## How do we best represent microbial communities in Earth system models?

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## Abstract

Microorganisms mediate the biogeochemical cycles of the Earth system and the atmospheric fluxes of greenhouse gases. Their activities respond to, and feedback on, changes in climate, and so estimating microbial impacts at global scales is important for climate science. Microbial activities involve complex interactions at the micro-scale between thousands of species and their environment. Some choice about how to reduce this complexity in Earth system models is required, given that representing the full complexity of microbial communities is not possible due to both conceptual and practical limitations. However, historically, microorganisms have been crudely represented in ways that limit model prognostic capabilities. As our understanding of microbial communities expands, Earth system models are in the midst of climbing up the ladder of complexity and resolution to incorporate more detailed, mechanistic descriptions of microbially mediated processes. How far should we climb up this hierarchy? In this talk, I do not attempt to fully answer this question, but I will argue that global biogeochemical models need a theoretically grounded framework with which to constrain parameterizations of diverse microbial ecosystems. As one path towards this goal, we can use the physical and chemical limitations underlying the distinct metabolisms that fuel microbial growth to develop first-principles descriptions that are simple enough to incorporate into current Earth system models. The benefit of this approach is that the presence or absence of microbial "metabolic functional types" emerges dynamically from ecological interactions, expanding model applicability to unobserved and future environments.