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**Friday, April 8, 2022**

**12:00-1:00 pm**

**Via Zoom:**

<https://uwmadison.zoom.us/j/95888467998?pwd=UTRuaVhCeJN1ZlREbUI2RWkzbzQwUT09>

## 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. By analyzing data from artificially constructed microbiomes of known composition, 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 algorithms to estimate model parameters. We conclude with examples of the utility of the method, and recommendations for the design and analysis of microbiome studies.