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YOU ARE INVITED TO ATTEND THE DEFENSE OF THE DOCTORAL DISSERTATION

"Development and Evaluation of Metataxonomic and Metagenomic Algorithms for Improved Taxonomic Classification"

By

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M.D./Ph.D. Program
B.A., Biochemistry, Vassar College

Thesis Advisor: W. Evan Johnson, Ph.D.
Professor, Division of Infectious Disease, Department of Medicine
Director, Center for Data Science

Wednesday, March 18th, 2026
12:00 P.M.
PHRI Executive Board Room
ICPH Building

Join Zoom presentation
https://rutgers.zoom.us/j/98896051426?pwd=ztA0bwbUeJZA6u8SpAAsn9pEBblbb3.1
Meeting ID: 988 9605 1426
Passcode: 735917

ABSTRACT

Accurate microbial identification remains central to modern microbiome research. However, conventional bioinformatic pipelines are limited by complications such as read mapping ambiguity, incomplete or biased databases and classifiers, and host genome contamination, all of which obscure the final composition and weaken downstream clinical or ecological interpretation. This work presents MetaScope, a novel, modular computational framework developed in R to address these core classification challenges. By refining a Bayesian reassignment model, MetaScope implements a classification-centric aggregation methodology that resolves ambiguous mappings to the highest taxonomic resolution supported by the data. This work also presents, MetaBlast, a novel secondary validation module, which allows for both classification confidence and grouped species reassignments to provide a statistically rigorous approach for handling high entropy sequences that standard tools often misclassify.

Comprehensive benchmarking against established tools, including QIIME2, DADA2, Kraken2, and Bracken, demonstrates that MetaScope significantly improves taxonomic classification across both 16S rRNA and metagenomic datasets. By increasing taxonomic accuracy and stabilizing downstream diversity estimates, MetaScope provides a scalable, high-resolution framework for next-generation microbial community analysis.