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To the editors of PLOS Computational Biology:

We submit for your review: "Biogeography & environmental conditions shape bacteriophage & bacteria interaction networks across the human microbiome" by Geoffrey Hannigan and colleagues. We believe this work to be especially well suited for publication in PLOS Computational Biology and highly relevant to a broader scientific readership as well as the general public. We previously discussed the appropriateness of this manuscript with co-Editor in Chief, Jason Papin, who indicated that this work was in spirit with his recent editorial on the value of computational biology in microbiome research.

Previous work has focused on studying the human microbiome bacterial and viral communities separately, 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 work-flows, 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: https://doi.org/10.1101/144642). All authors have read and approve the manuscript for publication.

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

Sincerely.

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Frederick G. Novy Collegiate Professor of Microbiome Research