



Channing Microbiome Seminar May 6th (Friday), 2022, 9AM (ET)

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Illuminating bacterial DNA methylation to understand microbiome and human epigenome

Abstract: As an increasing number of studies link microbiome with human diseases, researchers have also recognized the importance of high resolution microbiome analyses. Despite the rapid progress being made, significant challenges remain, stemming in part from the presence of highly similar bacterial species and strains with complex genomes. DNA methylation is highly prevalent in bacterial genomes, including three major forms: N6-methyladenine (6mA), N4-methylcytosine (4mC) and 5-methylcytosine (5mC). Importantly, the genetic material (chromosomes and plasmids) in a single strain all share the same methylation pattern, yet these patterns are highly variable not only between different species but also between different strains of the same species. Building on these rationales, we recently demonstrated that bacterial DNA methylation signatures can be exploited as natural epigenetic barcodes for binning metagenomic contigs and mapping mobile genetic elements (e.g. plasmids) to their host bacteria. In this seminar, I plan to introduce the foundations of bacterial epigenomes, technologies to profile them, and how to exploit bacterial DNA methylation for high resolution microbiome analyses. In addition, I will present our recent work that took a metagenomic approach to study the human epigenome, addressing an active debate over an epigenetic mark in multicellular eukaryotes.

Bio: Gang Fang, PhD is an Associate Professor in the Genomics Department at Icahn School of Medicine at Mount Sinai. The Fang lab develops long read sequencing-based methods to study the epigenomes of bacteria, microbiome and human. His lab pioneered the fast growing field of bacterial epigenomics (*Nature Biotechnology*, 2012; *Nature Reviews Genetics*, 2018; *Nature Microbiology*, 2019), and the use of DNA methylation as natural epigenetic barcodes for high resolution microbiome analysis (*Nature Biotechnology*, 2018; *Nature Methods*, 2021). In addition, his team also uses long read sequencing to understand human DNA methylation (*Science*, 2022) and alternative splicing (*Nature Genetics*, 2019) in brain disorders. Dr. Fang received his PhD degree in University of Minnesota, his MS degree in University at Buffalo, and his BS degree in Fudan University, China. Dr. Fang received multiple awards including: Best Network Model Award, Sage Congress (2010), Walter Barnes Lang Fellowship (2011), Best Dissertation Award at University of Minnesota (2013), Nash Family Research Scholar, Friedman Brain Institute (2016), Irma T. Hirschl / Monique Weill-Caulier Trust Research Award (2018).