

## PATRICK D SCHLOSS, PHD

Department of Microbiology & Immunology

1150 W MEDICAL CENTER DR. 1526 MSRB I ANN ARBOR, MICHIGAN 48109-0620

Phone: (734) 647-5801 Fax: (734) 764-3562 pschloss@umich.edu

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To the editors of Genome Research:

We submit for your review: "Biogeography and Environmental Conditions Shape Phage and Bacteria Interaction Networks Across the Healthy Human Microbiome" by Geoffrey Hannigan and colleagues. We believe this work to be especially well suited for publication in Genome Research and highly relevant to a broader scientific readership as well as the general public.

Previous work has focused on studying the human microbiome bacterial and viral communities seperately, relying on metrics such as community composition and diversity. These metrics fail to account for the relationships between bacteria and viruses, which account for much of the behavior of these two communities. To address this knowledge and methodological gap, we performed a re-analysis of three existing bacterial and viral metagenomic datasets using network-based techniques that allowed us to focus on the relationships between these interacting communities. Our findings provide new insight into the ecological networks of human bacterial and viral communities. The methods we implemented also provide an additional avenue for future microbiome researchers to build off of.

Our lab strives to set high standards of reproducibility and transparency, while generating and publishing high quality data. As such, all analysis workflows, scripts, and datasets have been made publicly available for other researchers to utilize.

The data presented in this manuscript are original and the manuscript is not under consideration elsewhere. A preprint version of this manuscript has been made available through BioRxiv (doi: PENDING). All authors have read and approve the manuscript for publication.

We suggest the following reviewers for this publication:

## Bonnie Hurwitz, PhD

Assistant Professor
Dept. of Agricultural and BioSystems Engineering
University of Arizona
Email: bhurwitz@email.arizona.edu

## John Kirby, PhD

Professor
Dept. of Microbiology and Immunology
Medical College of Wisconsin
Email: jkirby@mcw.edu

## K. Eric Wommack, PhD

Professor

Dept. of Plant and Soil Sciences

Dept. of Marine Biology and Biochemistry University of Delaware

Email: wommack@dbi.udel.edu

We thank you for your consideration and look forward to your response.

Sincerely,

Patrick D. Schloss Associate Professor

Kappy Frung