

Microbiome is a term used to describe the collection of all microorganisms that colonize our bodies. Whereas understanding the human genome has received enormous amount of attention in the last 15 years, the impact of host associated microbiome genomes (the metagenome) and their function in human health and disease is still in very early stages of being conceptualized. The recent surge in microbiome science has been afforded by increasing availability of technologies, such as high-throughput DNA sequencing, mass spectrometry, automated cell sorting, etc. Most notably, of course, the ability to sequence hundreds of individual microbiomes in a single run of a sequencing instrument has resulted in a perfect storm of microbial community profiling datasets addressing a vast array of biomedical questions. This presentation will motivate the need for microbiome specific data analytic techniques. I first describe a use case aiming to measure microbiomes of entire in-patient population and to utilize these data for development precision medicine approaches to triage and intervention. Next I will highlight a few promising analytic approaches and a general framework for integrating microbiome data coming from various high-throughput sources.