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Suite 305, Ashburn, VA 20147. *Statistical and computational approaches to microbiome analyses.*

Advances in DNA sequencing technology allow us to collect genomic data at a now cost-effective and efficient manner. Diagnostic companies and hospitals are equipping themselves with next-generation DNA sequencers, yet there remains significant constraint in our ability to manage and analyze these new volumes of data. Here we demonstrate some of the utility of using computational and statistical approaches for pathogen diagnosis as an example of translational research impacting personal medical outcomes. We demonstrate our approach with a variety of applications in human health and agricultural settings. In particular, we show the utility of our methods to identify pathogens, characterize microbial diversity, and test hypotheses associated with functional diversity of both host and pathogen. (Received January 10, 2015)