INTERNSHIP PROPOSAL

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Optimizing microbial intake strategies for therapeutic outcome: a mathematical modeling perspective

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Duration and available dates for the internship: up to 6 months, starting in January 2027 at the earliest

Location: Laboratoire de Chimie Bactérienne, Marseille

Deadline for applications: 30th November 2026

Send a cover letter and a CV – informal inquiries welcomed

Expected profile:
M2 student with sufficient mathematical background (e.g., applied maths, physics, interdisciplinary programs)

Contact: florence.bansept@univ-amu.fr

Short description of the host team:

Our group's research focuses on understanding the eco-evolutionary dynamics governing the composition and function of microbial communities. We are currently particularly interested in the mechanisms that allow the maintenance of the gut microbiome diversity and function, a key indicator of health. To study these questions, we use mathematical modeling, combining analytical and numerical techniques with stochastic simulations. We also exchange frequently and collaborate with experimentalists to inform our models' development.

Description of the internship project:

Animals' guts are home to a myriad of microbes forming an ecosystem, the microbiome, that fulfills important functions for its host, e.g., helping it with digestion. Correlations between microbiome composition and host health open up new therapeutic possibilities: manipulating the composition of the gut microbiome can lead to beneficial health outcomes. In our recent work, we developed a minimal model of a microbial community subjected to immigration spikes. We demonstrated that there are almost always microbial influx parameters that maximize community diversity, taken as an indicator of health [1]. However, several simplifying assumptions limited the translational scope of this model. One of them was to adopt a purely compositional framework, while from an empirical perspective, several different microbial compositions can lead to the same metabolic outcome available to the host, a concept called *functional redundancy*. This necessitates shifting our description to a functional perspective. Within this framework, interventions such as the administration of prebiotics, probiotics, or antibiotics aim to shift the system from a deleterious functional attractor to another, more beneficial one.

The aim of this internship will be to build on the previous work of the team [1] and emerging functional descriptions [2] to build a modeling framework based on classical consumer-resources assumptions. Classical analytical approximations will be rederived and numerical simulations will be performed, with a specific focus on community assembly. Indeed, immigration is often considered either continuous, or to happen sequentially,

one strain at a time, with ecological relaxation between each introduction. In reality, feeding events happen with a discontinuous pattern, bringing several strains into the system simultaneously. We will study how modifying these input regimes will modify the expected dynamical regimes and their dependency on the structure of resource preferences.

Interdisciplinarity and disciplines involved: This project proposes to use mathematical modeling to answer a biological question relevant for health. It will require tools from dynamical systems such as stability analysis and numerical solving. The host team is a team of theoretical biologists with various background ranging from fundamental physics to molecular biology, and is embedded within a microbiology lab. For this project, there is an active collaboration with the group of Thomas Roeder at Kiel University, working on the gut microbiome of drosophila.

Bibliography

[1] V. M. Marquioni et al., *Modulating microbial intake helps to maintain the gut microbiome diversity*, Comm Bio, 2026
[2] L. Fant et al., Eco-evolutionary dynamics lead to functionally robust and redundant communities, PLoS Comp Bio, 2026