

METANUTRITION: USING METAGENOMICS TO ANALYZE THE GUT MICROBIOME

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The gut microbiome is indispensable for supplementing mammalian nutrition requirements through fiber digestion. Microbial fermentation not only provides short chain fatty acids as a host energy source, but also produces supplemental levels of vitamins B and K. Recent commercial trends toward marketing of probiotic dairy products indicate increased public awareness and interest in promoting desirable bacterial communities, and the medical community has begun to use fecal transplants to restore gut communities after perturbation. But how can we sustain those introduced species? We must feed our microbes to help feed ourselves.

Metagenomics can provide a foundational understanding of microbial communities' metabolic capabilities. Shotgun sequencing targets whole communities, and next generation sequencing enables high coverage sampling at relatively high speeds and low cost. To that end, we have developed MMAP, a bioinformatics pipeline for the streamlined analysis of empirical data. We have combined existing programs and original algorithms to quantify bacterial gene ontology. The functional exploration of high-throughput sequencing data will help characterize gut microbiomes based on their collective strengths, weaknesses, and associations with a specific host or diet. If we use these profiles to infer the microbiota's basic growth patterns and requirements, we can provide the optimal dietary substrate to promote healthy, robust gut populations and optimize digestive performance within the host.