

[Algorithms for integrative functional metagenomics](#)

In studies of the human microbiome's role in health and disease, it is now practical to survey not just the "parts list" of its microbial residents, but their multi'omic metagenomes, metatranscriptomes, and other culture-independent functional molecular data. This raises two current computational challenges: how to provide the most precise bioinformatic solutions describing microbial community systems biology, and what new applications of these integrated data types can be developed? I will discuss the methods underlying our latest taxonomic and functional profilers for microbial communities, which provide strain-specific microbial identification and metabolic reconstruction. This level of detail can be used to uniquely identify individuals from their microbial communities by building "metagenomic codes," and I will conclude with downstream statistical analysis methods for associating microbial features with ecological, environmental, or health-related covariates in these or other multi'omic data.