

Co-activity networks reveal the structure of planktonic symbioses in the global ocean

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Abstract

Marine microbes interact with their siblings and the environment, forming complex networks of connected metabolic and signaling pathways. Such communities play crucial ecological and biogeochemical roles on our planet, forming the basis of the marine food web, sustaining Earth's biogeochemical cycles in the oceans, and regulating climate. Limited by the fact that most microbes are difficult to isolate and cultivate in lab-controlled environments, we are just starting to grasp the complexity and diversity of their interactions. Today, large-scale environmental surveys of microbial communities (e.g. Tara Oceans expeditions [1]) gathered large volumes of meta-omic and contextual data that are enabling the reconstruction of genomes of uncultivated microbial species (a.k.a. Metagenome Assembled Genomes, or MAGs) [2,3]. While classical co-occurrence analyses enable to predict potential interactions between these newly identified microbes [4], these approaches are inherently limited since true biotic interactions can hardly be disentangled from abiotic (environmental) effects.

Here, we propose a trait-based approach to enrich co-occurring information and uncover putative biotic interactions between marine bacterial MAGs by directly inferring genomic and growth traits from meta-omics data. Available metatranscriptomic data grant access to the expression of bacterial genomes in their environment, while new methods have emerged to infer bacterial replication rates based on differential coverage in a metagenomic sample. Across samples, these co-expression and co-growth signals can thus be exploited to reveal interactions between specific microbes and link their activities to the environmental context. In addition, we can use the functional content of these co-active genomes to predict their potential dependencies, in particular if they deviate from general scaling laws that govern the functional content of lab-cultivated microbial organisms [5]. Inferring and combining (meta-)genomic traits in a global framework can help to identify consortia of marine microbes and pave the way towards the functional understanding and the metabolic modeling of their interactions.

References

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