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

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Abstract

Microbes interact both with the environment and their siblings, sometimes forming highly connected networks of metabolic interactions. These communities play crucial ecological roles on our planet, sustaining Earth's biogeochemical cycles in the ocean, or impacting host nutrition, immunity, and development in our intestinal tract. Limited by the fact that most microbes can hardly be isolated and cultivated in lab-controlled environments, we are just starting to grasp the complexity and diversity of such interactions. Even when successful, laboratory experiments inherently lose valuable information about the richness and diversity of community functioning and interactions in situ. Today, large scale environmental surveys of microbial communities across Earth's ecosystems (e.g. Tara Oceans expeditions, Human Microbiome Project) gathered large volumes of meta-omic and contextual data that are enabling the reconstruction of genomes of uncultivated microbial species (Metagenome-Assembled Genomes – MAGs). While classical co-occurrence analyses enable to predict interactions between newly identified microbes, these approaches are inherently limited since true biotic interactions can hardly be disentangle from abiotic (environmental) effects. Here, we propose a trait-based approach to enrich co-occurring information and uncover putative biotic interactions among MAGs. Genomic and growth traits can directly be inferred from MAGs and meta-omics data. Notably, co-growth signals across samples and ecosystems can be used to reveal positive or negative interactions between co-occurring microbes. In addition, the functional content of MAGs can be used to predict microorganisms appearing to depend on others, in particular if they deviate from general scaling laws governing the functional content of microbial genomes. Inferring and combining (meta-)genomic traits in a global approach can help to identify consortia of microbes and pave the way towards the functional understanding and the metabolic modeling of their interactions.

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