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Kyle Bittinger

University of Pennsylvania, USA

Methods for characterizing fungal communities in the human microbiome

Fungi play an integral role in the human microbiota, the sum total of all microorganisms occupying the human body. When investigating the microbiota with high-throughput DNA sequencing approaches, fungi require the application of specialized methods to be characterized accurately. Here, we review some of the pitfalls and traps to avoid when analyzing combined communities of bacteria and fungi, and present methods for improving accuracy. We show how the methods can be applied to yield insight on the role of fungi in health and disease. Finally, we discuss the application of whole-genome shotgun metagenomic DNA sequencing to combined communities of bacteria and fungi.

Biography

Kyle Bittinger has completed his PhD in Physical Chemistry from MIT, and started his investigations on the human microbiome at the University of Pennsylvania in 2009. He helped to develop the widely used QIIME software for analysis of DNA sequence data. As part of the NIH Human Microbiome Project, his work focused on the role of diet in shaping the gut microbiota in health and disease. He directs the bioinformatics group at the CHOP Microbiome Center, part of the joint PennCHOP microbiome program.

kylebittinger@gmail.com