Capturing Seasonal Changes in Microbial Interactions Across Redox Dynamic Environments

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Microbes are responsible for the mediation of many biogeochemical processes, influencing the mobility of nutrients and contaminants. While the collection of microorganisms present in an environment define the potential metabolic behavior of a microbiome, it is the interactions among community members that determine their realized metabolic activity. This may be of particular importance in redox dynamic environments where temporally variable concentration gradients of redox-sensitive metabolites may lead to shifts in the activity and dominance of microbial guilds with unique metabolic capabilities.

In this work we present an approach for examining microbial community interactions that is based on mutual information and random matrix theory. Using temporally-resolved datasets collected from wetlands with different hydroperiods, we demonstrate that this approach is capable of capturing: highly dynamic microbial interactions, shifts in the overall architecture of interaction networks through time, shifts in both the average frequency and strength of interactions among community members with environmental conditions, and both stable and transient relationships among community members. This approach can be used to examine how changes in microbial interactions relate to changes in the abundance of redox active elements (e.g. Fe).

We present the pipeline developed to perform these analyses, which is publicly accessible in the U.S. Department of Energy's Systems Biology Knowledgebase (kbase.us). We will briefly describe how the KBase platform can be used for further analyses, including the generation of genome-enabled and community metabolic models of microbial taxa and interactions identified through interaction networks and the generation of biological reaction networks that can be used to inform reactive transport models.