research and education.
- David Sherman is responsible for software engineering and quality in the Poppy Station outreach association
- David Sherman is responsible for software and AI engineering in the UCIA outreach project

11.3.2 Productions (articles, videos, podcasts, serious games, ...)

- David Sherman developed the **Thymio 2+**, [7.1.14](#), a smart wifi router for the classroom that links allows students to use tablet computer to program mobile educational robots. The Thymio 2+ is distributed by **Mobsya** and currently equips more the 600 classrooms.
- **UCIA**, Usage et connaissances des intelligences artificielles, designed by the Ligue de l'Enseignement de la Gironde, Inria, and Poppy Station, is presented to young learners as a serious games combining cards, debates and negotiation, and manipulation of a two-wheeled robot capable of image recognition.
- David Sherman developed the robotics module of UCIA, [7.1.13](#), a serious game with four activities where the student plays user, trainer, and adversary of a simple AI system for self-driving vehicles.
- David Sherman helped produce training videos for the LUCIA robot used in by the UCIA project.

11.3.3 Participation in Live events

- David Sherman participated in two Teacher Training sessions for the UCIA project, in Bazas and Artigues-près-Bordeaux
- David Sherman participated in a live webinaire on Thymio in the classroom using the Thymio 2+ he developed.

11.3.4 Others science outreach relevant activities

- David Sherman is a member of the Scientific Advisory Board of **Enlightware GmbH**, Zürich, which makes educational software

12 Scientific production

12.1 Major publications

- [1] P. Almeida, C. Gonçalves, S. Teixeira, D. Libkind, M. Bontrager, I. Masneu-Pomarède, W. Albertin, P. Durrens, D. J. Sherman, P. Marullo, C. Todd Hittinger, P. Gonçalves and J. P. Sampaio. ‘A Gondwanan imprint on global diversity and domestication of wine and cider yeast *Saccharomyces uvarum*.’ In: *Nature Communications* 5 (2014), p. 4044. DOI: [10.1038/ncomms5044](https://doi.org/10.1038/ncomms5044). URL: <https://hal.inria.fr/hal-01002466>.
- [2] R. Assar, M. A. Montecino, A. Maass and D. J. Sherman. ‘Modeling acclimatization by hybrid systems: Condition changes alter biological system behavior models’. In: *BioSystems* 121 (June 2014), pp. 43–53. DOI: [10.1016/j.biosystems.2014.05.007](https://doi.org/10.1016/j.biosystems.2014.05.007). URL: <https://hal.inria.fr/hal-01002987>.
- [3] M. Bahram, T. Netherway, C. Frioux, P. Ferretti, L. P. Coelho, S. Geisen, P. Bork and F. Hildebrand. ‘Metagenomic assessment of the global distribution of bacteria and fungi’. In: *Environmental Microbiology* (13th Nov. 2020). DOI: [10.1111/1462-2920.15314](https://doi.org/10.1111/1462-2920.15314). URL: <https://hal.inria.fr/hal-03033570>.
- [4] A. Belcour, C. Frioux, M. Aite, A. Bretaudeau, F. Hildebrand and A. Siegel. ‘Metage2Metabo, microbiota-scale metabolic complementarity for the identification of key species’. In: *eLife* 9 (29th Dec. 2020). DOI: [10.1101/803056](https://doi.org/10.1101/803056). URL: <https://hal.inria.fr/hal-02395024> (cit. on pp. 7, 21).
- [5] B. Burgunter-Delamare, H. Kleinjan, C. Frioux, E. Fremy, M. Wagner, E. Corre, A. Le Salver, C. Leroux, C. Leblanc, C. Boyen, A. Siegel and S. Dittami. ‘Metabolic Complementarity Between a Brown Alga and Associated Cultivable Bacteria Provide Indications of Beneficial Interactions’. In: *Frontiers in Marine Science* 7 (21st Feb. 2020), pp. 1–11. DOI: [10.3389/fmars.2020.00085](https://doi.org/10.3389/fmars.2020.00085). URL: <https://hal.inria.fr/hal-02866101>.
- [6] K. Cerk, P. Ugalde-Salas, C. Ghassemi Nedjad, M. Lecomte, C. Muller, D. J. Sherman, F. Hildebrand, S. Labarthe and C. Frioux. ‘Community-scale models of microbiomes: articulating metabolic modelling and metagenome sequencing’. In: *Microbial Biotechnology* (20th Jan. 2024). DOI: [10.1111/1751-7915.14396](https://doi.org/10.1111/1751-7915.14396). URL: <https://inria.hal.science/hal-04409251> (cit. on p. 7).
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