Computational tools for predicting microbial function from gut metagenomes

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Abstract

The gut microbiome is involved in promoting or inhibiting (protecting against or contributing to the development of) many diseases, such as diabetes, inflammatory bowel disease, obesity, and cardiovascular disease, depending on the functions that the microbes encode. Elucidating the functional roles that the gut microbiome plays in disease mechanisms is crucial to improving treatment and diagnoses. Not only for improving treatments against pathogenic microbes, but also for improving health using microbes that confer beneficial functions to the host, such as anti-inflammatory effects. The initial analysis for most human microbiome studies is to identify and quantify the microbiome taxonomic composition. More recently, efforts are being made to predict the community wide functions. Function can be directly characterized by analyzing proteins or gene transcripts, from 'omic datatypes such as proteomics or transcriptomics, however, obtaining these datatypes can be challenging. Inferring microbial function from metagenomes could be helpful. **This study will discuss the available frameworks for predicting metagenomic functions, as well as provide key considerations for selecting the most appropriate tool given the question and data at hand.** A key consideration with these evaluations is to validate the predictions with paired proteomics or metatranscriptomics to assess accuracy.