Stoichiometric analysis of metabolic systems: from interacting microbial consortia to metabolic engineering

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Genome-enabled stoichiometric modeling approaches, such as elementary flux mode analysis (EFMA), are powerful systems biology tools for predicting and interpreting metabolic behavior on a continuum of size scales from single cells to communities of interacting cells. Briefly, these approaches construct *in silico* representations of cellular metabolism inferred from genome sequence analysis, omics data sets and culturing studies. The metabolic models define possible biochemical routes of cellular energy conservation and central metabolism, including details of electron transport, the acquisition of carbon, and anabolic processes necessary to synthesize biomass. EFMA identifies all biochemically distinct and non-decomposable routes through a metabolic network model. These distinct routes, and non-negative linear combinations thereof, describe all genome enabled physiologies and provide a relatively simple basis for predicting and dissecting microbial phenotypes. Stoichiometric modeling has been used by the speaker to study a wide variety of systems ranging from predicting genetic modifications for bioplastic synthesis in engineered systems, interpreting physiological behavior of bacteria under medically relevant stresses, and evaluating the transfer of mass and energy between distinct populations in natural microbial communities. Audience members will have the opportunity to select discussion topics relevant to their interests.