BRIGHAM AND WOMEN'S HOSPITAL

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Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar
April 22nd (Friday), 2022, 11AM (ET)

Zoom: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09
Meeting ID: 810 7095 9105
Passcode: 984617

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Statistical Analysis of Large-Scale Microbiome Profiling Studies: Batch Effects and Robust Testing

Abstract: Microbiome profiling studies of hundreds to thousands of individuals are being conducted within existing epidemiologic cohorts. Analysis of data from these studies offers comprehensive identification of bacterial taxa related to many health outcomes. However, the key characteristics of these studies (e.g., large sample size) also induce serious statistical challenges, particularly in combination with the difficulties inherent to microbiome data (e.g., high-dimensionality and sparsity). Some arising challenges include accommodating batch effects and robustly identifying taxa related to outcomes. We propose novel batch correction and individual-taxon analysis frameworks to address these problems. Our work is based on using two-part zero-inflated quantile regression, which makes minimal distributional assumptions while accommodating the zero-inflated nature of the data. We illustrate our work through simulations and application to data from several large-scale microbiome studies, including the CARDIA cohort.

Bio: *Michael Wu is a Professor in the Public Health Sciences Division of the Fred Hutchinson Cancer Center and an Affiliate Professor of Biostatistics at the University of Washington. His lab develops statistical and computational tools for many types of complex omics data, including GWAS, rare genetic variants, methylation, and, more recently, microbiome data. Previously, he served on the faculty at UNC-Chapel Hill and received his Ph.D. in Biostatistics from Harvard.*