



## Channing Microbiome Seminar November 4 (Friday), 2022, 9AM-10AM (ET)

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## Exploring functional landscapes of the human gut microbiome

**Abstract:** Microbial communities are critical determinants of a wide range of environments ranging from the human gastrointestinal tract, plant rhizosphere and extreme environments such as hydrothermal vents. A myriad of unknown and complex abiotic and biotic interactions dictates the dynamics and functional activities of microbial communities. The human gut microbiome is a dense and diverse microbial ecosystem that shapes human physiology, nutrition, and behavior. Key community-level functions performed by gut microbiota that impact human physiology include the production and degradation of key metabolites and colonization resistance to intestinal pathogens. In response to environmental perturbation or host dysfunction, the functional and compositional state of the gut microbiome can shift to an alternative state that negatively impacts human health. Developing the capability to predict and design the community-level functions of gut microbiota hold tremendous therapeutic potential. By combining high-throughput bottom-up assembly of human gut communities with computational modeling, we decipher the interaction networks shaping community dynamics and health-relevant functions. We exploit the data-driven models to design communities with desired behaviors including tailored metabolite profiles, enhanced resistance to invasion and optimized community diversity. Since microbiomes have immense heterogeneity at the single-cell level, we are developing and applying ultrahigh-throughput methods to analyze single-cell heterogeneity within microbiomes to provide a deeper understanding of interactions and microbiome dynamics. In sum, microbial interactions can be engineered to design microbial communities with desired target functions and building

microbiomes from the bottom-up is a powerful approach to exploring the structure-function landscapes of microbiomes.

*Bio: Dr. Ophelia Venturelli is an Assistant Professor in Biochemistry, Chemical & Biological Engineering, Biochemistry and Biomedical Engineering at UW-Madison. The Venturelli lab focuses on understanding and engineering microbiomes using systems and synthetic biology to address grand challenges facing society in human health, agriculture and bioprocessing. The lab aims to combine high-throughput experiments and computational modeling to predict, design and control microbiome functions. Dr. Venturelli began her appointment in 2016 after completing a Life Sciences Research Foundation Fellowship at UC Berkeley in the laboratory of Dr. Adam P. Arkin. Dr. Venturelli's postdoctoral research focused on combining high-throughput experimental data with dynamic computational models to decipher microbial interactions shaping assembly of synthetic human gut microbiomes. She received her PhD in Biochemistry and Biophysics in 2013 from Caltech with Richard M. Murray (co-advised by Hana El-Samad at UCSF), where she studied single-cell growth and gene expression dynamics and the role of feedback loops in a metabolic gene regulatory network. Dr. Venturelli has received numerous awards for her cross-disciplinary research including the Shaw Scientist Award (2017), Army Research Office Young Investigator Award (2017), NIH Outstanding Investigator Award (2017) and the Wisconsin Alumni Research Foundation Innovation Award (2019).*

Hosted by Yang-Yu Liu

