

Into the complexity of microbial communities

New research bridges colonization processes and complexity in interacting systems of microbes, adding to a body of work with implications for understanding how biodiversity is maintained and how it changes

Oeiras, 09 June 2021 - Microbial communities form complex ecosystems, built on networks of interactions. Gut bacteria, inside our bodies are an example, and we depend on them to help us digest food, to control our mood, or to protect us from infection. Nasopharyngeal multi-strain bacteria like *Streptococcus pneumoniae* are another example, often carried asymptotically but sometimes causing trouble to the host. Depending on underlying diversity, microbial community dynamics can lead to different outcomes between health and disease, and display different stability or resistance to invasion.

“Within the system, the fate of each member strain is inextricably linked with the fate of other strains. Depending on its interactions with others, a strain may persist or become extinct, may fluctuate over time, or reach a steady state”, explains Erida Gjini, former IGC principal investigator, now based at the Center for Computational and Stochastic Mathematics at Instituto Superior Técnico. But to understand the rules of coexistence in complex systems such as this, we need good theoretical models and strong mathematical analysis.

Translating the inner workings of a microbial ecosystem into the language of mathematics allows us to extract the principles and key parameters that govern it, making room for predictions and hypotheses that would otherwise remain inaccessible. In a study published in **Ecology and Evolution**, Erida Gjini and Sten Madec, from Institut Denis Poisson at the University of Tours, build on a [previously defined mathematical framework](#) and reveal a new parameter that explains how the same system can be found in different coexistence regimes. It all comes down to the ratio of single to co-colonization: how often strains are found to occur alone vs. how often they co-occur with others in a typical host (resource) unit.

The previously formalized mathematical framework uses an epidemiological model to understand how networks of many interacting microbes behave in the face of global parameter shifts. Although relative interaction strengths may remain fixed, the changing global parameter

dictates how these translate to coexistence dynamics. “It is this context that we have now understood in terms of what it means for effective pairwise interactions”, Erida explains.

We show that the critical quantity, responsible for strong qualitative shifts in the dynamics, is the ratio of single to co-colonization in the system, because it amplifies the role of asymmetry in how each pair of strains cooperates or competes between each other”, Erida Gjini says.

But what determines this ratio? “In our model, the mean cooperation or competition between all system members combines with reproduction number in a trade-off manner to determine the ratio of single to co-colonization. This becomes then the key tuner of the type of coexistence: the larger the ratio the more strains may coexist, but also the more complex their dynamics”, Erida Gjini details.

Instead of obtaining extremes of system behaviour as apparently disconnected and independent scenarios, the researchers now identify the parameter to gradually interpolate between them as ‘environment’ shifts. The study provides quantitative results both for fundamental understanding of biodiversity and for intervention design. Predictable changes in abundance between different microbes translate to predictable changes in system properties. Understanding how microbial communities respond to environmental gradients can generate valuable insights for control, and have applications in biotechnology and biomedicine.

Any exciting avenues for further exploration? The authors reveal that one definitely worth pursuing is the link between the single to co-colonization ratio, central to coexistence, and the stress-gradient hypothesis in ecology: harsh environments lead to cooperation, whereas benign environments lead to competition. “Our results suggest that the only way to keep the ratio constant is by trading-off mean interaction with others against global prevalence” Erida remarks. If prevalence goes down (lower reproduction potential), system members should universally cooperate more; if prevalence goes up (higher reproduction potential), system members should compete more, to preserve their coexistence configuration. “Although this seems a theoretical speculation at this point, it will be very interesting to examine this hypothesis in eco-epidemiological systems in the future, under the lens of this new model.”

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Original paper

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