QIIME scripts

# Method 1: Using fasta and qual file (single-end reads?)

1. Converting fasta and qual file to fastaq file
   1. >Convert\_fastaqual\_fastq.py -f filename.fasta -q filename.qual -o filename.fastaq
2. Create mapping file
   1. This file contains all of the information about the samples necessary to perform the data analysis. At a minimum, the mapping file should contain the name of each sample, the barcode sequence used for each sample, the linker/primer sequence used to amplify the sample, and a Description column. In general, you should also include in the mapping file any metadata that relates to the samples (for instance, health status or sampling site) and any additional information relating to specific samples that may be useful to have at hand when considering outliers (for example, what medications a patient was taking at time of sampling). Of note: the sample names may only contain alphanumeric characters (A-z,0-9) and the dot (.).
3. Validate mapping file
   1. >validate\_mapping\_file.py -m -m filename.txt -o  mapping\_output
4. Extract barcodes
   1. >extract\_barcodes.py -f filename.fastq -c barcode\_single\_end –bc1\_len 8 -o

# Method 2: Using fastaq file (paired-end approach)