1. Download the sequences from Box and upload them into CCR (/panfs/panfs.cbls.ccr.buffalo.edu/scratch/grp-pidiazmo). Files in this folder will be deleted if they are not accessed for 60 days.
2. Decompress the sequence files into fastq
3. Trim the first 25 bases of the sequences
4. Make the file list of sequences
5. Edit the sequence list with Excel or use [prepareFile4Mothur.m](https://github.com/liluacrobat/16S_Mothur_pipeline/blob/main/prepareFile4Mothur.m)
6. Run a first run with a sample till the step of generating align\_summary.txt to figure out the start and end place parameter.
7. Edit the parameter and submit the job of all the samples
8. Use Matlab to reorganize the taxonomy
9. Collect core files and summarize the OTU table