

Joint Conference

International Conference on

ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

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International Conference on

ECOLOGY AND ECOSYSTEMS

September 18-20, 2017 Toronto, Canada



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Reference-free shotgun metagenomics for the microbial ecologist

Traditionally, shotgun sequencing of complex microbial communities depends on reference genomes from known organisms. However, reference genomes are missing for the majority of the microbial diversity, making this approach inadequate for surveying complex microbial communities. The metagenomic species (MGS) concept allows detection and functional profiling of unknown species for which reference genomes are absent by clustering genes based on their abundance profiles. This method has already proven successful on the human gut microbiome, where it can identify up to five times more species than reference genomes can. The MGS concept has recently been expanded to include infants, mice, pigs, and marine microbial communities and can likely also be applied to terrestrial environments. Recent tests have found that the MGS concept is much more accurate and sensitive in detecting low-abundance taxa than a reference genome-based approach and, consequently, can provide reliable results at much lower sequencing depths, providing significant savings on sequencing costs. The MGSs typically consists of 1000-2000 genes representing core genomes and annotation of these genes allows identification of the functional potential of each MGS as well as insight into how metabolic pathways are distributed between the members of a microbial community. Furthermore, the majority of the MGSs appears to be only distantly related to known taxa and can provide a vantage point from which to describe new high-level taxa. The MGS concept is a very valuable tool for the microbial ecologist and allows surveying the microbial community at both a taxonomic and functional level of detail not previously possible.

Biography

Nikolaj Sørensen is a microbial ecologist with experience from a vast range of microbial habitats, including aquatic, terrestrial, and clinical microbial ecosystems. He makes extensive use of high-throughput sequencing in his work and is focused on bridging the gap between bioinformatics and microbial ecology. His holistic approach to microbial ecology comes from being actively involved in all steps of the scientific process, from study planning and sample collection through laboratory work and sequencing to bioinformatics and the ecological interpretation. He is the Director of scientific operations in the contract research organization clinical-microbiomics.

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