Combi Seminar

Wednesday, 11.9.22 | 1:30
held remotely: https://depts.washington.edu/gsrestrc/remote.htm

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Dr. Amy Willis

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"Model misspecification in microbiome studies"

The relative abundances of bacterial species in a microbiome are an important parameter to estimate given the critical role that microbiomes play in human and environmental health. By analyzing data from artificially constructed microbiomes, we show that high-throughput sequencing distorts the true composition of microbial communities. We propose a statistical model for microbiome data that reflects this observation, and a stable algorithm for estimating model parameters. Notably, our model and estimation procedure permit relative abundances to lie on the boundary of the simplex. We conclude with examples of the utility of the method, and recommendations for the design and analysis of microbiome studies. Our approach can be leveraged to select experimental protocols, design experiments with appropriate control data, and remove sample-specific contamination. This is joint work with David Clausen.