Longitudinal metagenome and metatranscriptome surveys on complex microbial communities

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Abstract
Understanding the composition and function of complex microbial communities remains a key goal of applied microbial ecology, as well as providing many opportunities for developing new thinking and methods in systems microbiology. The systematic analysis of such communities remains immensely complex, with particular challenges relating the lack of relevant reference genomes, the difficulty of recovering the genomes of member taxa from bulk community assemblies and the complexity of understanding whole community function. Here, I will describe recent studies we have performed using nucleic acid sequencing (DNA and/or RNA) using time-series designs in complex, unmodified microbial communities (sampled from full-scale wastewater plants), to study the organisation, diversity and plasticity of whole microbial community function. We show how monitoring the functional response of the community to perturbations of functional state, either natural or induced, can be coupled with metagenome assembly and network analysis to pinpoint taxa that are associated with specific functions. Our methods provide a general, systematic approach to probing composition-function relationships in intact microbial communities, highlight the limitations of laboratory studies to recapitulate within-community taxa interactions and suggests new routes for mechanistic level investigations.

Biography
Rohan Williams is Head of the Integrative Analysis Unit at the Singapore Centre for Environmental Life Sciences Engineering (SCELSE), an autonomous research centre in microbial ecology and biofilm biology co-hosted by the National University of Singapore and Nanyang Technological University. Williams holds a BAppSc in Physics from UTS (1994) and a PhD in Medicine from UNSW (2003), from 2004-2007 he was an NHMRC Peter Doherty Fellow at UNSW and between 2007-2011 he was a group leader at the John Curtin School of Medical Research at the ANU. He moved to Singapore in 2011 to take up a principal investigator role at SCELSE. His interests and expertise lie in statistical bioinformatics, design, analysis and interpretation of experiments using genomic technologies, systems microbiology and the analysis of complex microbial communities. twitter.com/rbhwilliams1