**NTM analysis protocol**

1. Sequence all samples in mothur
2. Cluster sequences at the following taxonomic levels:
   1. Family-
   2. Genus-
   3. OTU-
3. Calculate all α-diversity and select β-diversity measures with *mothur*
4. Calculate Shannon-β and γ-diversity with *entropart*
5. Combine the features listed in (2)-(4)
6. Perform regression for all features:
   1. For model #
   2. Separate data at the subject level
   3. For **subjects with >1 sample**, perform linear/logistic regression using the feature value as y-data and the relative (to first (+) culture) sample age as x-data
   4. Include the regression output as subject