BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

181 Longwood Avenue
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Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar
March 25th (Friday), 11AM (EDT)

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

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Model misspecification in microbiome studies

Abstract: The composition of bacterial taxa in a microbiome is an important parameter to estimate given the critical role that microbiomes play in human and environmental health. However, high throughput sequencing distorts the true composition of microbial communities. Sequencing mock communities -- artificially constructed microbiomes of known composition -- clearly illustrates that observed composition is a biased estimate of true composition, with certain taxa consistently overobserved or underobserved compared to their true relative abundance. We propose a statistical model for microbiome data that reflects this observation and illustrate its performance and usage in a variety of settings. We conclude with recommendations for the design and analysis of microbiome studies.

Bio: *Amy Willis is the Principal Investigator of the Statistical Diversity Lab and a tenure-track Assistant Professor in the Department of Biostatistics at the University of Washington. Amy and the StatDivLab develop tools for the analysis of microbiome and biodiversity data. Amy is passionate about reproducible science, meaningful data analysis, ecosystem and host health, and collaborating with scientists who share these values. Amy is the recipient of a NIH Outstanding Investigator Award, and a University of Washington Outstanding Faculty Mentor Award.*

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