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Analyzing determinants of gut microbiota using interaction network methods

The past twenty years have seen both a surge of interest in assessing ecological interactions using tools borrowed from network theory and an explosion of data on the occurrence of microbial symbionts thanks to next-generation sequencing. Ecologists now face huge datasets reporting microbial co-occurrences within different hosts, and have yet to understand them. I will present two methods to elucidate the determinants of multipartite interaction networks and apply them to experimental data on *Daphnia magna* and its interactions with gut microbiota and bacterioplankton. The first method is based on classifications and compares communities (modules) within networks to the grouping of nodes by treatment or similar controlling groups. The second method assesses the link between multivariate explanatory variables and network structure using redundancy analyses of ‘trait matrices’ obtained after singular value decomposition. In both methods, the significance of effects can be gauged through edge randomization. These two methods assess effects at different grains, the first one being coarser than the second. Our results suggest that bacterioplankton and gut microbiota communities are different. At coarse grains, the structure of the gut microbiota-based network was quite idiosyncratic, while the bacterioplankton-based network was related to both diet and genotype. At finer grains, *Daphnia*'s diet and genotype affected both networks, but the effect of diet on gut microbiota network structure was mediated solely by differences in microbial richness. Overall our results suggest little reciprocal effect between the two microbial communities, but fine-grained analyses presented a more nuanced picture, with bacterioplankton likely affecting the composition of the gut microbiota. Our methods are widely applicable to bipartite networks, can elucidate both controlled and environmental effects, and can even tease apart reciprocal effects of networks on one another. In *Daphnia magna*'s microbial networks, there is little reciprocal effect, but both networks are at least partly determined by the host's diet and/or its genotype.