# Towards a top-down framework to make microbial ecology predictive

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I propose a new framework to determine how microbial communities influence ecosystem processes. Rather than the established bottom-up approach where information on individual taxa is assembled to construct the function puzzle, I propose a top-down approach. First, I will offer tools to determine the dependence of microbial community processes on environmental factors (e.g., intrinsic temperature dependence of bacterial community growth rates) as measures of community response trait distributions. Second, I will show how the whole-community contribution to ecosystem functions can be estimated by parametrising response trait distributions (from above) with current environmental conditions. This synthetic information about microbial communities can then be linked with taxonomic community composition by comparative analysis of characterisations of environmental gradients combined with experimental findings. This could identify "biomarkers" that can capture microbial communities' regulation of ecosystem function and predict the susceptibility of community structure and functions to environmental change. This framework offers an alternative "top-down" complement to the "bottom-up" approaches that currently dominate microbial ecology.