Department of Biostatistics and Medical Informatics Seminar



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Friday, November 6, 2026
12:00-1:00 pm – Morgridge Hall Seminar Room 7560

Zoom Meeting: 966 3372 9112
https://uwmadison.zoom.us/j/96633729112?pwd=tHFc9i1dAAgmXe05uWtw8wXBIQZxGB.1 **Passcode: 621125**

Statistical Inference and Learning for Reproducible Microbiome Research

Abstract: Microbiome research offers new opportunities to understand human health and disease, yet findings from association studies are often inconsistent. Interpreting these differences requires reliable statistical inference and an understanding of genuine biological heterogeneity. This talk presents two complementary methodological developments addressing these challenges. I will first discuss a framework for estimating absolute-abundance association effects from relative microbial abundances derived from sequencing data. This framework produces more comparable effect estimates across studies when the underlying effects are homogeneous. Building on study-specific estimates and their uncertainty, I will then introduce a structure-learning meta-analysis approach that groups biological contexts with similar association profiles and identifies shared and context-dependent microbial signatures. Applications across diseases and colorectal neoplasia stages illustrate how these approaches reveal stable, biologically interpretable patterns of association heterogeneity across contexts that may be overlooked by existing meta-analysis methods.

Bio: ZhengZheng Tang, PhD, is an Associate Professor in the Department of Biostatistics and Medical Informatics and Associate Director for Biostatistics in the Center for Health Disparities Research at the University of Wisconsin–Madison. She develops statistical and computational methods for genetics, genomics, and microbiome research, with the goal of translating complex omics data into reproducible biological findings and clinically relevant insights. Her research has received sustained support from the National Institutes of Health. Her methodological work has been published in journals such as the Journal of the American Statistical Association, Nature Communications, Genome Biology, and the American Journal of Human Genetics.

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