Meeting #7 Agenda

Maddy to take minutes

1. How to merge the two individual graphs into a single graph for alpha diversity metrics?
2. The PiCRUST keeps giving an error when we try to input our files. It requires fastq files, but I'm not sure which directory it needs to be in in qiime2. We are having trouble with installing PiCRUST2.
3. Show the controlling for feeding mode significance metrics.

Minutes

wget https://github.com/picrust/picrust2/archive/v2.5.2.tar.gz
tar xvzf v2.5.2.tar.gz
cd picrust2-2.5.2/
mamba env create -f picrust2-env.yaml
conda activate picrust2
pip install --editable .

- Replace mamba with conda
- 15 to 30 mins to install
- Try to install in your working directory close to input files

Don't use picrust2

Rep-seqs.qza will be -s
Table-no-mito-no-chloro.qza as input
Output is a folder containing all the results so you can call it whatever you want
Filtering out features with less than 5 reads while doing it will make it take way longer so do a screen

Resubmit proposal with track changes/somehow made clear what you changed and resubmit and say resubmitting with track changes as per Avril's recommendation

- Make sure final manuscript is made using track changes as well

Ggpiecrust2 in R
You can choose input as DeSeq and since hayley and emily are doing DeSeq as well it would be good to consistent

No need for stats for core microbiome