Getting to the gray box: a challenge in soil microbiome modeling

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Soil microbiome models integrate existing genomic, physiological and physicochemical information to form a hypothesis about the roles of genes and organisms in a given environmental context. However, the data that one collects from the associated system is rarely rich enough to allow for reliable identification of model parameters and interaction topology. Microbial modeling remains a "gray box" in which known model structure provides little mechanistic insight into how genetic properties and dynamic couplings between microorganisms give rise to system level dynamics.

In order to solve the inference problem, the challenge is to develop coarse-grained model descriptions which tailor model complexity to information content of available data, preserve relevant mechanistic information and thus reveal emergent microbial behavior or functional redundancy. Here, we improve upon common informal model reduction approaches and use the recently developed Manifold Boundary Approximation Method [1] to show how original hypotheses about degradation pathways in a functional gene-centric model for herbicide degradation in the detritusphere [2] are systematically compressed into relevant microbial controls. We identify a minimal model with 11 effective parameters that preserves the predictive power of the original 61 parameter model in external perturbation scenarios.

In line with [3], we argue that coarse-grained inference models are key to understanding microbial ecosystems, to extract more information from experimental data and to make microbial functional diversity tractable. Our contribution is a proposal on how to perform the essential coarse-graining step which is scalable up to average-sized microbiome models with hundreds of reactions and can easily be integrated into a typical modeling workflow.

[1] Transtrum & Qiu (2014), *Physical review letters* **113** (9): 098701. [2] Pagel *et al.* (2016), *Soil Biology and Biochemistry* **103**, 349-364. [3] Hanemaaijer *et al.* (2015), *Frontiers in microbiology* **6,** 213