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Global epistasis and the emergence of function in microbial consortia

The many desirable functions provided by microbial communities emerge from a complex web of interactions between organisms and their environment. This complexity poses a significant obstacle to engineering microbial consortia, which is hindering our ability to harness the potential of microorganisms for all types of biotechnological applications.

In this talk I will present recent work from our group, where we show that the collective impact of ecological interactions between community members leads to the emergence of simple statistical models that predict ecological function with high precision. These predictive models mirror the patterns of *global epistasis* reported in genetics, and they can be quantitatively interpreted in terms of pairwise microscopic interactions between community members.

Our results illuminate an unexplored path to optimizing many target functions of microbial communities, bringing the tasks of predicting biological function at the genetic, organismal, and ecological scales under the same quantitative formalism.