

Commands used for the Qiime2 pipeline to process sample reads
all lines run directly into a bash terminal in an environment with the Qiime2-2022.2 package loaded

imports manifest files to a qiime artifact

**qiime tools import --type 'SampleData[SequencesWithQuality]' --input-path
[PATH_TO_MANIFEST_FILE] --output-path [OUTPUT_PATH_TO_READS.QZA] --input-format
SingleEndFastqManifestPhred33V2**

dereplicates sequences

**qiime vsearch dereplicate-sequences --i-sequences [PATH_TO_NEW_READS.QZA] --o-
dereplicated-table [PATH_TO_DEREP_TABLE] --o-dereplicated-sequences
[PATH_TO_DEREP_SEQUENCES]**

aligns to custom classifier

see classifier generator script for how classifiers were created

**qiime feature-classifier classify-sklearn --i-classifier [PATH_TO_CORRESPONDING_CLASSIFIER]
--i-reads [PATH_TO_DEREP_SEQUENCES] --p-confidence 0.8 --o-classification
[PATH_TO_TAXONOMY.QZA]**

generates a .qzv file of relative abundance

this can be exported to a csv at any taxonomic level from <https://view.qiime2.org/>

#the resulting csv at the genus level was imported to R for processing

**qiime taxa barplot --i-table [PATH_TO_DEREP_TABLE] --i-taxonomy
[PATH_TO_TAXONOMY.QZA] --o-visualization [PATH_TO_TAXONOMY.QZV]**