

INTERNATIONAL RELATIONS



INTERNSHIP SUBJECT

2895 - Modelling wild mice gut microbiome as an ecological metacommunity

Context

The communities of bacteria, fungi and viruses living inside larger multicellular organisms are increasingly recognised as key modulators of their host's health and function. These microbial ecosystems called **host microbiomes** harbor large biodiversity and, especially in the case of large host organisms such as vertebrates, are deeply embedded in the physiology of their host. Mammalian gut microbiomes, for instance, are known to directly influence the immune system, hormonal status, metabolism and brain of their hosts, consequently affecting their behavior and survival. Despite their importance, we know little about why microbiomes vary between individuals. One reason for this knowledge gap is that microbiomes have been extensively studied as individual traits, even though they actually are **open ecosystems**, with microbes constantly dispersing in and out of the host. In particular, **transmission between hosts** seems to play a key role in shaping microbiome composition.

In collaboration with colleagues from the University of Oxford, UK, a **Bayesian model of microbial transmission dynamics** between hosts has been developed and applied to a study system of intensively tracked **wild wood mice**. This observational system provides unique **time series data on the gut microbiome, social network and space-use patterns** of wild social vertebrates. The model relies on the idea that gut microbiomes can be considered as "island ecosystems" separated by oxygen-rich out-of-host environment, where most gut microbes cannot thrive. The host islands are connected by temporary bridges created by social interactions (e.g., touch) and shared environments (e.g., exposure to same soil). The key model parameters inferred from the data are **the temporal rates of colonization and extinction** of the different microbes in the different host individuals.

Assignment

Applying the above model to the bacterial communities (16S rRNA) of wood mice led to highlighting **striking differences in the transmission patterns of different bacterial taxa**, in particular according to whether they are anaerobes or aerobes, spore-forming or not, pathogens or commensal. To complement our understanding of gut microbiome variation, the sequencing of **fungal communities** from the same samples is planned for the fall. The internship will consist in applying the model to this new dataset, and compare the fungal transmission patterns with those found for bacteria. In particular, fungal communities are expected to follow transmission routes more tightly connected to social contacts than most bacterial taxa.

The main activities will be:

- Assign ecological functions to the different fungal taxa by matching sequences to reference databases;
- Adapting the Bayesian metacommunity model to the specificities of the new data, if needed;
- Applying the model and interpreting the results in light of the comparison with the bacterial results.

Host team

The intern will be jointly supervised by Guilhem Sommeria-Klein, Inria Bordeaux, and Raulo Aura, University of Oxford. The intern will be hosted in Pleiade team, a joint research group between Inria and **INRAE**, in **Bordeaux, France**. Pleiade is an **interdisciplinary research group** at the frontier of **computer science, mathematics, bioinformatics and biology**. Pleiade is a member of the **Inria Associated Team VALPO**, in association with the Inria team SISTM (Marta Avalos-Fernandez, Bordeaux, France), the CIMFAV at the University of Valparaíso (Cristian Meza, Valparaíso, Chile), and the University Adolfo Ibáñez (Inria Chile, Santiago). This internship project is in line with the stated objective of the associated team, namely the statistical analysis of longitudinal compositional and high-dimensional microbiome data to predict health outcomes.

Required Skills

The candidate is expected to have interest in microbial ecology and the statistical analysis of biological data, to be proficient in at least one scripting and data analysis language (e.g., R or Python), and to be at least familiar with the mathematical notations used in statistics. Prior experience with running bioinformatic pipelines, with Bayesian inference and the use of a probabilistic programming language (such as Stan), as well as background knowledge of microbial ecology are appreciated. Oral and written proficiency in English is expected.

General Information

- **Research Theme :** Computational Biology
- **Locality :** Talence
- **Level :** Master
- **Period :** 5th January 2025 -> 3rd April 2025 (3 months)

 *These are approximative dates. Please contact the training supervisor to know the precise period.*

- **Deadline to apply :** 1st July 2025 (midnight)

Contacts

- **Training Supervisor :** Guilhem Sommeria-Klein / guilhem.sommeria-klein@inria.fr
- **Second Training Supervisor :** Raulo Aura / aura.raulo@biology.ox.ac.uk
- **Team Manager :** David Sherman / David.Sherman@inria.fr

More information

- **Inria Team :** PLEIADE
- **Inria Center :** Centre Inria de l'université de Bordeaux