

## Modeling the Many Microbes Inside Us

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Microbial communities, from plankton to the human microbiome, present similar community structures. They are for instance composed of many rare species and a few abundant ones. How a large number of species can coexist in those complex communities and why they are dominated by rare species is still not fully understood. Those communities also present similar dynamical behavior. To study the dynamics of microbial communities, we analyzed the properties of various experimental time series and looked for their common characteristics. We investigated whether the most popular model for ecosystem modeling, namely the (stochastic) generalized Lotka-Volterra models, could reproduce those properties. We showed that this is the case upon certain conditions. In particular, the noise in the growth rates of the various species should be large, meaning that environmental noise is dominant at the observed timescale. Moreover, we showed that if we add a global maximal capacity, representing the limited available resources, the heavy-tailed abundance distributions arise as an emergent property. The long-term goal in the field is to build predictive dynamical models, and eventually to be able to control community composition - and especially to understand how to restore healthy flora in case of disease.

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