High-order interactions promote diversity in productive microbial communities

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Understanding the composition and dynamics of microbial communities associated with the human body (collectively known as the microbiome) is essential to comprehend important aspects of human physiology and health. Accordingly, the study of species interactions and their effects on the structure and stability of the microbiome has become a major topic of experimental and theoretical research. A growing body of empirical evidence has revealed that cooperative interactions are widespread across microbial communities and could be a key factor involved in species co-occurrence [1]. However, mathematical models suggest that highly diverse communities can only be stable if competition is the dominant mode of interaction. In particular, results based on generalized LotkaVolterra (gLV) equations show that mutualism destabilizes complex microbiomes, and this effect becomes stronger as the number of species increases [2].

Traditional gLV approaches have two major limitations: they (i) assume zero-growth stationary states, and (ii) exclude interactions involving more than two species (high-order interactions). The zero-growth assumption is not realistic in scenarios where there is sustained growth, such as the gut microbiome or industrial bioreactors, whereas the existence of potentially relevant high-order interactions has been increasingly acknowledged in microbiological studies. To overcome such limitations, we developed a model based on replicator equations with non-lineal fitness and conducted systematic analytical and numerical analyses to determine the effect of high-order interactions, network connectivity, and interaction spectrum (the fraction of mutualistic, exploitative, and competitive interactions) on the stationary composition of a randomly assembled community.

Our simulations show that permanence (the fraction of species that persist in the stationary state) increases with the fraction of exploitative interactions in the initial sample, as well as with the degree of mutualism (if connectivity is high) or competition (if connectivity is low). In the absence of high-order interactions, the replicator-based community dynamics purges most diversity initially present in the set of interactions and favors small clusters of mutualistic species or, if those do not exist, disjoint sets of non-interacting species. In contrast, the addition of high-order interactions allows for coexistence of species involved in a diverse range of ecological relations, which may also include order-2 interactions.

Strikingly, a theoretical examination of the stationary states shows that neither of these characteristics are the underlying determinants of high bio-diversity. In particular it can be demonstrated that for stationary states associated to high bio-diversities to exist, either the mean interactions acting on every species should be similar, or specific relations between the species abundances and the different interaction terms need to be established. Moreover, we found that the changes in the behavior of the system observed when high-order interactions are included are likely the result of a relaxation in the existence conditions for the stationary state of the replicator equations. However, when a mixture of interactions of different orders is considered, the lower order ones tends to dominate the others. Accordingly, we derived an analytical expression for the scaling factor that high-order terms must fulfil to have a qualitative impact in the dynamics of the community.

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