A GENERALIZED MODEL OF AQUATIC MICROBIAL METABOLISM BASED ON THERMODYNAMIC, KINETIC, AND STOICHIOMETRIC THEORY

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Thermodynamic theory is frequently invoked to explain metabolic variability in aquatic microbial ecosystems. However, existing mechanistic thermodynamic models tend to incorporate details of cellular function, which limits their generality and comparability with basic measurements of solute dynamics. We have developed a generalized computer model that aggregates thermodynamic, kinetic, and stoichiometric hypotheses, for the purpose of simulating solute dynamics in sediments of the recently restored Timberlake Wetland, coastal North Carolina, USA. The model uses a linear optimization scheme to maximize standing stock of microbial biomass as a function of (1) the availability of energy from potential redox reactions and (2) the availability of elements necessary for growth. Here, we review the heuristics of the development process, leading up to a relatively flexible and parsimonious model that can mechanistically reproduce the biogeochemical patterns frequently observed along redox gradients. The model is designed to co-evolve with the growing dataset from Timberlake, in order to quantitatively illustrate what we *do* (and perhaps more importantly *do not*) understand regarding how previous land use and climate change may influence greenhouse gas emission and nutrient retention.