

TEMPLE UNIVERSITY
Department of Mathematics

Applied Mathematics and Scientific Computing Seminar

Room 617 Wachman Hall

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Linking Microbial Metabolism to Microbial Community Environment

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Abstract. For environmental microbial communities, environment is destiny in the sense that, frequently, microbial community form and function are strongly linked to chemical and physical conditions. Moreover, most environments outside of the lab are physically and chemically heterogeneous, further shaping and complicating the metabolisms of their resident microbial communities: spatial variation introduce physics such as diffusive and advective transport of nutrients and byproducts for example. Conversely, microbial metabolic activity can strongly effect the environment in which the community must function. Hence it is important to link metabolism at the cellular level to physics and chemistry at the community level.

In order to introduce metabolism to community-scale population dynamics, many modeling methods rely on large numbers of reaction kinetics parameters that are unmeasured and likely effectively unmeasurable (because they are themselves coupled to environmental conditions), also making detailed metabolic information mostly unusable. The bioengineering community has, in response to these difficulties, moved to kinetics-free formulations at the cellular level, termed flux balance analysis. These cellular level models should respond to system level environmental conditions. To combine and connect the two scales, we propose to replace classical kinetics functions (almost) entirely in community scale models and instead use cell-level metabolic models to predict metabolism and how it is influenced and influenced by the environment. Further, our methodology permits assimilation of many types of measurement data.