Mateusz M. Pluciński
Department of Environmental Science, Policy and Management, University of California, Berkeley. Berkeley, CA, 94720
e-mail: `mateusz@berkeley.edu`

Human social network structure is reflected in sequence data for commensal bacteria

DNA sequence data has traditionally been used to infer transmission networks only in the context of epidemics and outbreaks of pathogens, but it can analogously be applied to cases of ubiquitous commensal bacteria in order to infer information about host contact networks. Here, we show that multilocus DNA sequence data, based on multilocus sequence typing schemes (MLST), from isolates of commensal bacteria circulating in an endemic equilibrium can be used to infer both the local and global properties of the contact networks of the populations being sampled. Indeed, we show that MLST data obtained from simulations of spread on a small-world network can be used to robustly estimate the small world parameter controlling the degree of structure in the contact network. Moreover, the pairwise distances in the network — degrees of separation — correlate with genetic distances between isolates meaning that how far apart two individuals in the network are can be inferred from MLST analysis of their commensal bacteria. This result has important consequences, and we show an example from epidemiology — how this result could be used to test for infectious origins of diseases of unknown etiology. We also extend our previous work to include the study of the spread of commensal bacteria on scale-free networks; in particular, we examine the role of highly connected individuals in determining the overall distribution of sequence types.