Studying the human microbiome: From systems biology to multi-meta-omic analysis

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The human microbiome represents a vastly complex ecosystem that is tightly linked to many host-related processes and that directly impact human health. To date, however, most studies have focused on characterizing the composition of the microbiome in health and in disease and on comparative analyses, and relatively little effort has been directed at studying and modeling the microbiome as an integrated and comprehensive biological system. In this talk, I will highlight the pressing need for the development of predictive system-level models of the microbiome and discuss potential computational frameworks for metagenomic-based modeling of this microbial system. I will describe several preliminary attempts at constructing such models at the cellular, ecological and supra-organismal levels, accounting for the complex web of interactions in the microbiome. Specifically, I will demonstrate the use of network-based and constraint-based models to study various aspects of the microbiome, predicting both microbe-microbe and microbe-host interactions. These models allow us to obtain valuable insights into the forces that govern the assembly of the microbiome and into disease-associated organizational shifts. Finally, I will discuss routes for integrating various modeling approaches and multiple meta-omic datasets for obtaining a comprehensive, multi-scale, mechanistic understanding of the microbiome and exciting future clinical applications facilitated by this research.