**PINNELL QIIME2 MANIFEST FILE CREATION**

For starters, navigate to your [ProjectID]/metadata/ directory. Keep in mind that you need to use your username not mine throughout (i.e., not ljpinnell).

**STEP 1. List the absolute path to the forward reads and output to a new file (R1.txt):**

ls /scratch/users/ljpinnell/16S\_ReAnalysis/reads/\*R1.fastq.gz > R1.txt

**STEP 2: Same thing for the reverse reads (R2.txt):**

ls /scratch/users/ljpinnell/16S\_ReAnalysis/reads/\*R2.fastq.gz > R2.txt

**STEP 3: Used sed (find and replace) to get sampleIDs from R1.txt.**

First step is to replace the paths (i.e., /scratch/users/ljpinnell/16S\_ReAnalysis/reads/) with nothing and write the results a temporary file (tmp1):

sed ‘s@/scratch/users/ljpinnell/16S\_ReAnalysis/reads/@@g’ R1.txt > tmp1

Next, remove the ‘\_1.fastq.gz’ part of the lines and write to new file:

sed ‘s@\_R1.fastq.gz@@g’ tmp1 > sampleIDs.txt

Then remove the temporary file

rm tmp1

This leaves us with three files (sampleIDs.txt, R1.txt, R2.txt).

**STEP 4: Combine the three files with paste and write to manifest file:**

paste sampleIDs.txt R1.txt R2.txt > manifest.tsv

This creates a tab-delimited file combining the three pieces.

**STEP 5: Add tab-delimited headers to the manifest file**

First, use nano to open the manifest and use text-editor abilities in command line

nano manifest.tsv

Then you are going to add the following headers above the three columns. Between each header use to tab to space the headers. Don’t worry, it won’t look like the headers are lined up with the columns correctly but if you use tab to separate them it’ll be correct!

sample-id forward-absolute-filepath reverse-absolute-filepath

Exit and save from nano and the manifest file is all good to go and should be located inside your metadata/ directory!