October 15, 2018

To the Editors of *Nature Ecology & Evolution,*

Today we are excited to submit, for your consideration, a brief communication entitled “Applying ecological network theory to re-estimate global viral diversity: host sharing matters.”

Our manuscript grapples with a fundamental question at the intersection of virology, ecology, and evolutionary biology: how many viruses are there on Earth? Though global diversity studies are often treated as an academic exercise, this particular problem is of tremendous economic and policy importance: the standing estimate of 1.6 million viruses recently published in *Science* has been used to justify the $1.2 billion currently allocated for the Global Virome Project over the coming decade.

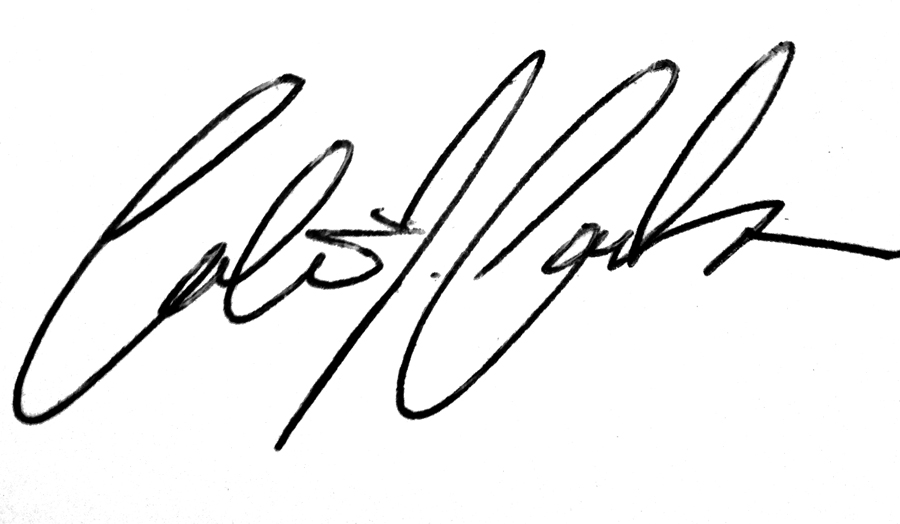
Our study applies ecological network theory to revise that estimate to a much lower figure (roughly 37,000 viruses including about 9,000 with the potential to infect humans). This reduction results from the fact that many viruses have multiple hosts (that is, exhibit host sharing). Host sharing produces a power-scaling relationship between host and virus diversity, instead of the previously-assumed linear relationship. As we show in our paper, this pattern is not unique to viruses, and is readily illustrated for many types of ecological interactions.

Whereas previous estimates infer global viral diversity in mammals and birds from the profile of only two well-described, virus-rich species (a bat and a macaque), our study re-analyzes a large dataset to make a more confident estimate of viral diversity. In the process, we find an unexpected result: zoonotic DNA viruses probably outnumber zoonotic RNA viruses, even though at present they are significantly underdescribed, and usually considered lower priority for viral discovery projects.

Our results have simple but critical implications for one of the largest scientific undertakings ever attempted. More importantly, our paper helps make an important link between ecological theory and the efforts currently underway to achieve global pandemic prevention. We believe this will be of broad interest to ecologists, virologists, network theorists, and potentially the economists and policymakers involved in global health security.

We eagerly await your comments and are happy to provide any additional documentation as needed.

On behalf of the authors,



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