(qiime2-2019.1) d47h244:20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence users$ time /Volumes/iMacPro\_Pegasus/MacPro\_Data/Graf\_Data/Graf\_lab/TestermanT/20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence/Qiime2\_script\_v2\_gg\_sv\_UPDATED\_0.8\_confidence\_tax.sh

Input directory path where FASTQ files are contained (no subdirectories): /Volumes/iMacPro\_Pegasus/MacPro\_Data/Graf\_Data/Graf\_lab/TestermanT/20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence/All\_reads\_Qiime2

Input file path for map file (.txt): /Volumes/iMacPro\_Pegasus/MacPro\_Data/Graf\_Data/Graf\_lab/TestermanT/20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence/04122019\_mapping\_file.txt

Specify sampling depth for alpha and beta diversity statistics: 1000

FASTQ directory is /Volumes/iMacPro\_Pegasus/MacPro\_Data/Graf\_Data/Graf\_lab/TestermanT/20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence/All\_reads\_Qiime2

Map file path is /Volumes/iMacPro\_Pegasus/MacPro\_Data/Graf\_Data/Graf\_lab/TestermanT/20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence/04122019\_mapping\_file.txt

Sampling depth is 1000

Database is Greengenes and Silva

Imported /Volumes/iMacPro\_Pegasus/MacPro\_Data/Graf\_Data/Graf\_lab/TestermanT/20190426\_Flavo\_dilution\_final\_parameters\_0.8\_tax\_confidence/All\_reads\_Qiime2 as CasavaOneEightSingleLanePerSampleDirFmt to demux-paired-end.qza

Sequences imported

Saved Visualization to: demux-paired-end.qzv

Running external command line application(s). This may print messages to stdout and/or stderr.

The command(s) being run are below. These commands cannot be manually re-run as they will depend on temporary files that no longer exist.

Command: run\_dada\_paired.R /var/folders/67/6dbph7ys1d3240bqc4wgn7380000gp/T/tmpd5122nm9/forward /var/folders/67/6dbph7ys1d3240bqc4wgn7380000gp/T/tmpd5122nm9/reverse /var/folders/67/6dbph7ys1d3240bqc4wgn7380000gp/T/tmpd5122nm9/output.tsv.biom /var/folders/67/6dbph7ys1d3240bqc4wgn7380000gp/T/tmpd5122nm9/track.tsv /var/folders/67/6dbph7ys1d3240bqc4wgn7380000gp/T/tmpd5122nm9/filt\_f /var/folders/67/6dbph7ys1d3240bqc4wgn7380000gp/T/tmpd5122nm9/filt\_r 250 250 0 0 2.0 2 consensus 1.5 0 400000

R version 3.4.1 (2017-06-30)

Loading required package: Rcpp

DADA2 R package version: 1.6.0

1) Filtering ....................

2) Learning Error Rates

2a) Forward Reads

Initializing error rates to maximum possible estimate.

Sample 1 - 5153 reads in 693 unique sequences.

Sample 2 - 33191 reads in 12983 unique sequences.

Sample 3 - 42573 reads in 17308 unique sequences.

Sample 4 - 63598 reads in 16795 unique sequences.

Sample 5 - 35866 reads in 13517 unique sequences.

Sample 6 - 113355 reads in 40510 unique sequences.

Sample 7 - 39264 reads in 15081 unique sequences.

Sample 8 - 22056 reads in 7790 unique sequences.

Sample 9 - 30703 reads in 11682 unique sequences.

Sample 10 - 41921 reads in 14871 unique sequences.

selfConsist step 2

selfConsist step 3

selfConsist step 4

selfConsist step 5

Convergence after 5 rounds.

2b) Reverse Reads

Initializing error rates to maximum possible estimate.

Sample 1 - 5153 reads in 991 unique sequences.

Sample 2 - 33191 reads in 10928 unique sequences.

Sample 3 - 42573 reads in 15262 unique sequences.

Sample 4 - 63598 reads in 15313 unique sequences.

Sample 5 - 35866 reads in 10817 unique sequences.

Sample 6 - 113355 reads in 39037 unique sequences.

Sample 7 - 39264 reads in 12100 unique sequences.

Sample 8 - 22056 reads in 10518 unique sequences.

Sample 9 - 30703 reads in 9468 unique sequences.

Sample 10 - 41921 reads in 15866 unique sequences.

selfConsist step 2

selfConsist step 3

selfConsist step 4

selfConsist step 5

Convergence after 5 rounds.

3) Denoise remaining samples ..........

The sequences being tabled vary in length.

4) Remove chimeras (method = consensus)

6) Write output

Saved FeatureTable[Frequency] to: table.qza

Saved FeatureData[Sequence] to: rep-seqs.qza

Saved SampleData[DADA2Stats] to: denoising-stats.qza

dada2 filter and denoise complete

Saved Visualization to: table.qzv

Saved Visualization to: rep-seqs.qzv

Saved FeatureData[AlignedSequence] to: aligned-rep-seqs.qza

Saved FeatureData[AlignedSequence] to: masked-aligned-rep-seqs.qza

Saved Phylogeny[Unrooted] to: unrooted-tree.qza

Saved Phylogeny[Rooted] to: rooted-tree.qza

Saved FeatureTable[Frequency] to: core-metrics-results/rarefied\_table.qza

Saved SampleData[AlphaDiversity] % Properties(['phylogenetic']) to: core-metrics-results/faith\_pd\_vector.qza

Saved SampleData[AlphaDiversity] to: core-metrics-results/observed\_otus\_vector.qza

Saved SampleData[AlphaDiversity] to: core-metrics-results/shannon\_vector.qza

Saved SampleData[AlphaDiversity] to: core-metrics-results/evenness\_vector.qza

Saved DistanceMatrix % Properties(['phylogenetic']) to: core-metrics-results/unweighted\_unifrac\_distance\_matrix.qza

Saved DistanceMatrix % Properties(['phylogenetic']) to: core-metrics-results/weighted\_unifrac\_distance\_matrix.qza

Saved DistanceMatrix to: core-metrics-results/jaccard\_distance\_matrix.qza

Saved DistanceMatrix to: core-metrics-results/bray\_curtis\_distance\_matrix.qza

Saved PCoAResults to: core-metrics-results/unweighted\_unifrac\_pcoa\_results.qza

Saved PCoAResults to: core-metrics-results/weighted\_unifrac\_pcoa\_results.qza

Saved PCoAResults to: core-metrics-results/jaccard\_pcoa\_results.qza

Saved PCoAResults to: core-metrics-results/bray\_curtis\_pcoa\_results.qza

Saved Visualization to: core-metrics-results/unweighted\_unifrac\_emperor.qzv

Saved Visualization to: core-metrics-results/weighted\_unifrac\_emperor.qzv

Saved Visualization to: core-metrics-results/jaccard\_emperor.qzv

Saved Visualization to: core-metrics-results/bray\_curtis\_emperor.qzv

Classification step

Saved FeatureData[Taxonomy] to: taxonomy-gg.qza

Saved FeatureData[Taxonomy] to: taxonomy-silva.qza

Saved Visualization to: taxonomy-gg.qzv

Saved Visualization to: taxonomy-silva.qzv

Saved Visualization to: taxa-bar-plots-gg.qzv

Saved Visualization to: taxa-bar-plots-silva.qzv

Script complete

real 58m26.215s

user 367m20.907s

sys 45m21.547s