

From genome-scale to ecosystem-level models of microbial metabolism

Abstract: Metabolism, in addition to being the “engine” of every living cell, plays a major role in the cell-cell and cell-environment relations that shape the dynamics and evolution of microbial communities, e.g. by mediating competition and cross-feeding interactions between different species. Despite the increasing availability of metagenomic sequencing data for numerous microbial ecosystems, fundamental aspects of these communities, such the maintenance of diversity, the unculturability of many isolates, and the conditions necessary for taxonomic or functional stability, are still poorly understood. In our lab, we develop and test mechanistic computational models for the dynamics and evolution of interactions between different organisms based on the knowledge of their entire metabolic networks, with applications in the study of natural and synthetic microbial communities.

Relevant Papers:

<http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1001002>

[http://www.cell.com/cell-reports/fulltext/S2211-1247\(14\)00280-0](http://www.cell.com/cell-reports/fulltext/S2211-1247(14)00280-0)

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