

Mixed Model Regressions for the Fit of the Human Microbiome Project to Biodiversity Models

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Set working directory

Import the data.

```
HMP_meta <- read.csv("../data/HMP-Data/ppAll_V35_map_noTimeseries.txt", sep="\t") # read csv file
```

Wrangle the data so that it matches the labels in the file containing r_m^2 values.

```
HMP_meta$NAP <- sub("$", ".may1", HMP_meta$NAP )
```

We know from theory and previous analyses from this study that N_0 , S_0 , and $N_m ax$ are not independent, so we include them as interactions from the start.