AMS SEMINAR

Title: Adaptive Statistical Methods for Human Microbiome Studies

SPEAKER · HYUNWOOK KOH, PH.D.

Hyunwook Koh is an Assistant Professor in the AMS department at SUNY Korea. He completed his Ph.D. degree in Biostatistics at New York University. Then, he worked as a Postdoctoral Research Fellow in the Department of Biostatistics at Johns Hopkins University. He primarily works on statistical methods for high-dimensional compositional data analysis with applications to human microbiome studies. Email: hyunwook.koh@stonybrook.edu

ABSTRACT

The human microbiome is the totality of all microbes inhabiting in and on the human body. The roles of the microbiome on human health or disease have been increasingly studied by the recent advance in high-throughput sequencing technologies. For example, the microbiome perturbation has been associated with a variety of health or disease status (e.g., obesity, diabetes, cancer, brain disorder), medical interventions (e.g., antibiotic or probiotic use) and behavioral or environmental factors (e.g., diet, residence, smoking, birth mode). However, the high complexity of the microbiome data (e.g., high-dimensionality, compositionality, zero-inflation, phylogenetic correlations) makes the downstream data analysis challenging, and thus there is a strong need for more sophisticated statistical methods. In this seminar, we study the human microbiome from the very beginnings of the subject to recent statistical methods (e.g., α- and β-diversity analysis). Then, we further discuss the potential and promise in statistical method development.

TIME & METHOD

Time: 4:30 PM - 5:30 PM; November 20, 2020; **Method:** Online via Zoom

Zoom Meeting ID: 485-595-6497; **Passcode:** 504784