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Optimizing biodiversity in metagenomics via compressed sensing. Preliminary report.

Metagenomics is the study of microbial DNA that is extracted directly from a community of organisms in a given environment. Metagenomic analysis has clarified diverse processes ranging from global nutrient cycling to human disease and has proven to be a powerful tool for understanding the ubiquitous communities of bacteria that exist in our world, many of which can be studied only via their DNA. This pursuit presents a number of unique challenges including producing massive amounts of data that can be only approximately compared to very incomplete databases. We will present an approach based on compressed sensing, and discuss an extension that involves optimizing the biological diversity of a given sample. This is based on a recently proposed generalization of biodiversity metrics introduced by Leinster and Cobbold (2014). (Received September 22, 2015)