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Correlation-based and model-based inference in complex virus-microbe communities ASHLEY R. COENEN, School of Physics, Georgia Institute of Technology, JOSHUA S. WEITZ, School of Biological Sciences and School of Physics, Georgia Institute of Technology — Microbes are found in high abundances in the environment and in human-associated microbiomes, often exceeding one million per milliliter. Viruses of microbes are estimated to turn over 10 to 40 percent of microbes daily and, consequently, are important in shaping microbial communities. Yet, the interactions among microbes and viruses are difficult to pin down *in situ*. Deducing which pairs interact in complex virus-microbe communities (the "inference problem") remains an open question. Here, we test two approaches to the inference problem with *in silico* experiments. The first approach uses correlations between population time series to indicate interaction. Contrary to widespread use, our results suggest that correlation is a poor indicator of interaction when interactions are not already known *a priori*. The second approach extends recent work (Jover, Romberg, and Weitz, *Roy Soc Open Science*, 2016) by discretizing a nonlinear mechanistic model to infer virus-microbe as well as microbe-microbe interactions. We find that, unlike the correlation-based approach, the model-based inference is robust to variation in network structure and life history traits. In addition, inference is possible even when microbe-microbe competition is heterogeneous.

Ashley R. Coenen
School of Physics, Georgia Institute of Technology

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