Abstract Submitted
for the MAR13 Meeting of
The American Physical Society

Phage-bacteria infection networks: From nestedness to modularity[1] CESAR O. FLORES, Georgia Institute of Techonology, SERGI VALVERDE, University Pompeu Fabra, JOSHUA S. WEITZ, Georgia Institute of Techonology — 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 re-evaluated 38 prior studies and demonstrated that phage-bacteria infection networks tend to be statistically nested in small scale communities (Flores et al 2011). Nestedness is consistent with a hierarchy of infection and resistance within phages and bacteria, respectively. However, we predicted that at large scales, phage-bacteria infection networks should be typified by a modular structure. We evaluate and confirm this hypothesis using the most extensive study of phage-bacteria infections (Moebus and Nattkemper 1981). In this study, cross-infections were evaluated between 215 marine phages and 286 marine bacteria. We develop a novel multi-scale network analysis and find that the Moebus and Nattkemper (1981) study, is highly modular (at the whole network scale), yet also exhibits nestedness and modularity at the within-module scale. 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.

[1] CFG acknowledges the support of CONACyT Foundation. JSW holds a Career Award at the Scientific Interface from the Burroughs Wellcome Fund and acknowledges the support of the James S. McDonnell Foundation

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Date submitted: 11 Nov 2012 Electronic form version 1.4