**Codes used in Microbiome Section Report (G2)**

1. **START in Ubuntu**

# import my files into qiime2 and create the artefact

qiime tools import \

--input-path demux.qza \

--output-path sequences

1. **In R Studio**

# Load required packages

```{r}

library(dada2)

```

# Load sequences

```{r}

path <- "sequences"

list.files(path)

```

# Read in file names

```{r}

# Forward and reverse fastq filenames have format: SAMPLENAME\_R1\_001.fastq and SAMPLENAME\_R2\_001.fastq

fnFs <- sort(list.files(path, pattern="\_R1\_001.fastq", full.names = TRUE))

fnRs <- sort(list.files(path, pattern="\_R2\_001.fastq", full.names = TRUE))

# Extract sample names, assuming filenames have format: SAMPLENAME\_XXX.fastq

sample.names <- sapply(strsplit(basename(fnFs), "\_"), `[`, 1)

```

# Inspect read quality

```{r}

plotQualityProfile(fnFs[1:2])

```

```{r}

plotQualityProfile(fnRs[1:2])

```

1. **In Ubuntu using qiime2**

# quality control of forward and reverse reads based on histogram

# it uses the demux.qza file to trim and truncate reads

# the output a rep-seqs file, a table of the sequences, and stats

qiime dada2 denoise-single \

qiime dada2 denoise-paired --i-demultiplexed-seqs demux.qza --p-trim-left-f **15** --p-trunc-len-f **150** --p-trim-left-r **0** --p-trunc-len-r **120** --o-representative-sequences rep-seqs.qza --o-table table.qza --o-denoising-stats stats.qza

# the code creates a visualizations for the Table and Sequences

# it tabulates the stats file

# an output would be a visualization of the stats file

qiime metadata tabulate \

--m-input-file stats.qza \

--o-visualization stats.qzv

# creating a table summarizing the data

# it uses the table files

# results in an output of a metadata file

qiime feature-table summarize \

--i-table table.qza \

--o-visualization table.qzv \

--m-sample-metadata-file metadata.tsv

# creating a table of the sequences, output a visualization

# it uses the rep-seqs file

# results in a visualization of the rep-seqs file

qiime feature-table tabulate-seqs \

--i-data rep-seqs.qza \

--o-visualization rep-seqs.qzv

# adjusted the following code by adjusting the names of the files I personalized

qiime feature-table summarize \

--i-table table.qza \

--o-visualization table.qzv \

--m-sample-metadata-file metadata.tsv

qiime feature-table tabulate-seqs \

--i-data rep-seqs.qza \

--o-visualization rep-seqs.qzv

# qiime uses a specific database as a classifier

# input the reads

# output of the taxonomy

qiime feature-classifier classify-sklearn \

--i-classifier gg-13-8-99-515-806-nb-classifier.qza \

--i-reads rep-seqs.qza \

--o-classification taxonomy.qza

# making a visualization of the taxonomy.qza file to a qzv

qiime metadata tabulate \

--m-input-file taxonomy.qza \

--o-visualization taxonomy.qzv

# filters the taxonomy, excluding contaminants of mitochondria and chloroplast genetic material

qiime taxa filter-table \

--i-table table.qza \

--i-taxonomy taxonomy.qza \

--p-exclude mitochondria,chloroplast \

--o-filtered-table table.qza

# making a visualization of the table.qza file to a qzv (now excluding mitochondria and chloroplast DNA)

qiime metadata tabulate \

--m-input-file table.qza \

--o-visualization table.qzv

# input the table.qza of the data (now excluding mitochondria and chloroplast DNA)

# input the metadata file

# output of the taxonomy bar plots through a .qzv file

qiime taxa barplot \

--i-table table.qza \

--i-taxonomy taxonomy.qza \

--m-metadata-file metadata.tsv \

--o-visualization taxa-bar-plots.qzv

# generating a phylogenetic tree for diversity analysis

# input sequences

# output of alignment, masked aligned, unrooted and rooted phylo trees.

qiime phylogeny align-to-tree-mafft-fasttree \

--i-sequences rep-seqs.qza \

--o-alignment aligned-rep-seqs.qza \

--o-masked-alignment masked-aligned-rep-seqs.qza \

--o-tree unrooted-tree.qza \

--o-rooted-tree rooted-tree.qza

#generating the phylogenetic core metrics

# input the phylogenetic tree

# input the table excluding mitochondria and chloroplast DNA

# setting parameters for the sampling-depth based on the visualization of the table.qzv file

# using the metadata file to make an output of the phylogenetic core metrics

qiime diversity core-metrics-phylogenetic \

--i-phylogeny rooted-tree.qza \

--i-table table.qza \

--p-sampling-depth \

--m-metadata-file metadata.tsv \

--output-dir core-metrics-results

# analysis of the alpha-group-significance, specific to Shannon Diversity and Observed Features

# input specific core-metric outputs

# output visualizations of core-metric outputs

qiime diversity alpha-group-significance \

--i-alpha-diversity core-metrics-results/shannon\_vector.qza \

--m-metadata-file metadata.tsv \

--o-visualization core-metrics-results/shannon\_vector.qzv

qiime diversity alpha-group-significance \

--i-alpha-diversity core-metrics-results/observed\_features\_vector.qza \

--m-metadata-file metadata.tsv \

--o-visualization core-metrics-results/observed\_features\_vector.qzv

# analysis of beta-group-significance, specific to the metadata columns sex, population, and flock

# input core-metric output from beta analysis

# specific metadata file

# specify what column on the metadata file should be used as data

# output of visualization of the specific core-metric result

# pair-wise parameters

qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results/bray\_curtis\_distance\_matrix.qza \

--m-metadata-file metadata.tsv \

--m-metadata-column sex \

--o-visualization core-metrics-results/bray\_curtis\_distance\_sex.qzv \

--p-pairwise

qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results/bray\_curtis\_distance\_matrix.qza \

--m-metadata-file metadata.tsv \

--m-metadata-column population \

--o-visualization core-metrics-results/bray\_curtis\_distance\_population.qzv \

--p-pairwise

qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results/bray\_curtis\_distance\_matrix.qza \

--m-metadata-file metadata.tsv \

--m-metadata-column flock \

--o-visualization core-metrics-results/bray\_curtis\_distance\_flock.qza \

--p-pairwise