module load bio3

module load qiime/2-2020.2

source activate qiime2-2020.2

#Import data (sequences + barcodes)

#Files in FL103 folder are “sequences.fastq.gz” and “barcodes.fastq.gz”

qiime tools import \

--type EMPSingleEndSequences \

--input-path ~/FL103/barcodes\_unfiltered/ \

--output-path ~/FL103/FL103seqs\_unfiltered.qza

#demultiplexing

qiime demux emp-single \

--i-seqs ~/FL103/FL103seqs\_unfiltered.qza \

--m-barcodes-file ~/FL103/FL103\_MapFile.txt \

--m-barcodes-column BarcodeSequence \

--p-no-golay-error-correction \

--o-per-sample-sequences ~/FL103/demux\_unfiltered.qza \

--o-error-correction-details ~/FL103/demux-details\_unfiltered.qza

#summarize demux results

qiime demux summarize \

--i-data ~/FL103/demux\_unfiltered.qza \

--o-visualization ~/FL103/demux\_unfiltered.qzv