



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

Channing Microbiome Seminar

December 17 (Monday), 2018, 11am @ 3rd-floor conference room



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Illuminating Bacterial Epigenomes: Technologies, Pathogens and Microbiome

Abstract: Bacterial genome contains three types of DNA methylation: N6-methyladenine, N4-methylcytosine and 5-methylcytosine. While their biological roles were thought to be limited to bacterial defense, increasing evidence supports that they are important regulators of bacterial gene expression, especially in the context of infectious diseases. The lack of tools to analyze the frequency and distribution of methylated residues in bacterial genomes has prevented a full understanding of their functions. In the past few years, advances in DNA sequencing technology, including single-molecule, real-time sequencing and nanopore-based sequencing, have provided new opportunities for systematic detection of all three forms of methylated DNA at a genome-wide scale and offer unprecedented opportunities for achieving a more complete understanding of bacterial epigenomes. Indeed, as the number of mapped bacterial methylomes approaches 2,000, increasing evidence supports roles for methylation in regulation of gene expression, virulence and pathogen-host interactions. I will present our work that pioneered this fast growing field of bacterial epigenomics, and our more recent work that exploits the use of DNA methylation for high resolution microbiome analysis.

Short Bio: Gang Fang is an Associate Professor in the Genomics Department at Icahn School of Medicine at Mount Sinai. He is also part of the Icahn Institute for Genomics and Multiscale Biology. The Fang lab pioneered the fast growing field of bacterial epigenomics, and developed the foundational methods that enabled the effective use of third-generation sequencing technology for direct detection of DNA modifications. Recently, his lab pioneered the use of DNA methylation for high resolution microbiome analysis. Dr. Fang received his PhD degree in University of Minnesota in 2012, his MS degree in University at Buffalo, 2007, and his BS degree in Fudan University, China, 2005. Dr. Fang received multiple awards including: Joint Mayo Clinic - IBM Research Traineeship (2007), Best Network Model Award, Sage Congress (2010), Walter Barnes Lang Fellowship (2011), Best Dissertation Award at University of Minnesota (2012), Kavli Frontiers in Science Fellow (2013), Nash Family Research Scholar, Friedman Brain Institute (2016), Hirschl Research Award, Irma T. Hirschl Trust (2018).

Hosted by Yang-Yu Liu

