

# 2025 Activity Report

RESEARCH CENTRE: Inria Paris Centre

IN PARTNERSHIP WITH: Institut Pasteur

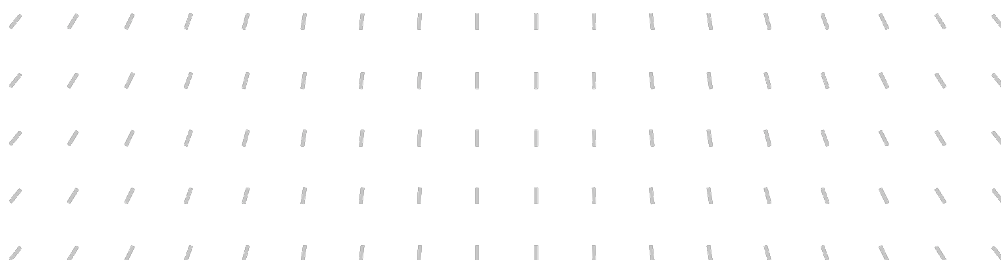
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Project-Team

## INBIO

Experimental and Computational Methods for  
Modeling Cellular Processes

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## **Project-Team INBIO**

*Creation of the Project-Team: 2019 November 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

- A3.1.1. – Modeling, representation
- A6.1.1. – Continuous Modeling (PDE, ODE)
- A6.1.4. – Multiscale modeling
- A6.3.3. – Data processing
- A9.2.1. – Supervised learning

### Other research topics and application domains

- B1.1.2. – Molecular and cellular biology
- B1.1.4. – Genetics and genomics
- B1.1.7. – Bioinformatics
- B1.1.10. – Systems and synthetic biology
- B2.2.4. – Infectious diseases, Virology
- B2.4.2. – Drug resistance
- B5.10. – Biotechnology
- B9.8. – Reproducibility

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## 1 Team members, visitors, external collaborators

### Research Scientists

- Gregory Batt [Team leader, Inria, Senior Researcher, HDR]
- Sean Kennedy [Institut Pasteur, Researcher, from Feb 2025]

### Post-Doctoral Fellows

- Angelica Frusteri Chiacchiera [Institut Pasteur]
- Nathalie Laforge [Institut Pasteur, from Apr 2025]
- Esteban Lebrun [Institut Pasteur, until Sep 2025]
- Eléonore Pourcelot [Institut Pasteur]

### PhD Students

- Alicia Da Silva [Inria]
- Henri Galez [Institut Pasteur]
- Cecilia Pires De Oliveira Capela [Institut Pasteur]

### Technical Staff

- Agnès Baud [Institut Pasteur, Engineer]
- Maïté Gomard [Institut Pasteur, Technician, from Feb 2025]
- Sara Napolitano [Institut Pasteur, Engineer]

### Interns and Apprentices

- Ines Dahlal [Institut Pasteur, Apprentice]

### Administrative Assistants

- Nelly Maloïsel [Inria, 25%]
- Mélanie Ridel [Institut Pasteur, 20%]

### Visiting Scientist

- Lorenzo Pasotti [Pavia University]

## 2 Overall objectives

The main objective of our research is to understand, control, and optimize cellular processes in single cells and at the population level. We combine experimental and theoretical work within a single team.

Our focus is on developing methods and models that take stochasticity of intracellular processes and heterogeneity of cell populations into account. To this end, we use both mixed-effects models as well as continuous-time Markov chains and their diffusion approximations. We develop methods for efficiently calculating with such models and use them to design optimally informative experiments and to reverse engineer unknown cellular processes from experimental data. Furthermore, we deploy models in order to optimally construct and optimally control synthetic gene circuits.

We have recently started to set up our own biology laboratory at Institut Pasteur. We develop novel experimental platforms that are designed to be fully automated, controllable by our own software, and capable of updating the experimental plan in response to incoming measurements. Optogenetic actuation of intracellular processes, coupled to real time fluorescence measurements by microscopy or flow cytometry, then allows us to connect cellular processes with models and algorithms in real time.

The spirit of our work is that experimental platforms and circuits should be constructed with our theoretical work in mind, while our mathematical methods should be usable to address concrete experimental questions in the lab.

## 3 Research program

### 3.1 Cybergentics – real time control of biological processes

Cells have evolved uncountable numbers of feedback circuits to regulate their functionalities in the presence of changing environmental conditions. But can such feedback control also be externalized and placed under control of scientists? Early work on this topic suggested that **optogenetic systems, allowing for external regulation of gene expression**, have the potential to serve as an interface between cells and experimental platform that gives a computer the power to stir the functioning of cells via the application of light. We develop all the tools required to realize automated computer control of intracellular processes. On the experimental side, we develop yeast strains that are equipped with optogenetic promoters to drive various functionalities. On the mathematical side, we develop models and software to equip our experimental platforms with the appropriate programs to realize successful feedback control, both at the level of single cells (microscopy) and at the level of populations (bioreactors and plate reader).

### 3.2 Platforms for automated reactive experiments

The core scientific activity of the team is to connect mathematical methods with biological applications in our lab. The interface between the two sides, that is the experimental platforms, is therefore of crucial importance for the success of our activities. However, platforms that can be purchased by vendors are typically delivered without the capacity to adapt the experimental plan in response to incoming measurements, a functionality that is crucially needed for deploying our computational methods (e.g. feedback control). Therefore, we develop novel experimental platforms and/or extend existing platforms with additional software and hardware that allows us to perform automated reactive experiments. Concretely, we develop a **microscopy platform and control software for yeast that uses a digital micromirror device to expose single cells to targeted light signals** that can be adjusted in real time in response to measurements taken from the cell. Furthermore, we develop a platform of 16 parallel **small scale automated bioreactors**, each equipped with controllable LEDs to allow for optogenetic gene expression and long-term reactive experiments in tightly controlled conditions. Automation of the platform is achieved via a low-cost open-source **pipetting robot that samples all reactors to a benchtop cytometer** in which single cell gene expression is measured in all sampled cells of all reactors. Finally, we develop **software to take full control of a commercial plate reader with liquid injection capabilities** (Tecan Spark). This platform allows us to use a Raspberry Pi to pilot 96 parallel reactive experiments where optical density is used as a readout of bacterial growth.

## 4 Application domains

### 4.1 Preamble

Since most of our research is at the interface of mathematics and biology, there often is no clear split between mathematical research objectives and applications. For instance, feedback control of gene expression is simultaneously a mathematical and an applied problem.

## 4.2 Understanding resistance and tolerance to antibiotic treatments

The non-susceptibility of pathogenic bacteria to antibiotic treatments is a major health problem. Bacteria might escape treatments in two ways: being resistant or being tolerant. Whereas resistant bacteria can multiply in presence of antibiotics, tolerant bacteria can merely survive. Yet, tolerance is increasingly recognized as a major player in treatment failure. In particular, an increasing fraction of commensal and pathogenic *E coli* bacteria express extended-spectrum  $\beta$ -lactamases and/or carbapenemases. When individual bacteria die as a consequence of antibiotic treatments, these enzymes are released and hydrolyze the antibiotic molecules in the environment, conveying a transient protection to the remaining bacteria that lasts until the enzymes are degraded themselves. Understanding how this collective antibiotic tolerance (CAT) shapes population dynamics is difficult yet important for **optimally killing bacterial populations**: when a second antibiotic dose is applied directly after a first dose it will not be effective since the antibiotics will be degraded by the enzymes released from bacteria killed after the first dose; when the second dose is applied too late the surviving bacterial population will have regrown to a large size. Our plate reader platform allows us to apply complex temporal patterns of antibiotic treatments to bacteria over nearly two days. Paralleling such treatments in the 96 well plates allows us to generate rich data sets and to calibrate population dynamics models that can be used to optimize temporal treatment plans. One of the applied objectives of our team is to use these capacities to study a collection of fully-sequenced clinical isolates treated with a broad range of clinically important antibiotics and grown in various media. Ideally, this will lead to an approach that can be used to assay tolerance to antibiotics in hospitals instead of, or in addition to, standard antibiotic susceptibility tests, detecting resistance.

## 4.3 Optimization of protein production in yeast

Many proteins are of technological or therapeutical importance. The yeast *S. cerevisiae* is an interesting organism for protein bioproduction since it combines a relatively fast growth rate with good capacities to perform post-translational modifications needed for protein maturation and full functionality. However, imposing a strong demand on protein production to the cell places a significant burden on its physiology, either at the protein production level or at the maturation and secretion levels. Using systems and synthetic biology approaches, we aim at **better understanding the origins of the production bottlenecks** and then using modeling and control approaches, we aim at finding **optimal control solutions** for bioproduction. Three different strategies are envisioned. In the first approach, bioproduction stress sensors are used to observe in real time the physiological state of the cell, and the demand is externally tuned based on the stress level of the cell population. In the second approach, the stress sensor is used to tune the response capacities of the cell to the external demand, thus creating an internal feedback loop. In the third approach, we control the fraction of the producing cells by engineering an artificial differentiation system that implements the partial differentiation of grower cells into producer cells. The optimization problem is then to find the optimum ratio based on the external environment of the cells.

# 5 Latest software developments, platforms, open data

## 5.1 New platforms

**Participants:** Henri Galez, Gregory Batt.

We have developed InSillyClo, an open-source web application to assist large-scale Golden Gate cloning and MoClo workflows. It is a convenient platform to support laboratory work.

Systems and synthetic biology developments often require the construction of many variants of a genetic circuit of interest, resulting in large-scale cloning campaigns. Golden Gate and Modular Cloning (MoClo), two powerful technologies enabling the scale-up of cloning workflows, play a central role for efficient circuit construction. These workflows include a number of dry-lab tasks, which are time-consuming and error-prone at scale. No software tool was available to handle these tasks in a dedicated, time-saving, and user-friendly manner.

InSillyClo supports an easy specification of genetic designs at any scale, followed by the automated generation of comprehensive workflow-related data. Moreover, InSillyClo leverages Modular Cloning with a versatile typing system of parts to generate user-defined workflows. InSillyClo is open source, accessible with or without user registration, and can also be used locally.

The webapp is accessible at <https://insillyclo.pasteur.cloud>.

## 6 New results

### 6.1 InSillyClo, a user-friendly web application to assist large-scale Golden Gate cloning and MoClo workflows

**Participants:** Henri Galez, Gregory Batt.

Systems and synthetic biology developments often require the construction of many variants of a genetic circuit of interest, resulting in large-scale cloning campaigns. Golden Gate and Modular Cloning (MoClo), two powerful technologies enabling the scale-up of cloning workflows, play a central role for efficient circuit construction. These workflows include a number of dry-lab tasks, which are time-consuming and error-prone at scale. Currently, no software tool is available to handle these tasks in a dedicated, time-saving, and user-friendly manner. We present InSillyClo, an open-source web application to assist large-scale Golden Gate cloning and MoClo workflows. It supports an easy specification of genetic designs at any scale, followed by the automated generation of comprehensive workflow-related data. Moreover, InSillyClo leverages Modular Cloning with a versatile typing system of parts to generate user-defined workflows. InSillyClo is open source, accessible with or without user registration, and can also be used locally.

### 6.2 Harnessing CRISPR interference to resensitize laboratory strains and clinical isolates to last resort antibiotics

**Participants:** Angelica Frusteri, Gregory Batt, Lorenzo Pasotti.

The global race against antimicrobial resistance requires novel antimicrobials that are not only effective in killing specific bacteria, but also minimize the emergence of new resistances. Recently, CRISPR/Cas-based antimicrobials were proposed to address killing specificity with encouraging results. However, the emergence of target sequence mutations triggered by Cas-cleavage was identified as an escape strategy, posing the risk of generating new antibiotic-resistance gene (ARG) variants. Here, we evaluated an antibiotic re-sensitization strategy based on CRISPR interference (CRISPRi), which inhibits gene expression without damaging target DNA. The resistance to four antibiotics, including last resort drugs, was significantly reduced by individual and multi-gene targeting of ARGs in low- to high-copy numbers in recombinant *E. coli*. Escaper analysis confirmed the absence of mutations in target sequence, corroborating the harmless role of CRISPRi in the selection of new resistances. *E. coli* clinical isolates carrying ARGs of severe clinical concern were then used to assess the robustness of CRISPRi under different growth conditions. Meropenem, colistin and cefotaxime susceptibility was successfully increased in terms of MIC (up to > 4-fold) and growth delay (up to 11 h) in a medium dependent fashion. ARG repression also worked in a pathogenic strain grown in human urine, as a demonstration of CRISPRi-mediated re-sensitization in host-mimicking media. This study laid the foundations for further leveraging CRISPRi as antimicrobial agent or research tool to selectively repress ARGs and investigate resistance mechanisms.

### 6.3 Investigation of dynamic regulation of TFEB nuclear shuttling by microfluidics and quantitative modelling

**Participants:** Sara Napolitano.

Transcription Factor EB (TFEB) controls lysosomal biogenesis and autophagy in response to nutritional status and other stress factors. Although its regulation by nuclear translocation is known to involve a complex network of well-studied regulatory processes, the precise contribution of each of these mechanisms is unclear. Using microfluidics technology and real-time imaging coupled with mathematical modelling, we explored the dynamic regulation of TFEB under different conditions. We found that TFEB nuclear translocation upon nutrient deprivation happens in two phases: a fast one characterised by a transient boost in TFEB dephosphorylation dependent on transient calcium release mediated by mucolipin 1 (MCOLN1) followed by activation of the Calcineurin phosphatase, and a slower one driven by inhibition of mTORC1-dependent phosphorylation of TFEB. Upon refeeding, TFEB cytoplasmic relocalisation kinetics are determined by Exportin 1 (XPO1). Collectively, our results show how different mechanisms interact to regulate TFEB activation and the power of microfluidics and quantitative modelling to elucidate complex biological mechanisms.

#### **6.4 Predicting neonatal infection in PPRM with vaginal microbiology and metagenomics: a prospective cohort study**

**Participants:** Sean Kennedy, Agnès Baud.

Early-onset neonatal sepsis (EONS) due to ascending infection is a potentially preventable complication of preterm premature rupture of membranes (PPROM). Our objective was to determine whether the analysis of bacteria from vaginal swab samples is predictive of the risk of EONS in PPRM. In a prospective 3-center observational cohort, patients with PPRM were enrolled between 22 and 36 weeks' gestation (WG) + 6 days. Vaginal swab samples at delivery were analyzed using two different approaches, classical bacterial cultures and shotgun metagenomic sequencing analysis. A metagenomics score was constructed combining the characterization of the vaginal microbiome and the presence of pathogens and the optimal cut-off to predict EONS was tested on a receiver operating curve. 563 PPRM cases were enrolled, with 646 liveborn neonates. PPRM occurred < 32 WG in 41.9 % and deliveries were < 34 WG in 41.0%. The incidence of EONS was 29/646 (4.5%). When considering all central and peripheral microbiological samples available for 26 neonates, the main pathogens isolated were *Escherichia coli* in 14 cases (53.8 %), other gram-negatives in 5 (19.2%), strict anaerobes in 3 (11.5%); there was a single case (3.8%) each with Group B *Streptococcus* (GBS), *Streptococcus anginosus*, *Staphylococcus aureus* and *Ureaplasma urealyticum*. We studied the prediction of EONS among 272 mothers and their 310 neonates (20 EONS, 6.4%) with both culture and metagenomic data available. A culture positive for a major or intermediate pathogen in the vaginal sample at delivery had a sensitivity of 80.0 % and a specificity of 37.9%, adjusted odds ratio (aOR) of 1.6 to predict EONS. The presence of *E. coli* was associated with an EONS risk of 10.6% vs 4.9%, in the absence of *E. coli*. The metagenomics score was highly associated with EONS, with an area under the receiver operating curve of 0.75. At the optimal cutoff value, sensitivity was 70%, specificity was 85%. A metagenomics score greater than 40 was associated with a significantly increased risk of EONS with an aOR of 8.9 in multivariate analysis adjusted for latency period and gestational age. In conclusion, in PPRM, conventional microbial culture of maternal vaginal samples was associated with EONS, but its predictive values remain insufficient to guide perinatal care. Metagenomic microbial signatures improved predictive values. This opens the perspective for a rapid point-of-care test.

## **7 Partnerships and cooperations**

### **7.1 Visits of international scientists**

**Participants:** Lorenzo Pasotti.

Lorenzo Pasotti, assistant professor at the Department of Electrical, Computer and Biomedical Engineering and at the Centre for Health Technologies of the University of Pavia (Italy) has been invited for three months in the InBio team.

## 7.2 National initiatives

- **PPR Antibiorésistance Anoruti** (2021-2025) on the “Analysis of non-response to antibiotics in vivo: application to Escherichia coli urinary tract infections”, coordinated by I. El Meouche (Inserm).

The objective of Anoruti is to identify the different factors involved in the fact that some bacteria sensitive to an antibiotic in vitro do not respond to treatment in vivo.

- **PPR Antibiorésistance Seq2Diag** (2021-2026) on “Whole genome sequencing and artificial intelligence to characterize and diagnose antibiotic resistance and capacity to escape treatment”, coordinated by P. Glaser (Institut Pasteur).

Genomic sequencing has revolutionized microbiological surveillance and molecular epidemiology. The objective of the Seq2Diag project is to provide a proof of concept for its use in hospital and veterinary laboratories as a diagnostic tool for in silico antibiotic sensitivity testing.

- **ANR JCJC SmartSec** (2022-2025) on “Matching maximal host capacities: stress-informed, self-tuning bioproduction circuits”, coordinated by Francois Bertaux (Lesaffre) with Gregory Batt and Sara Napolitano (Inria and Institut Pasteur).

Bioproduction requires diverting resources normally used by host cells for growth and self-replication towards the production of desired molecules. Achieving maximal resource diversion without compromising the essential functions of the host is of critical importance, but is particularly challenging. To tackle this challenge, SmartSec aims at designing host-aware circuits, with application to the production of secreted proteins.

- **Inria/IFPEN PhD fellowship Screen2learn** (2023-2026) on “A screening and learning approach for protein secretion in yeast”, obtained by Alicia da Silva, supervised by Gregory Batt (Inria/Institut Pasteur) and Senta Blanquet (IFPEN).

This project aims to generate data and train a prediction tool for optimizing the production of secreted proteins in yeast. We will quantify secretion levels in different genetic contexts and for libraries of enzyme variants. We will screen for libraries of novel enzymes involved in vegetable biomass degradation, with application to second generation biofuel production.

- **Ferments du Futur Precompetitive projects Screen2Drive** (2024-2026) on “CRISPR-based screens to identify key factors to drive yeast consortia dynamics in fermented food”, coordinated by Gregory Batt (Inria and Institut Pasteur) and Thibault Nidelet (INRAE).

The optimization of fermentation processes is hindered by a too superficial understanding of interactions between yeast species. The Screen2Drive project uses CRISPR-based functional screens and deep-sequencing to identify key genes altering yeast interactions. Our expected goals are to improve fermentation results and develop genetic tools to engineer non-model yeasts.

- **ANR Générique TrojanYeast** (2024-2028) on “Engineering probiotic yeasts to prevent and treat Clostridia-induced intestinal infections”, coordinated by Gregory Batt (Inria and Institut Pasteur), with Bruno Dupuy (Institut Pasteur) and Pierre Lafaye (Institut Pasteur).

This project aims to engineer a probiotic yeast to fight Clostridioides difficile and Clostridium perfringens gut infections. This yeast will produce endolysins to kill the bacteria and nanobodies to neutralize their toxins. We will utilize modular cloning, lab automation, and anaerobic culture platforms to screen and optimize these constructs. If successful, this approach could offer a novel and effective alternative to antibiotics.

- **ABIES doctoral school PhD fellowship CyberStable** (2024-2028) on “Cybergenetic solutions to enforce genetic stability in synthetic biology applications”, obtained by Cecilia Capela, supervised by Gregory Batt (Inria and Institut Pasteur) and Sara Napolitano (Institut Pasteur and Inria).

In CyberStable, we investigate the effects of a bioproduction burden on genetic stability in yeast. We will quantify the impact of induction demands on cell physiology, stress, and genetic stability for various hard-to-secrete proteins. We will also use an artificial differentiation system to engineer more stable production systems. By understanding these complex processes, our research aims to improve the efficiency and reliability of synthetic biology applications.

- **PPR Antibiorésistance NASPEC** (2021-2026) on “Narrow spectrum antibiotics to fight the convergence of bacterial resistance”, coordinated by M. Arthur (Paris Cité University).

The NASPEC project aims to develop antibiotics that target multi-resistant Gram-negative bacteria, while reducing the collateral damage caused by antibiotic therapy on the commensal flora. In order to achieve selective activity on pathogens, two antibiotics from the beta-lactam family will be combined within the same molecule to obtain inactive pro-drugs. Metagenomic analyses will be used to study the potential impact of these molecules on the intestinal flora. The results of this project will provide a rational pipeline for the development of new therapeutic molecules, which will undergo preclinical development with an industrial partner at the end of the project.

### 7.3 Regional initiatives

- **Equipment grant BioConvS Region Ile-de-France PlatPath** (2024-2025) on “Automated platform to engineer pathogenic strain libraries via optimized conjugation”, coordinated by Sara Napolitano (Institut Pasteur and Inria) and Angelica Frusteri (Institut Pasteur and Inria).

This project aims to develop an automated platform for constructing collections of engineered pathogenic bacteria through optimized bacterial conjugation. The platform will include a liquid handler robot, a plate reader, a biosafety cabinet, and control software. It will enable the high-throughput and robust engineering of bacterial collections, particularly for studying antimicrobial resistance in clinical isolates.

## 8 Dissemination

### 8.1 Promoting scientific activities

#### 8.1.1 Scientific events

Gregory Batt has been a member of the scientific committee of the 32nd International Conference on Yeast Genetics and Molecular Biology (Yeast 2025, Paris).

#### 8.1.2 Journal

- Gregory Batt has been a reviewer for *Cell Reports Methods*.
- Sean Kennedy has been a reviewer for *Microbial Drug Resistance*, *Scientific Reports*, and *mBio*.
- Lorenzo Pasotti has been a reviewer for *Science Advances*, *ACS Synthetic Biology*, and *Frontiers in Lab on a Chip Technologies*.

#### 8.1.3 Invited talks

- Gregory Batt has been an invited speaker at the 2nd Berlin-BioTECH Symposium “Autonomous Discovery in Bio- and Chemical-Engineering” (Berlin Nov 2025) and at the “FdF Scientific Day” organized by Ferments du Futur (Saclay, Oct 2025).
- Sean Kennedy gave an invited presentation at the Medical Center of Tromsø (Norway, Oct 2025).

- Lorenzo Pasotti gave an invited presentation at the 34th Annual Conference of the European Society for Biomaterials (ESB 2025), September 7-11, Turin, Italy.

#### 8.1.4 Scientific expertise

- Gregory Batt has been a jury member for the PhD of Nattawt Leelakorn (University of Copenhagen, October 2025) and of Cyprien Guerin (Université Paris Saclay, December 2025). He is also a member of the thesis advisory committees of Manon Perrot (Institut Pasteur) and Felix Knotte (University of Würzburg). Gregory Batt is also a core member of the coordination group of the AI initiative at Pasteur, led by Laurent Essioux.
- Henri Galez received a Best Poster Award at the Yeast 2025 conference for his work on InSillyClo.
- Sean Kennedy served as the primary examiner for the PhD defense of Typhaine Le Doujet at the Arctic University of Norway in October 2025. He has also been a reviewer for the INSERM internal review. He is also a member of the selection committee of the Pasteur Roux-Cantarini call for proposals.
- Sara Napolitano has been a reviewer for the annual general call for proposals (AAPG) of the French National Research Agency (ANR).
- Lorenzo Pasotti has been a committee member for PhDs in Information Engineering - Control, Optimization and Complex Systems (Jun 2025) at the University of Florence, Italy. He has also been a reviewer and a jury member for the PhD thesis of Sara Letrari (Dep. Molecular Medicine) at the University of Padua, Italy. He has also been a reviewer for the annual general call for proposals (AAPG) of the French National Research Agency (ANR).

#### 8.1.5 Research administration

Gregory Batt is the director of the Computational Biology department at Institut Pasteur. Department heads are responsible for research animation (organization of department seminars and of department retreats), are involved in group leader recruitments (regular G5 calls), are involved in the mentoring of recently hired group leaders, have a campus-wide coordination role as representatives of the group leaders and of all department members, and have an advisory role to the direction on scientific and administrative topics (department head meetings).

Moreover, he is a representative of the department directors (DDrep) to discuss with the direction, and participates to the comité de direction (CoDir) of Institut Pasteur.

He is also a member of the freeze clean initiative, aiming at rationalizing the park of -80°C fridges at Pasteur (the larger in Europe, costing > 3M€/year in electricity).

He is also a member of the Comité des Equipes Projets and the Bureau du Comité des Equipes Projets at Inria Paris.

Alicia da Silva and Henri Galez are PhD student representatives, Sara Napolitano is an engineer representative, and Mélanie Ridet is an administrative support representative at the Computational Biology Department Council at Institut Pasteur.

## 8.2 Teaching - Supervision - Juries - Educational and pedagogical outreach

### 8.2.1 Teaching

- Henri Galez took part in a three-day code development hackathon focused on the Python package pyDNA, which supports biological sequence manipulation. The hackathon was held at the Technical University of Denmark (DTU) in September 2025.
- Sean Kennedy gave a course on "the vaginal axis" as part of a teaching session entitled "The Power of the Microbiota" at the "Institut de Formation Supérieure Biomédicale" (Paris-Saclay University).
- Lorenzo Pasotti gave courses on "Bioinformatics and Synthetic Biology" at the Bioengineering Master of University of Pavia, on "Bioinformatics" at the Biotechnology Master of University of Pavia (Italy), and on "Bioengineering and Instrumentation in Sport" at the Sport Science Bachelor of University of Pavia (Italy).

### 8.2.2 Supervision

- Gregory Batt is co-supervising with Senta Blanquet and Etienne Jourdier (IFPEN) the PhD work of Alicia da Silva, “A screening and learning approach for protein secretion in yeast”. Started in Oct. 2023.
- Sara Napolitano and Gregory Batt are co-supervising two PhD students:
  - Henri Galez, “Engineering an autocrine-like system for screening libraries of protein secreting strains in yeast”. Started in Sept. 2022.
  - Cecilia Pires De Oliveira Capela, “Cybergenetic solutions to enforce genetic stability in bioproduction applications”. Started in Nov. 2024.
- Sara Napolitano supervised the work of Ines Dahlal, a dual-education student in "bachelor universitaire de technologie" with specialization in Medical Technology and Biotechnology at Cergy Paris University.

## 9 Scientific production

### 9.1 Publications of the year

#### International journals

- [1] A. Frusteri Chiacchiera, M. Casanova, M. Bellato, A. Piazza, R. Migliavacca, G. Batt, P. Magni and L. Pasotti. ‘Harnessing CRISPR interference to resensitize laboratory strains and clinical isolates to last resort antibiotics’. In: *Scientific Reports* 15.1 (2nd Jan. 2025), p. 261. DOI: [10.1038/s41598-024-81989-5](https://doi.org/10.1038/s41598-024-81989-5). URL: <https://inria.hal.science/hal-04930229>.
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