

Cesar O. Flores, School of Physics, Georgia Institute of Technology, Atlanta, GA, USA

Sergi Valverde , Complex Systems Lab and Institute of Evolutionary Biology, University Pompeu Fabra, Barcelona, Spain

Joshua S. Weitz, School of Biology & School of Physics, Georgia Institute of Technology, Atlanta, GA, USA

Phage-Bacteria Interaction Networks: From Nestedness to Modularity

Bacteriophages (viruses that infect bacteria) are the most abundant biological life-forms on Earth. However, very little is known regarding the structure of phage-bacteria infections. In a recent study we showed that phage-bacteria infection assay datasets are statistically nested in small scale communities while modularity is not statistically present (Flores et al 2011). We predicted that at large macroevolutionary scales, phage-bacteria infection assay datasets should be typified by a modular structure, even if there is nested structure at smaller scales. We evaluate and confirm this hypothesis using the largest study of the kind to date (Moebus and Nattkemper 1981).

The study in question represents a phage-bacteria infection assay dataset in the Atlantic Ocean region between the European continental shelf and the Sargasso Sea. We present here a digitized version of this study that consist of a bipartite network with 286 bacteria and 215 phages including 1332 positive interactions, together with an exhaustive structural analysis of this network. We evaluated the modularity and nestedness of the network and its communities using a variety of algorithms including BRIM (Bipartite, Recursively Induced Modules), NTC (Nestedness Temperature Calculator) and NODF (Nestedness Metric based on Overlap and Decreasing Filling). We also developed extensions of these standard methods to identify multi-scale structure in large phage-bacteria interaction datasets. In addition, we performed an analysis of the degree of geographical diversity and specialization among all the hosts and phages.

We find that the Moebus and Nattkemper (1981) study, as anticipated by Flores et al. (2011), is highly modular and not significantly nested (computed in comparison to null models). More importantly is the fact that some of the communities extracted from Moebus and Nattkemper dataset were found to be nested. We examine the role of geography in driving these modular patterns and find evidence that phage-bacteria interactions can exhibit strong similarity despite large distances between sites. We discuss how models can help determine how coevolutionary dynamics between strains, within a site and across sites, drives the emergence of nested, modular and other complex phage-bacteria interaction networks

Bibliography:

Moebus K, Nattkemper H (1981). Bacteriophage sensitivity patterns among bacteria isolated from marine waters. *Helgol Meeresunters* 34: 375-385.

Flores CO, Meyer JR, Valverde S, Farr L, Weitz JS (2011). Statistical structure of host-phage interactions. *Proc Natl Acad Sci US A* 108: E288-E297.