

Disentangling environmental effects in microbial association networks

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Preliminary ABSTRACT

Ecological interactions among microbes are fundamental for ecosystem functioning. Yet most of them remain unknown. High-throughput omics can help unveiling microbial interactions by inferring species associations over time or space, which can be represented as networks. Associations in these networks can indicate ecological interactions between species or alternatively, similar or different environmental preferences, in which case the association is environmentally-driven. Therefore, prior to network analysis and interpretation, it is important to disentangle these associations and determine whether two species are associated because they interact ecologically or because they are associated to an abiotic or biotic environmental factor.

We developed an approach to determine whether or not two species are associated in a network due to environmental preference. We use a combination of four methods (Sign Pattern, Overlap, Interaction Information, and Data Processing Inequality) that aim

to detect what associations in a network are environmentally-driven. Our approach was tested on simulated networks as well as on real marine microbial networks constructed with temporal and spatial community composition data. For the network constructed with 10 years of monthly microbial-plankton abundance data, we found that 14% of the associations were predicted to be environmentally-driven. In the network, constructed with 120 samples from the surface global ocean, 16% of the associations were predicted to be environmentally-driven.

We conclude that it is crucial to determine and quantify environmentally-driven associations in microbial association networks in order to generate more accurate hypotheses on ecological interactions. We implemented our approach in a publicly available software tool called EnDED (Environmentally-Driven Edge Detection).