

## Modeling of Context-dependent Microbial Interactions in Biopolymer Degradation Networks

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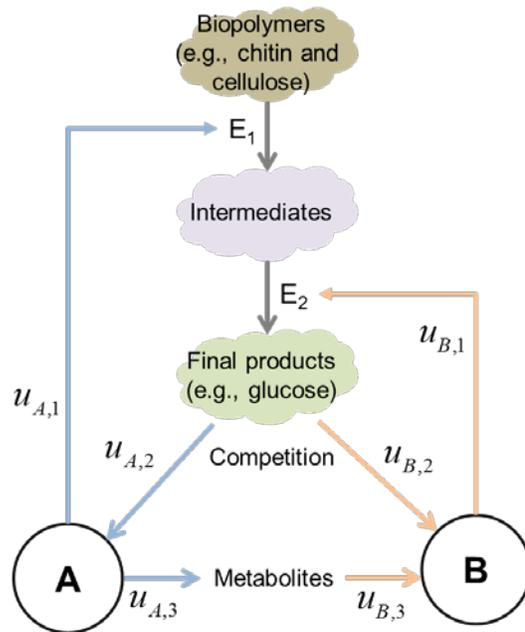
**Project Goals: PNNL's Soil Microbiome SFA aims to achieve a systems-level understanding of the soil microbiome's phenotypic response to changing moisture through spatially explicit examination of the molecular and ecological interactions occurring within and between members of microbial consortia. Integrated experiments will be designed to confront both the scaling challenges and inter-kingdom interactions that regulate networks of biochemical reactions. Individual- and population-based models for predicting interspecies and inter-kingdom interactions will be parameterized using experimental data, and predictions will be tested in soil to reveal spatially explicit microbial interactions. Discoveries from controlled experiments will be tested and validated in the field, using moisture gradient experiments at a new local field site. Data will be captured and shared through the establishment of a Soil Microbiome Knowledgebase (SMK). Knowledge gained will provide fundamental understanding of how soil microbes interact to decompose organic carbon and enable prediction of how biochemical reaction networks shift in response to changing moisture regimes.**

Degradation of biopolymers (such as chitin and cellulose) in soil is a key element of the terrestrial carbon cycle. Bacteria and fungi are known to play as major mediators of the degradation process in soil systems<sup>1</sup>, but we have little understanding of how microorganisms interact with each other in degradation process under a dynamically varying environment. While *in silico* tools are often useful for improving the understanding of such a complex phenomenon in microbial communities<sup>2</sup>, successful dynamic modeling examples for microbially-driven degradation processes are rare. A primary challenge may be ascribed to the difficulty in modeling a biological regulatory process, the mechanistic details of which are unknown in general<sup>3,4</sup>. To address this challenge, we developed a modeling approach that enables simulating regulatory behavior of species by viewing microorganisms as dynamic control systems optimally modulating metabolic interactions with other species to maximize the survival chance of their own<sup>5</sup>. For conceptual understanding, we considered simplified degradation networks where microbes simultaneously cooperate (through the division of labor by synthesizing distinct degradation enzymes) and compete (for the consumption of digestible nutrients obtained as the final products of the degradation process) (Fig. 1). Our model not only enables predicting community dynamics that change interspecies interactions depending on the context, but also helps to characterize complex interactions by quantifying relative portions of cooperation and

competition. We also found that survival strategies of microbes could depend on a specific setting of interspecies interactions, e.g., species can choose to cooperate by providing nutrient sources to a competing partner if it can help to reduce the competition. As such, the developed conceptual model provides various interesting predictions that can be used as *ab initio* hypotheses on interspecies interactions in natural microbial communities. The developed interspecies interaction model will be parameterized based on the data collected from our field sampling and controlled experiments, ultimately to predict metabolic changes in soil microbiomes in response to moisture perturbations.

## References

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**Figure 1.** A conceptual biopolymer degradation network considered for understanding context-dependent interspecies interactions. Control actions of species A and B (denoted by  $u_A$  and  $u_B$ ) dynamically vary depending on environment and the partner organism's response.

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