

Oceanography Seminar

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“Towards a mechanistic model of marine microbial community metabolism”

Marine microbial communities mediate the transformations of Earth’s major bio-elements through an intricate web of inorganic and organic ‘conduits,’ connecting microbes to microbes, and connecting microbes to global biogeochemical cycles. As part of a collaborative effort to simulate these processes within the North Pacific Subtropical Gyre microbiome, my objective is to identify and quantify the fluxes through each conduit within and between the numerically dominant microbial groups. Genome-scale metabolic models, detailed and stoichiometrically balanced networks of the many biochemical transformations within a cell, are being reconstructed from the ‘pangenomes’ of each taxonomic group in an effort to capture the phylogenetic, physiological and metabolic microdiversity within each group. I will discuss the deployment of new algorithms for the network reconstruction of 48 individual strains of the abundant cyanobacterium *Prochlorococcus*, as well as hundreds of hypothetical *in silico* strains adapted to growth in a variety of environments. Analysis of the fluxes and growth rates of each strain, evaluated using a convex optimization approach (flux balance analysis and its family of variants), reflects the extensive microdiversity within the *Prochlorococcus* genus, suggesting a metabolic basis for the broad ecological niche space it occupies. By leveraging laboratory and field data, including environmental ‘omics datasets, realistic simulations will be designed to predict the winners and losers within the broad environmental niche spaces they occupy. I will discuss a roadmap to community simulations and their implementation within a trait-based general circulation model framework.

Thursday April 5, 2018 3:00p.m. MSB 100