**Power and Sample Size Calculation for Microbiome Differential Abundance Studies**

**Authors:**

Michael Agronah1, Dr Benjamin Bolker2

1 *Department of Mathematics & Statistics, McMaster University,ON Canada.*

*2 Departments of Mathematics & Statistics and of Biology, McMaster University, ON Canada.*

**Abstract:**

Determining an appropriate sample size for a study is a crucial step in planning scientific research. Appropriate sample sizes avoid both overinflated and inadequate sample sizes. Collecting too many samples wastes resources, time and effort of human subjects, and lives of experimental animals. Insufficient sample sizes, a much more common problem, waste even more resources through the inability to detect biologically meaningful differences.

Microbiome studies are particularly challenged by sample size, particularly in studies of human subjects or expensive animal models.

We analyzed seven real case-control microbiome datasets and developed a novel method for simulating microbiome data. We present a new approach for sample size and power calculation as a function of effect size (fold change) and mean abundance. We also quantify the expected total number of significant taxa within differential abundance studies.

Differential abundance microbiome studies require larger sample sizes than currently prevalent in the literature to achieve adequate statistical power. Our framework will help researchers make informed decisions about appropriate sample sizes.