

# **Microbial Community Profiling and Metagenomic Sequencing**

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The quantity of bacterial cells that live upon and within a human host is an order of magnitude greater than the number of human cells that make up the body itself. This diverse population of bacteria comprises the human microbiome and variations in these communities have implications in general human health and disease. High throughput sequencing can be utilized to assay the composition and diversity of microbial communities but analysis of these data presents unique computational challenges. The system we are developing allows for visualization and manipulation of sequencing results as well as hypothesis testing across microbial communities. The system is very flexible and integrates diversity analysis, rarefaction curves and other important measures of community differences into a framework that is easy to use for biological researchers.