



181 Longwood Avenue Boston, Massachusetts 02115-5804 **Department of Medicine** *Channing Division of Network Medicine*

Channing Network Science Seminar

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Computational Systems and Ecosystems Biology of Microbial Metabolism

Cellular metabolism consists of a complex network of biochemical reactions required to convert nutrient molecules to energy and building blocks of life. Last decade has witnessed a rapid progress in the construction of genome-scale stoichiometric-based models of metabolism compiling all biochemical reactions occurring in an organism derived from its annotated genome. In this talk, I review my recent work on the development of efficient computational systems biology tools to analyze and redesign metabolic networks in single- and multi-species microbial systems. First, I introduce a class of computational pipelines to rationally design promising metabolic reprogramming strategies for biotechnological/biomedical applications. The focus is then shifted to microbial ecosystems, where I introduce OptCom, a multi-level and multi-objective optimization framework for the metabolic modeling and analysis of microbial communities using genome-scale metabolic models. Next, I introduce dynamic OptCom, an extension of OptCom, to capture the impact of dynamic changes in the environment on the function and structure of microbial communities. This is followed by a brief discussion of the recent advances on the metabolic modeling of microbial ecosystems in dynamic spatially heterogeneous environments.

Bio: Ali Zomorrodi is a postdoctoral associate in Daniel Segre's group at Boston University. He obtained his PhD in Chemical Engineering from Pennsylvania State University-University Park. He holds an MS in Industrial & Manufacturing Engineering from Pennsylvania State University, an MS in Chemical Engineering from Tehran Polytechnic and a BS in Chemical Engineering from Sharif University of Technology. Ali's current research is concerned with the game-theoretic and evolutionary analysis of microbial communities in homogenous and heterogeneous environments using genome-scale metabolic models. He has recently co-authored a textbook on using mathematical optimization to analyze and redesign metabolic networks.

Hosted by Yang-Yu Liu

