



Towards a top-down framework to make microbial ecology predictive

Johannes Rousk and Lettice Hicks

Lund University, Microbial Ecology - MEMEG, Department of Biology, LUND, Sweden (johannes.rous@biol.lu.se)

Understanding the role of ecological communities in maintaining multiple ecosystem processes is a central challenge in ecology. Soil microbial communities perform vital ecosystem functions, such as the decomposition of organic matter to provide plant nutrition. However, despite the functional importance of soil microorganisms, attribution of ecosystem function to particular constituents of the microbial community has been impeded by a lack of information linking microbial processes to community structure.

Here, we propose a new conceptual framework to determine how microbial communities influence ecosystem processes, by applying a “top-down” traits based approach. By determining the dependence of microbial community processes on environmental factors (e.g. the intrinsic temperature dependence of bacterial growth rates) we show that we can define the response trait distribution of the community. We then demonstrate that the whole community contribution to ecosystem function can be predicted, by parameterising the response trait distribution with current environmental conditions. In a final step, we show how this information on function can be linked to the taxonomic community composition (amplicon assessments of microbial community composition) in order to identify “biomarker” taxa that capture microbial communities’ regulation of ecosystem processes. Ultimately, these biomarkers may be used as indicator taxa, enabling predictions of microbial community trait distributions and estimates of ecosystem function from community composition information combined with environmental metadata.