Metabolic fitness landscapes in fluctuating environments

Duration and available dates for the internship: 7 weeks to 6 months, starting in January 2025 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 [1], [2]. We also exchange frequently and collaborate with experimenters to inform our models' development.

Description of the internship project:

Natural selection favors organisms that are better to reproduce and survive. The "survival of the fittest" reflects the fit between an organism's phenotype and its environment: an organism's *fitness* quantifies how good it is at exploiting the environments in which it lives. At the cellular level, environmental exploitation is achieved through metabolism: enzymes process substrates into products that eventually help reproduction or survival. For that reason, we expect enzymes to have evolved towards being very efficient. Assuming that fitness is a function of enzymatic efficiencies, we can draw metabolic *fitness landscapes* to predict how evolution should shape their phenotypes. Thus far, it has mainly been considered that fitness coincides with the metabolic flux reached at biochemical steady-state. However, there are several cases where this homeostatic assumption is unrealistic: for instance, microbial cells living in animals' guts face recurrent feast and famine cycles due to intermittent feeding. **Here, we propose to study how environmental fluctuations impact metabolic fitness landscapes.**

Expected results / deliverables of the internship:

During this internship, the intern will expand the ODE model presented in [3], where metabolic fitness landscapes are studied under the assumption of a constant concentration of nutrient in the environment. The student will introduce a fluctuating term in the nutrient supply, so that no steady-state is reached. An analytical approximation of the landscape based on simple assumptions will be derived, before relying on numerical simulations for more realistic scenarios. It is thus expected that the student will have a strong mathematical background and the ability to develop numerical models (e.g., using R or Python).

Interdisciplinarity and disciplines involved (5 lines)

This work is at the crossroads of evolutionary ecology, biochemistry and cell biology. The student will develop mathematical models derived from first principles to help bridge the gap between these fields. Depending on their background, the student will thus combine an evolutionary approach with applied maths and one or several different fields including cell metabolism and ecology. As the internship is based in a molecular microbiology lab, the intern will also benefit from the feedback of experimenters specialised in cell biology.

Contact: florence.bansept@univ-amu.fr

References

[1]	F. Bansept, K. Schumann-Moor, M. Diard, W.-D. Hardt, E. Slack, et C. Loverdo, « Enchained growth and cluster dislocation: A possible mechanism for microbiota homeostasis », *PLOS Comput. Biol.*, vol. 15, n° 5, p. e1006986, mai 2019, doi: 10.1371/journal.pcbi.1006986.

[2]	F. Bansept, N. Obeng, H. Schulenburg, et A. Traulsen, « Modeling host-associating microbes under selection », *ISME J.*, vol. 15, n° 12, p. 3648-3656, 2021, doi: 10.1038/s41396-021-01039-0.

[3]	F. Labourel et E. Rajon, « Resource uptake and the evolution of moderately efficient enzymes », *Mol. Biol. Evol.*, mai 2021, doi: 10.1093/molbev/msab132.