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Title of the internship: Maximizing the diversity of gut microbial communities via controlled intermittent feeding

Duration and available dates for the internship: 8 weeks to 6 months, starting in January 2026 at the earliest

Short description of the host team:

Our group's research focuses on understanding the eco-evolutionary dynamics governing the composition of the gut microbiota. We are currently particularly interested in the mechanisms that allow the maintenance of the microbial community diversity, 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:

A multitude of microbes inhabit animal bodies. They can be found, for instance, on the skin, in the genital tract, or in the mouth, and many important biochemical functions have been associated with these microbes [1]. In the gut, where they are the most abundant, microbes degrade complex fibers that the host cannot digest by itself, and form byproducts that can be absorbed by intestinal epithelial cells. Changes in the composition of the gut microbiome have been correlated with a wide range of diseases, including diabetes, psoriatic arthritis, Crohn's disease, psychological conditions, and cancer [2]. To quantify such connections, descriptive measures of the microbiome have been employed. Among them is the Shannon diversity index: it has been shown that lower values of this index are linked to poor host health status.

In a recent study [3], our team developed a mathematical model to investigate how microbial immigration affects the Shannon diversity of the gut microbiome. We found that there exists an immigration rate that maximizes observed diversity. Assuming that microbial inflow into the gut mostly originates from ingested food, it must be possible to maximize diversity through controlled feeding patterns, which can be derived from our model. However, to which extent our findings are robust to the mathematical assumptions we made on microbial interactions remains unclear. This project aims to investigate this question by modifying the original set of equations to include Generalized Lotka-Volterra dynamics [4] and testing whether our quantitative results hold under these changes.

Expected results / deliverables of the internship:

At the end of the internship, the student is expected to have learned how to analyze sets of differential equations — both analytically and numerically — which are frequently used to model ecological dynamics. The characterization of the *Maximal Diversity Strategy* [3] emerging from the equations in a two-type system constitutes the primary outcome of this internship, and its extension to the many-type case is the ultimate goal.

Interdisciplinarity and disciplines involved:

This project relies on dynamical systems techniques applied to the ecology of microbial communities, particularly — though not exclusively — within the gut environment. Accordingly, its development involves biological aspects of bacterial interactions and the gut microbiome, as well as the analysis of nonlinear differential equations and numerical integration methods.

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References

[1] C. Huttenhower *et al.*, "Structure, function and diversity of the healthy human microbiome," *Nature*, vol. 486, no. 7402, pp. 207–214, June 2012, doi: 10.1038/nature11234.

[2] A. M. Valdes, J. Walter, E. Segal, and T. D. Spector, "Role of the gut microbiota in nutrition and health," *BMJ*, p. k2179, June 2018, doi: 10.1136/bmj.k2179.

[3] V. M. Marquioni, A.-C. Hofacker, J. V. Villavicencio, and F. Bansept, "Optimizing microbial intake helps to maintain the gut microbiome diversity," Mar. 10, 2025, *bioRxiv*. doi: 10.1101/2025.03.05.641598.

[4] I. Akjouj *et al.*, "Complex systems in ecology: a guided tour with large Lotka–Volterra models and random matrices," *Proc. R. Soc. Math. Phys. Eng. Sci.*, vol. 480, no. 2285, p. 20230284, Mar. 2024, doi: 10.1098/rspa.2023.0284.