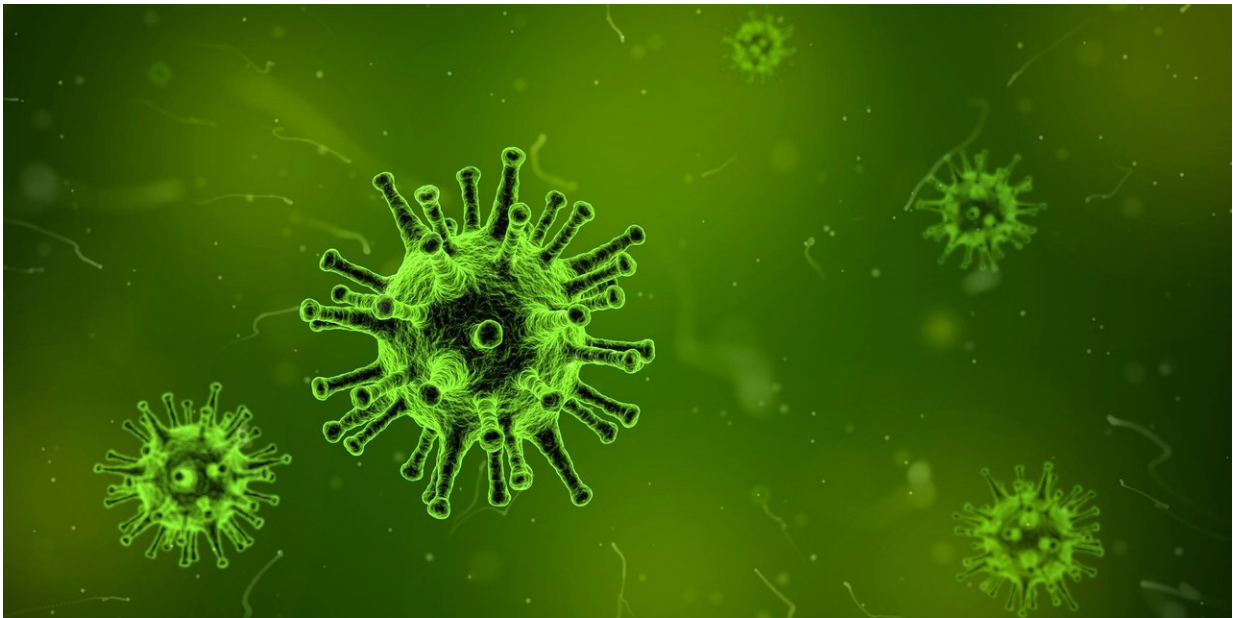


Novel framework to infer microbial interactions

December 11 2017



Credit: CC0 Public Domain

Inferring the underlying ecological networks of microbial communities is important to understanding their structure and responses to external stimuli. But it can be very challenging to make accurate network inferences. In a paper published in *Nature Communications*, researchers at Brigham and Women's Hospital detail a method to make the network inference easier by utilizing steady-state data without altering microbial communities.

"Existing methods require assuming a particular population dynamics model, which is not known beforehand," said Yang-Yu Liu, PhD, of the Channing Division of Network Medicine. "Moreover, those methods require fitting temporal abundance data, which are often not informative enough for reliable inference."

To obtain more informative temporal data, researchers have to introduce large perturbations to alter the [microbial communities](#), which are not only difficult in practice but also potentially ethically questionable, especially for human-associated microbial communities. The new [method](#) developed by BWH investigators avoids this dilemma.

"The basic idea is very simple. If one steady-state sample differs from another only by addition of one species X, and adding X brings down the absolute abundance of Y, then we can conclude X inhibits the growth of Y," said Liu. The team showed that this simple idea can be extended to more complicated cases where steady-state samples differ from each other by more than one species. They verified that, if enough independent steady state data were collected from the microbial communities, then the microbial interaction types (positive, negative and neutral interactions) and the structure of the [network](#) could be inferred without requiring any population dynamics modeling. The method proposed by the team resembles other network reconstruction methods based on steady-state data, but unlike the previous methods, no perturbations are required to be applied to the system. Furthermore, a rigorous criterion was established by the team to check if any given steady-state data was consistent with the Generalized Lotka-Volterra (GLV) model—a classical population dynamics model in ecology that mathematically describes the relationships between species. The team found that if the microbial community followed the GLV model, then the steady-state data could also be used to deduce the [model](#) parameters—interspecies interaction strengths and growth rates.

The method was systematically validated using simulated data generated from different classic population dynamics models with various levels of complexity. Then it was applied to real data collected from four different synthetic microbial communities, finding that the inferred ecological networks either agree well with the ground truth or can predict the response of systems to perturbations.

Additional insights into microbial ecosystems will emerge from a better understanding of their underlying ecological networks. Inferring ecological networks of human-associated microbial communities using the method developed here will facilitate the design of personalized microbe-based "cocktails," as the authors write, to treat diseases related to microbial dysbiosis.

"I am quite excited about this method, because it may pave the way to mapping more complex microbial communities such as the human gut microbiota, which in turn will help us design better microbiome-based therapies," said Liu.

More information: Yandong Xiao et al, Mapping the ecological networks of microbial communities, *Nature Communications* (2017).
[DOI: 10.1038/s41467-017-02090-2](https://doi.org/10.1038/s41467-017-02090-2)

Provided by Brigham and Women's Hospital

Citation: Novel framework to infer microbial interactions (2017, December 11) retrieved 28 April 2024 from <https://phys.org/news/2017-12-framework-infer-microbial-interactions.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.