

**Course Title**

Statistical and Computational Methods for Microbiome Data Analysis

**Category**

methodology

**Target Audience**

graduate students and practitioners interested in microbiome research

**Prerequisites for Participants**

Basic knowledge of multivariate statistics and R programming

**Computer and Software Requirements**

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**Course Description****Abstract**

The human microbiome plays a critical role in human health and disease. A thorough understanding of the microbiome and its link to health promises to revolutionize precision medicine. Vast amounts of high-throughput data have been generated from 16S rRNA sequencing or metagenomic sequencing technologies to characterize the human microbiome in different anatomical sites (e.g., oral, skin, vaginal, gut, and lung). Large collaborative efforts such as the Human Microbiome Project (HMP) have curated valuable databases. New computational and statistical methods are being developed to understand the function of microbial communities. In this short course, we will start with a brief introduction to how microbiome data are obtained and then provide detailed presentations on the statistical and computational methods for analyzing microbiome data. We will focus on preprocessing, exploratory data analysis (e.g., data visualization, dimension reduction, diversity calculation), and more advanced statistical analysis (e.g., association analysis, mediation analysis, network analysis). We will demonstrate how to use some state-of-the-art tools to conduct these analyses. Open questions and future research directions on microbiome data analysis will also be discussed. Participants will get a good understanding of existing methods and future directions for microbiome data analysis and be able to perform basic processing and analysis of microbiome data after taking the short course.