

Presentation title: Great expectations or why sequencing platforms are not magic work

Abstract:

Environmental microbial sequencing (e.g. amplicon sequencing, metagenomics, metatranscriptomics) provides a culture-independent means to investigate the composition, genomic potential and activity of microbial communities.

These approaches have been rapidly and widely adopted with the result that the corresponding data typically constitutes a critical component of many studies. Unfortunately, highly complex microbiomes coupled with poor experimental design and unrealistic goals have all too often lead to doomed studies, disappointment and tears. In this tag-team talk, we provide an overview of environmental microbial sequencing techniques, with a focus on appropriate experimental design and bioinformatic analyses. We aim to provide a broad overview of what can be achieved with a HiSeq and some derring-do: and what cannot. We will illustrate our main points with a few case studies.