# Prediction of community-level function in microbial communities.

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Short project Description
Controlling microbial communities may have enormous benefits for human health, bioremediation, land use or biofuel production. It is recognized that some important challenges could be addressed with a rational management of complex natural communities. An open question, however, is how to predict the function of natural microbial community, given the vast number of microbial species that coexist. In previous work, we observed that natural microbial communities could be "domesticated" by growing them in a standardized, albeit complex, environment [1]. Exploiting this approach we recently showed that there is a surprising reproducibility in the dynamics of resurrected communities, leading to well differentiated functional classes [2]. On the other hand, Sanchez lab at CNB has shown that there are simple principles that allow us to predict the function of a focal strain, when it is introduced in a known community [3]. The question we would like to explore is whether this theoretical formalism can be expanded to larger communities, in particular to predict the functional outcome of the encountering between two or more communities, for which we have experimental data available.

[1] Pascual-García, A., & Bell, T. (2020). Community-level signatures of ecological succession in natural bacterial communities. Nature communications, 11(1), 2386.

[2] Pascual-García, A., Rivett, D., Jones, M. L., & Bell, T. (2023). Replaying the tape of ecology to domesticate wild microbiomes. bioRxiv, 2023-07.

[3] Juan Diaz-Colunga, Abigail Skwara, Jean C. C. Vila, Djordje Bajic, Álvaro Sánchez, (2023) Global epistasis and the emergence of ecological function bioRxiv

Scope: Master Project. Fair programming skills are required,