

Inferring microbial interactions with their environment from genomic and metagenomic data

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Abstract

Microbial communities organize through a complex set of interactions between microbes and their environment, and the resulting metabolic impact on the host ecosystem can be profound. Microbial activity has been shown to impact human health, leading to a myriad of treatments meant to manipulate the resident microbiota of the human gut. Additionally, microbes of plant rhizospheres have a strong influence on plant growth and resilience. Finally, microbial communities impact decomposition in terrestrial ecosystems, influencing the way that carbon is stored in soil and removed from the atmosphere. In order to understand, predict, and influence this process, we must first infer the network of interactions between microbes and environmental metabolites.

Using our previously developed algorithm for simulating microbial communities from genome-scale metabolic models (GSMs), we infer the set of microbe-metabolite interactions within a microbial community in a particular environment. Because these interactions depend on the available environmental metabolites, we refer to the networks that we infer as *metabolically contextualized*, and so name our tool MetConSIN: Metabolically Contextualized Species Interaction Networks.