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On prediction and predictability in microbial community functions

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Microbial communities carry out metabolic functions critical to the persistence of life on this planet through the cycling of nutrients in natural environments and host-microbiome interactions. Community metabolism emerges from a hierarchy of processes, including gene expression, ecological interactions, and environmental factors. Making quantitative predictions about community functions thus requires distilling from this complexity appropriate informative features. In this talk I will present the results of two efforts to make predictions of synthetic microbial community functions using the features of (1) community gene content in the model system of bacterial denitrification, and (2) community composition in a reanalysis of existing various synthetic community function datasets. Both investigations offer lessons about features that are potentially informative for predicting process rates in complex natural microbiomes.