Run Suzie’s version of Jiwoong’s 16s pipeline

1. Create a file on your desktop and add all of your 16s reads to this file.
2. Add your metadata file to this file. This should be a tab delimited file. Make sure your first column is named “sample-id”. The other columns can have any name. The name of your metadata file should be “metadata.txt”.
3. Move the scripts folder (that I provide) to this file. The scripts inside this file should be: “classifier.qza”, “parse\_manifest.py”, “table.extendLines.pl” and “table.mergeLines.pl”. If you do not have these files, then this script will not work.
4. The only thing you will need to edit in the qiime2 script before running is the path to the file with the sequences. This is on one of the topmost lines that says cd {PATH to folder}.
5. Once this is done, you will run the script by typing in sh {PATH to folder}.
6. This might take a couple of hours to run locally.