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Introduction

Power analyses are important for experimental study design so that the researcher has an idea of how many experiment subjects are needed to minimize Type II error. Most NIH funding applications require sample size and power analyses. In microbiome studies power analyses can be difficult not just because the true effect size is unknown, but also because the composition of the microbiome in control and experimental groups (i.e. beta diversity) is generally unknown. However, if the study intends to use pairwise distances and PERMANOVA to measure diversity then we can use methods from the R package *micropower* (Kelly et al. 2015) to perform power analyses as long as we have previously available datasets characteristic of one of the groups (most likely the control) and some idea of the effect size. The basic idea behind *micropower* is to simulate distance matrices given prior population parameters computed from previous studies, then simulate a range of effect sizes, rarefaction curves, etc. to estimate PERMANOVA power from the simulated distance matrices.

micropower is a great package that I've used to perform power analyses for researchers wanting to do 16s and whole genome shotgun metagenomics experiments. However it comes without a tutorial or much documentation - there is a [gist available](#) though - so it's not entirely clear how to use it. Following is a (more in-depth than the gist) walkthrough of what such an analysis looks as well as what you will need to consider for your own power analysis.