



181 Longwood Avenue
Boston, Massachusetts 02115-5804

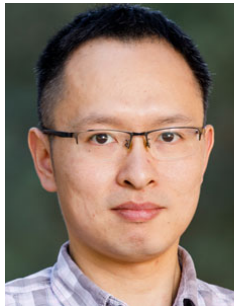
Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar October 7th (Friday), 2022, 11AM-12PM (ET)

Zoom: <https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09>

Meeting ID: 810 7095 9105

Passcode: 984617



Qiyun Zhu, Ph.D.

Assistant Professor at School of Life Sciences
Arizona State University, USA

<https://qiyunlab.github.io/>



Upgrading microbiome data science with relationship graphs

Abstract: Central to microbiome research is the inference and analysis of a high-dimensional feature table where features represent microbial components present in the community. These tasks have unique challenges stemming from the complex hierarchical relationships in biological systems. Utilizing relationship graphs, such as phylogenetic trees or gene interaction networks, is a promising yet difficult option that could bring significant merits in decoding microbiomes. My research group at ASU is pursuing this goal through four directions. First, we are building reference databases for microbiome research. This includes deliberately sampled reference genomes and gene catalogs, and phylogenetic trees of genomes and genes constructed using rigorous approaches. Second, we are developing software tools to enable microbial community analysis by exploiting a tree or network structure behind the features. Our methodology advances beyond current approaches by permitting graph-guided microbial classification which has high resolution and flexibility. Three, we are developing computational methods for combined structural and functional analysis of microbiomes. This is achieved through an algorithm permitting efficient mapping between sequencing data and gene annotations. Fourth, we are developing an adaptive feature engineering algorithm that explores the feature space along a graph to infer the optimal feature membership and resolution that maximize supervised prediction model performance. These works will improve the understanding of the diversity and dynamics of microbiomes and their roles in the host or natural environment.

Bio: Qiyun Zhu is a computational biologist with expertise in phylogenetics, comparative genomics, metagenomics and multiomics. He received his Ph.D. in Biological Sciences from University at Buffalo and did his postdoctoral training at J. Craig Venter Institute and University of California San Diego. His research interests include the development of computational tools and resources to improve the analytics of microbiome data, the study of various host and environmental microbiomes and their influence on human health, and the investigation of the

evolution of microbes and their hosts, with a focus on vertical and horizontal genetic connections between organisms. He led or made significant contributions to a number of microbiome research projects, covering diverse topics such as pathology, nutrition and anthropology, from a variety of sources including host gut, cancer tissue, build environment, ocean and more. He strives to expand understanding of the microbial world through its multiple levels: genes, genomes, lineages, communities, hosts and environments.

Hosted by Tong Wang & Yang-Yu Liu