ERC Starting Grant 2025

Research proposal Part B1

UNDERSTANDING MICROBIOME CONTROL BY ENGINEERING MICROBE-BIOTOPE SYMBIOSES

Acronym

eSYMBIONT

Principal Investigator

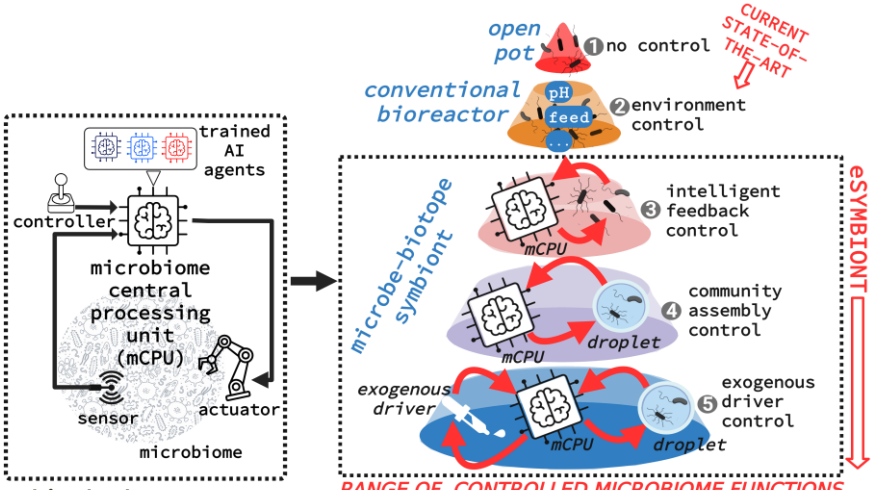
Daniel Rios Garza

Host Institution

INRAE – PROSE/Antony

Proposal Duration

60 months



Graphical abstract

I propose to expand the range of controlled microbiome functions by engineering microbe-biotope symbioses. mCPUs are artificially intelligent agents trained by reinforcement learning.

Executive Summary

Humanity's impact on the planet is influenced by approximately one trillion microbial species, which exist within highly complex and interconnected microbiomes. What if we could control these microbiomes to solve pressing challenges like pollution and climate change? In practice, today, we lack the knowledge to do so.

Theoretical models suggest that microbiomes can be controlled by adjusting their environment—the biotope—tuned by continuous feedback from a desired outcome. In fact, both animals and plants evolved such strategies to control their microbiomes. However, translating these theoretical models into practical applications presents significant challenges; techniques for tracking microbiomes are slow, expensive, and labor-intensive. Even when we manage to track them, we lack the information-processing tools necessary to predict which actions will lead to a desired outcome.

I hypothesize that artificial intelligence (AI) agents can overcome these challenges by learning to control microbiomes in real-time through experience. AI excels at learning abstract concepts and non-linear relationships from vast amounts of multidimensional data. Using an innovative model system, I will develop with my team AI agents to control the most fundamental energy exchanges within complex microbiomes: their electrical currents. Electroactive microbes are widespread across the biosphere, and their electrical signatures reflect complex microbe-microbe and microbe-environment interactions. Our AI agents will accomplish three important tasks for electroactive microbiomes:

1. They will interpret the microbiome's state and take actions that control its electrical activities.
2. They will control which species are included in the system and in what sequence.
3. They will control the addition of exogenous agents to modulate the microbiome's function.

Creating a real-world controller will offer a new perspective on microbiome-based bioprocesses, where autonomously trained AI agents steer the system toward desired functions. Our model system will generate fundamental insights that can improve microbiome-based environmental biotechnologies and lay the foundations for the emerging field of microbiome control.

SECTION A
THE SCIENTIFIC PROPOSAL

The Opportunity & Challenge

Controlling microbiomes can solve humanity's most pressing challenges

Microbes are directly involved in humanity's most pressing challenges (*1*, *2*), with their functions and malfunctions profoundly impacting our existence (*3*). For example, certain microbes capture and fix greenhouse gases, while others produce and release them into the atmosphere. Some microbes help us digest food, synthesize vitamins, and resist invasive pathogens, while others cause deadly diseases. Microbial functions rarely depend on a single microbe; instead, they emerge from vast interconnected ecosystems of microbes known as microbiomes (*4*). **Expanding our ability to control microbiomes promises to solve some of humanity's most pressing health, environmental, and economic challenges**.

Controlling microbiomes is an open challenge

Efforts to control microbiomes often involve connecting control knobs (i.e., biotic and abiotic factors under our control) with desired microbiome functions (*5*–*9*). These efforts include introducing new species, targeting specific populations with antibiotics or bacteriocins, or modifying environmental conditions (*10*–*13*). However, controlling microbiomes has proven to be challenging for several reasons:

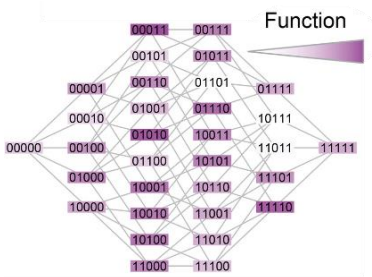


Fig.1. *Five control knobs (e.g., temperature, feed, pH) combine in 32 different ways. Each combination potentially affects a microbiome function (purple gradient) (after ref. (17)).*

Microbiomes are shaped by dynamic interactions between dozens or thousands of diverse species and their environments. These interactions are often poorly understood, nonlinear, and constantly changing. E.g., an introduced strains with desirable functions might be killed by resident phages or antimicrobial peptides (*14*, *15*). At the same time, efforts to engineer resistance into such strains could inadvertently promote the spread of antimicrobial resistance.

Altering microbiome properties can lead to unforeseen consequences. Attempts to boost a single "good" bacterium might inadvertently create conditions favoring a pathogenic one (*16*). Furthermore, external inputs interact with each other and the system (*17*). Added molecules may change their structure due to fluctuations in pH or temperature or the actions and interactions of microbes, leading to a combinatorial explosion between control knobs and their effects (**Fig.1**). **Overall, it remains a significant challenge to predict how interventions translate into specific microbiome effects.**

Background and hypotheses

Theory predicts that feedback control strategies are effective in controlling complex, interconnected systems like microbiomes

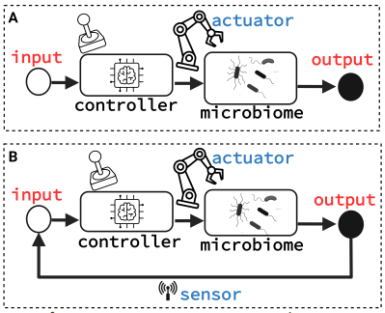


Fig. 2. *Two strategies to control complex system like microbiomes. (A) The conventional open-loop and (B) feedback (or closed-loop) control.*

Theoretical models predict that complex, nonlinear biological systems like microbiomes can be controlled through feedback control strategies (*6*, *7*, *18*, *19*), also known as closed-loop control strategies (**Fig. 2B**). These strategies involve selecting control knobs and continuously adjusting the intensity or duration of interventions based on their effects on the targeted microbiome function. While feedback control is typically used to keep environmental parameters stable, I am referring here to its use in directly controlling the microbiome. This means adjusting environmental conditions to influence microbiome functions, rather than maintaining constant conditions (**Fig.2**).

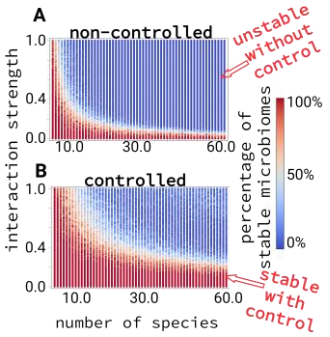


Fig. 3. *Fraction of stable microbiomes in 10,000 GLV simulations. Here, I simulated random microbiomes with increasing interaction strengths and number of species. Adding a controller (B) increases the range of stable microbiomes (red vs. blue points).*

Feedback control can expand the range of controllable microbiome functions by making the system more stable and easier to control. Based on the generalized Lotka-Volterra (GLV) model, commonly used to model microbiomes (*20*), communities are only expected to be stable when their interactions are sufficiently weak or when only a few species strongly interact (**Fig. 3A**). This stability-complexity tradeoff was first shown by Robert May in the 1970s (*21*) and, recently,

for human and sponge-associated microbiomes (*22*). However, as I show in **Fig. 3B,** introducing a feedback controller can significantly shift the stability-complexity tradeoff in the GLV model. This suggests that feedback control expands the range of controllable microbiome functions similar to how technology maintains complex systems far from their natural equilibrium state using feedback control, as seen in airplanes in flight, cars in motion, and heated homes in winter.

Two key bottlenecks prevent us from implementing feedback control strategies for microbiomes in practice. First, they require continuously monitoring microbiome composition and/or function: microbiome monitoring techniques like high-throughput sequencing and metabolomics are slow, expensive, and resource-intensive. Second, they require intelligent information processing to determine which actions to take, given the microbiome's current state (**Fig. 2B**): predicting how biotic and abiotic interventions translate into desired effects in microbiomes is challenging. As a result, **feedback control strategies, although promising theoretically** (*6*, *8*, *9*, *23*)**, lack experimental validation.**

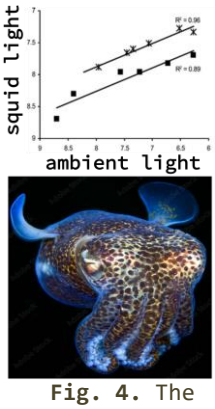


Fig. 4. The Hawaiian bobtail squid controls *V. fischeri* to produce light. Two experiments reproduced from ref. (32)

The way animals and plants control their microbiomes, shows how feedback control could work in practice—the natural microbe-biotope symbioses

Animals and plants achieve dynamic, real-time control over their microbiomes through microbe-biotope symbioses. Here, the host acts as the biotope—i.e., the specific environment where the microbiome thrives, continuously sensing its microbiome and taking actions to promote beneficial functions. In nature, active control often suppresses selfish behavior (*24*), a key mechanism in host-microbiome coevolution (*25*, *26*).

For example, legumes rely on microbiomes in their root nodules to fix nitrogen, a costly function. In return, the plant supplies nutrients. If some nodules fail to fix sufficient nitrogen, the plant stalls their nutrient supply (*27*). Similarly, the mammalian gut recognizes the unique electrical signature of its microbiome (*28–31*). This signature emerges from interactions between electrogenic bacteria and metabolic byproducts. By sensing these electrical signals (via electrotaxis), immune cells can target microbes at locations with atypical signatures (*31*). Another example is the Hawaiian bobtail squid, which isolates *Vibrio fischeri* from seawater and controls it to produce specific light intensities using ambient light as a feedback cue (*32*). Lighting up allows the squid to hide its shadow from moonlight while hunting and evading predators (**Fig. 4**).

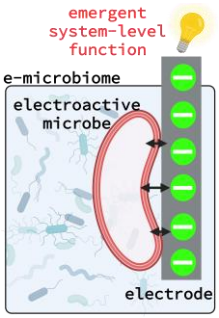


Fig. 5. *Electroactive microbes in e-microbiomes interact with electrodes, generating an electrical signature.*

In contrast, many microbiome-based bioprocesses rely on open-loop interventions (**Fig. 2A**) to control the biotope. These interventions lack feedback mechanisms to adjust their input based on desired outcomes (*33*). Biotope parameters like pH, temperature, and flow rate are typically held constant during operation, despite their potential roles in modulating microbiome function (*34–39*). Optimization relies on modeling, which requires deep knowledge of the microbiome—often lacking—or on empirically optimizing conditions, usually one at a time. **My hypothesis is that to control microbiomes effectively, we need to engineer microbe-biotope symbioses using nature's chief mechanism: feedback control.**

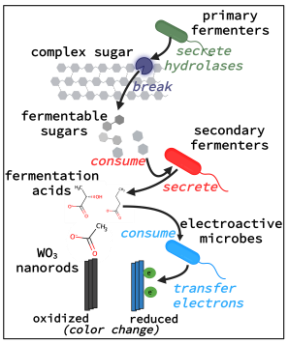


Fig. 6. *The electrical signature, measured by the oxidation of WO_3 nanorods is the result of a myriad of biotic and abiotic interactions.*

Innovative Model System

Electromicrobiomes (e-microbiomes) are attractive model systems for feedback control in practice—the engineered microbe-biotope symbioses

Recent discoveries show that many of the Earth's microbiomes are e-microbiomes, i.e. microbiomes containing microorganisms that electrically interact with each other and their environments (*40–45*). Electroactive microorganisms influence various environments by "plugging in" (connecting electrically) to other cells and minerals, or by extracellularly reducing redox-active molecules like flavins and humic compounds (*46–49*). E-microbiomes are common across anaerobic biomes, including animal guts, anaerobic digestors, and anaerobic soils and sediments (*50–53*).

Key properties make e-microbiomes attractive for studying microbe-biotope symbioses:

1) Measurable electric signatures: Microbial extracellular electron exchanges generate measurable electric signatures that we can monitor using electrodes (**Fig. 5**) or colorimetric assays (**Fig. 6**) (*54*, *55*). These

signatures reflect the most fundamental energy exchanges within the microbiome (*56*). Between these exchanges and the system's molecules (like complex sugars, amino acids, vitamins, etc.) lie complex species-species and species-environment interactions (**Fig. 6**) (*57–59*). Producing a desired electrical signature requires aligning these interactions, similar to managing other microbiome functions like maintaining healthy gut communities, producing tasty fermented foods, or reducing greenhouse gas emissions (*60–62*).

2) Feasible interface to wire the microbe-biotope symbioses: E-microbiomes offer a unique opportunity to create a rapid feedback loop between external interventions and the microbiome's electrical activity (*63*). This interface will allow me to develop microbiome processing units (mCPUs) capable of managing the system's inherent complexity while sensing and controlling its functions (**Fig. 7**). **By learning to modulate the electrical currents of e-microbiome, we can gain valuable insights into controlling the emergent functions of complex microbiomes in practice.**

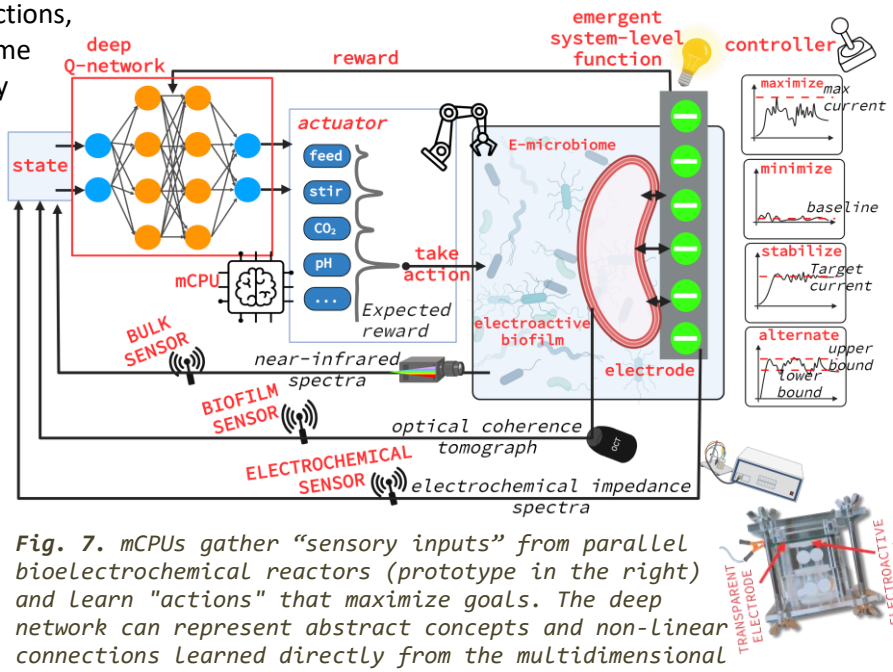


Fig. 7. *mCPUs gather "sensory inputs" from parallel bioelectrochemical reactors (prototype in the right) and learn "actions" that maximize goals. The deep network can represent abstract concepts and non-linear connections learned directly from the multidimensional data.*

3) Promising biotechnological systems: Engineered e-microbiomes can convert industrial and domestic waste into electricity and valuable molecules, making them promising biotechnological systems (*51*). E-microbiome research offers a solid baseline for understanding system performance and variability. Known performance and variation will allow me to benchmark mCPUs against stablished microbiome engineering strategies (*41*, *56*, *64*).

Scientific Objectives

Toward engineered systems mimicking natural microbe-biotope symbioses

I will bring artificial microbe-biotope symbionts into reality by integrating microbiomes and intelligent feedback controllers in three steps:

1. **Wiring feedback control:**

I will develop artificially intelligent controllers called microbiome central processing units (mCPUs, **Fig. 7**). mCPUs will be trained using deep reinforcement learning, an approach inspired by how animals adapt their behavior based on environmental cues (*65*). The basic ideas of this approach are illustrated by its success in beating the Atari video game Breakout (**Fig. 8**) (*66*). Controlling microbiomes, however, is a significantly more challenging task: **mCPUs need to process multidimensional biological data and make decisions in a highly dynamic and unpredictable environment**. Nevertheless, this is feasible since reinforcement learning is an active research field that has recently enabled the control of complex systems like drones and self-driving cars using multisensory data (*67*).

Fig. 8. *AI agent trained to "sense" high-dimensional pixel data and decide on control moves that—based on previous experience—maximize the score. The agent learned that by digging a hole in the left corner it achieves a jackpot. From ref. (66)*

2. **Controlling the microbiome assembly process:**

To enhance controllability, I will systematically reduce complex microbiomes into minimal functional units while controlling them with mCPUs. The functionality of microbiomes largely depends on their composition and assembly history (*68*, *69*). Although multi-species communities can outperform isolated strains by dividing tasks and collectively resisting stress (*70–72*), they are often unpredictable and difficult to control (*73*, *74*). Studies indicate that small consortia or even isolates can outperform open microbiomes in specific functions (*75–77*). For example, certain bacteria isolated from complex e-microbiomes produce nearly double the current densities of their original mixed cultures under the same conditions (*78*). Similar to the squid

depicted in **Fig. 4,** which isolates a lowly abundant ocean microbe, to then control its luminescence. Achieving the same control is unlikely in a complex mixture. By controlling key variables of the community assembly process—namely, which species are included and in what order—I will improve the ability of mCPUs to control microbiomes.

3. **Incorporating external control elements:**

I aim to connect mCPUs to biotic and abiotic control knobs to expand the range of controllable microbiome states. Microbiomes naturally interact with various external factors (*79–81*). By integrating and controlling a range of molecules and microbes not present in the original setup, I aim to significantly enhance the range of controllable functions. This approach aligns with recent theoretical frameworks proposing that by controlling specific sets of microbes—referred to as "minimal control elements"—we can influence the entire microbiome composition (*6*, *8*, *18*). This is feasible because species within a microbiome influence each other, allowing for the design of control chains that connect external levers to intrinsic interactions (as illustrated in **Fig. 9**).

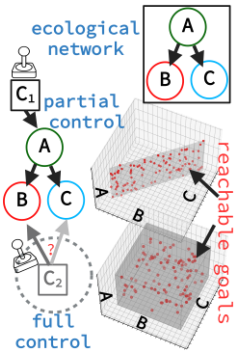


Fig. 9. *Species "A" influences species "B" and "C". By controlling its composition (lever C_1), we influence "B" or "C" (the third component is uncontrollable). For full-state control, at least a second lever (C_2) is needed. Simulation based on (6)*

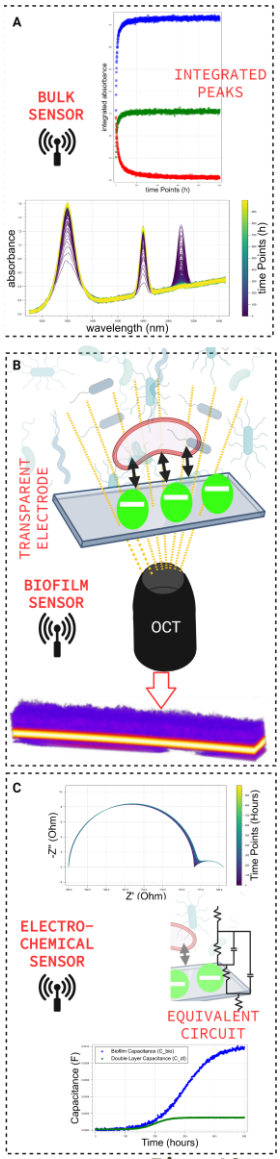


Fig. 10. *Illustration of a e-microbiome sensed in real-time. (A) simulated near-infrared data from the bulk medium (two molecules produced, one consumed) ranges from (82); (B) illustrative OCT setup, with an example image from (85); (C) Simulated electrochemical impedance spectroscopy (EIS) with equivalent circuit and ranges based on (88).*

PROGRAMME OF RESEARCH

Approach and Feasibility

Research Task 1 (RT-1): Engineering intelligent feedback control with microbiome processing units (mCPUs)

(Years 1-3, 1 postdoc)

To investigate the emergence of intelligent feedback control in microbe-biotope interactions, we will develop artificially intelligent agents (mCPUs) to control the electrical signatures of e-microbiomes (**Fig. 7**). Acting as "microbiome brains", mCPUs will learn from experience to process sensory information and take actions that maximize control goals, potentially discovering new strategies, similar to the learning process in the Atari game shown in **Fig. 8.** mCPUs will be trained through shared experiences between parallel reactors, acquiring real-time data from the main compartments of the system: bulk medium, the biofilm, and their electrochemical interface (**Fig.10**) (*63*, *82–89*).

I have already secured funds for parallel near-infrared spectroscopy (**Fig. 10A**) and optical coherence tomography measurements (**Fig. 10B**). Additionally, the neural network and training data will be open-source and easily accessible, building on my experience with miaSIM (*90*) and DNNGIOR (*91*).

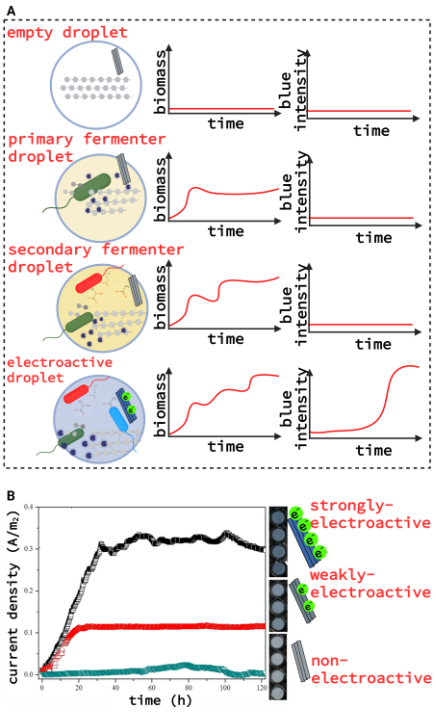


Fig. 11. *Droplets containing WO3 nanorods and complex substrates change to blue when all ecological roles are present, as seen in plates (55). approximately 1000 droplets are incubated per round.*

RT-2. Controlling the assembly of e-microbiomes by isolating minimal, controllable ecological units

(Years 2-4, 1 PhD)

To investigate the role of community assembly processes in microbiome control, we will develop a new method to decompose complex e-microbiomes into minimal functional units—i.e., minimal syntrophic consortia capable of exchanging electrons with extracellular acceptors (**Fig. 6**). We will achieve this with dilution-to-extinction experiments conducted in an automated high-throughput microfluidic droplet system

(Millidrop, concept illustrated in **Fig. 11** and (*55*)). This system allows droplets to be incubated under homeostatic conditions, monitored over time, stored, and later recovered. The Millidrop developers are located near our lab and are committed to helping my team extend their technology, initially developed for isolates, to study minimal ecological units.

RT-3. Expanding controllability with exogenous drivers

(Years 3-5, 1 PhD)

To investigate microbiome control under the influence of exogenous factors, we will progressively expand the action-space of mCPUs by introducing a panel of biotic and abiotic elements not present in the original system. The biotic factors will consist of minimal ecological units obtained in RT-2, while the abiotic factors will include electron shuttles, micronutrients, and alternative carbon sources, which commonly shape e-microbiomes (*47*, *48*, *52*, *56*). Building on my experience in microbiome modeling (*20*, *90*, *92–95*), we will define a spectrum of theoretically possible states—based on metabolic models and thermodynamic constraints—that mCPUs fail to reach. Employing our array of parallel reactors and automations (developed in RT-1), we will incrementally add external factors to the mCPU action sets, aiming to reach previously unreachable states. Sequencing and metabolomics will help elucidate ecological control chains (**Fig. 9**) and explain why particular external factors enhance controllability, thereby enriching our theoretical models of the system.

Risk Assessment and Mitigation

Engineered microbe-biotope symbioses are at the frontier of microbiome control, and bringing them to reality is a risky but rewarding challenge. Key conceptual risks exist: What if the neural network fails to learn the connections between sensing and actions? What if actions prove ineffective in driving functions? What if learning is too slow or computationally/experimentally prohibitive?

In our favor, theoretical results show that feedback control is effective for microbiomes (**Fig. 3**)—animals and plants use such mechanisms in practice (**Fig. 4**). Furthermore, deep reinforcement learning achieved remarkable success in processing information from high-dimensional sensors to control complex systems in many different fields (*96*) (exemplified in **Fig. 8**). Regardless of the outcome, I will learn the strengths and limitations of intelligent feedback control from a real-world example. This empirical knowledge—currently lacking—is instrumental for optimizing microbiome control strategies and for refining theoretical models (*8*, *23*).

Interdependency between key objectives is another risk. What if mCPUs turn out to be ineffective controllers, and, for example, underperform current open-loop strategies? Systematically selecting minimal ecological units for finer microbiome control still represents significant advance. As a fallback, we will study microbiome control on the minimal ecological units and external drivers using models I recently co-developed (*37*).

Like some of my previous projects (*37*, *94*, *97*), this project presents operational challenges that require coordination across diverse fields such as artificial intelligence, reactor engineering, and electromicrobiology. To overcome these challenges, I formed a consultative committee composed of three highly experienced scientists in engineering bioelectrochemical systems: Theodore Bouchez, Yannick Fayolle, and Elefteria Ntagia, e.g., (*98–105*). They will provide my team with periodic consultations. I will also recruit a postdoc with a PhD in deep learning applied to empirical systems, who will fill in gaps in deep reinforcement learning.

Expected Outcomes and Scientific Breakthroughs

By engineering microbe-biotope symbioses in a real-world model system, I want to promote a timely transformation in microbiome bioprocesses, where intelligent, dynamic, and autonomously trained controllers replace static open-loop systems. Combining e-microbiomes with deep reinforcement learning potentially solves two key bottlenecks that currently prevent microbiome feedback control in practice: expensive, labor-intensive monitoring and the lack of intelligent information processing.

By developing mCPUs for e-microbiomes, I immediately benefit from a local network of collaborators who apply e-microbiomes to convert and valorize waste (*101*, *105*). These collaborations enable the translation of our findings directly into their on-going work.

Similar architectures, where AI agents control microbiome phenotypes by adjusting the biotope, can already be envisioned for several other microbiome bioprocesses, including anaerobic digesters, wastewater treatment plants, and environmental biorefineries. The experience gained in this project will lead to new collaborative efforts focused on optimizing environmental bioprocesses through microbiome control.

This project goes beyond the state of the art by developing the first real-world example of an intelligent microbiome feedback controller. I anticipate high-impact publications and active participation in international microbiome meetings.

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SECTION B
CURRICULUM VITAE AND TRACK RECORD

Personal Details

Garza, Daniel Rios
ORCID: 0000-0003-3865-2146
Website: https://danielriosgarza.github.io/

Current position

2023-… **Researcher "Chargée de recherches"**
Université Paris-Saclay, INRAE, PROSE, Antony, France
Current topics:

- Microbiome systems ecology
- Modelling and controlling microbiomes in bioprocess

Position is 100% focused on research, no teaching duties.

Previous position

2020-23 **Postdoc at the Rega Institute (KU Leuven, Belgium)**
Advisor: Karoline Faust
Topics:

- Gut microbiome ecology and multistability
- Model development and experimental validation with synthetic microbiomes

Postdoc funded by Karoline Faust's ERC STG "EcoBox".

Education

2014-2020 **Ph.D. in Computational Biology at the Radboud University, The Netherlands**
Thesis: Exploring microbial ecology and evolution with genome-scale metabolic models [link]
Supervisors: Bas Dutilh and Martijn Huynen
PhD fully funded by my own grant.

2013-2014 **M.S. in Virology**
Evandro Chagas Institute – Brazil

Research Achievements

As a young researcher, I spent the past decade studying microbes and microbiomes [see ref. 1 of list below]. I independently collaborated with computational and experimental biologists to build theoretical models and design experimental systems to challenge and refine my models. My work has been recognized with publications in top journals (Nature Microbiology, Cell Systems, Gut Microbes) and invitations to speak at national and international conferences (BioSB, ISME, INI).

Ground-breaking microbiome research: patterns learned from metabolism

- I developed MAMBO [2], an open source computational framework that has been used by several research groups (more than 98 citations since 2018) to predict the environmental molecules shaping microbiome composition.
- I also created algorithms to predict why certain bacteria are enriched in cancer while others are depleted [3].

- In collaboration with my co-supervised PhD student Meine Boer from Utrecht University, I developed a deep neural network that significantly outperforms state-of-the-art methods for metabolic reconstruction. Our models have similar quality to manually curated models that take months to complete [4].

Microbiomes are too complex to be fully captured by the conventional models used in natural sciences. These studies innovated by using metabolism as a unifying system to uncover the mechanistic basis for patterns observed in genomic and metabolomic microbiome data. However, to fully grasp microbiome dynamics, it is essential to connect these mechanisms to empirical data, bridging the gap between theoretical models and real-world observations.

Breakthroughs across scales: from theory to informative experimental systems

- I supervised the development of miaSIM, a Bioconductor R package that implements dynamic microbiome models while greatly simplifying the process of developing, sharing, and comparing theoretical models with empirical datasets [10].
- In a comprehensive Cell Systems perspective, I discussed new methods for incorporating metabolism into microbiome models [5].
- In collaboration with experimental biologists, we showed how certain microbes impact cancer cells [6] and how the interactions between microbes are dynamic and change when physical and chemical environments change or are altered by the microbes themselves [7].
- I also discovered a novel mechanism of multistability in microbiomes using mini-bioreactors, models, and theoretical simulations [8].

My research highlights the limitations of traditional theoretical ecology frameworks when applied to microbiomes. While mathematical models incorporating metabolic flexibility and dynamic interactions excel in small experimental systems, a significant gap remains between these models and a comprehensive understanding of full-scale microbiomes. For example, the model I developed in [8] required the parametrization of over one hundred variables to explain the dynamic states of just three microbes [see model description].

Innovative approaches: towards microbiome control

Despite extensive research into the structure, function, and ecology of Earth's microbiomes, much of this knowledge has yet to be translated into effective strategies for engineering microbiomes to meet specific goals, as we recently discussed for gut microbiomes [9].

Can we engineer microbiomes that are too complex to be captured by conventional models and, at the same time, bridge the gap between small-scale models and real-world microbiome control?

An often-overlooked aspect of microbial interactions are their physical modes of communication. In the microbial world, communication often occurs through sound waves, electromagnetic radiation, and electric currents. My plan is to bridge the gap between small-scale models and real-world microbiomes by training state-of-the-art deep learning methods to interpret and manipulate these physical signals. To pursue this promising new research direction, I am establishing a research group in a scientific unit where my expertise in microbiome modelling, machine learning, and ecology can be combined with the necessary scientific and technical support needed to engineer real-world microbe-biotope symbioses.

Selected Research Outputs

N° publications: 22; N° citations: 510 (Aug. 2024)

Publications

1) **Garza** & Dutilh (2015) From cultured to uncultured genome sequences: metagenomics and modeling microbial ecosystems. *Cellular & Molecular Life Sciences*

   cited 169 times

2) **Garza** et al. (2018) Towards predicting the environmental metabolome from metagenomics with a mechanistic model. *Nature Microbiology*

   cited 98 times

3) ***Garza** et al. (2020)* Metabolic models predict bacterial passengers in colorectal cancer. *Cancer & Metabolism*

   cited 40 times

4) Boer, Melkonian, Zafeiropoulos, Haas, **Garza**, Dutilh (2024) Improving genome-scale metabolic models of incomplete genomes with deep learning. *iScience* (in press)

5) **Garza** et al. (2023) Metabolic models of human gut microbiome: advances and challenges. *Cell Systems*

6) Taddese, **Garza**, et al. (2020) Growth rate alterations of human colorectal cancer cells by 157 gut bacterial. *Gut Microbes*

7) Liu, **Garza**, et al. (2023) Starvation responses impact interaction dynamics of human gut bacteria *Bacteroides thetaiotaomicron* and *Roseburia intestinalis*. *The ISME Journal*

8) **Garza**, et al. (2024) Phenotype switching explains the emergence of alternative stable states in a gut microbial community. [BioArxiv] Submitted to Nature Microbiology

9) Liu, *Garza*, et al. (2024) Exploiting gut microbial traits and trade-offs in microbiome-based therapeutics. *Nature Reviews in Bioingineering*

Open-source software

10) Gao, Şimşek, Gheysen, Borman, Li, Lahti, Faust, **Garza** (2023) miaSim: an R/Bioconductor package to easily simulate microbial community dynamics. *Methods in Ecology and Evolution*

Peer Recognition

Invited talks

- ✓ Utrecht Bioinformatics Center (2018) *Predicting microbiome signatures from metabolic models*.
- ✓ BioSB (2019) *Interpreting microbes in their environments with metabolic models*.
  Main Dutch bioinformatics and systems biology conference
- ✓ School on the analysis of microbial time series data (2021) - *simulating microbial interactions with the miaSim package*.
- ✓ Economic principles in cell physiology (2022) Dynamics *and metabolic strategies in gut bacterial consortia*.
- ✓ ISME 18 (2022). *Hunger games: exploring the ecology of dynamic life strategies in a synthetic ecosystem of human gut bacteria*.
  Main international conference in microbial ecology
- ✓ BioSB Metagenomics Advanced Course (2022) *metabolic modelling of microbiomes*.
- ✓ INI (2022) Microbial communities: current approaches and open challenges. *Exploring the dynamic metabolic strategies of a gut bacterial consortium*.
  Selective conference funded by the Isaac Newton Institute for Mathematical Sciences in Cambridge
- ✓ FindingPheno Mechanistic models training (2023). *Simulating microbial ecology with dynamic models*.
- ✓ Modeling microbial ecology at multiple scales (2021) tutorials on microbial community modeling
  Tutorials I co-organized (https://modelmems.github.io/).

Ad hoc Reviews (~10 per year)

Nature Microbiology, Nature Communications, Nature ecology and evolution, Microbiome, Elife, mSystems, Journal of the Royal Society Interface, Applied and Environmental Microbiology, Journal of Virology, BMC Genomics, etc.

Guest scientific editor of Frontiers in Cell and Developmental Biology.

Awards & Grants

Personal grant for a full PhD in Nijmegen. CNPQ (2014)

Best PhD paper for the tumors of digestive tract topic. RadboudUMC (2019)

Best TED talk. CMBI (2018)

Grant for a high-risk exploratory idea. Explorae (2024)