module load bioinfo Qiime/2-2020.2

cd /scratch/scholar/clapp5/project

qiime demux emp-paired \

--m-barcodes-file file.tsv \

--m-barcodes-column barcode-sequence \

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

--i-seqs emp-paired-end-sequences.qza \

--o-per-sample-sequences demux.qza \

--o-error-correction-details demux-details.qza

qiime demux summarize \

--i-data demux.qza \

--o-visualization demux.qzv

qiime dada2 denoise-paired \

--i-demultiplexed-seqs demux.qza \

--p-trim-left-f 0 \

--p-trim-left-r 0 \

--p-trunc-len-f 240 \

--p-trunc-len-r 180 \

--o-table table.qza \

--o-representative-sequences rep-seqs.qza \

--o-denoising-stats denoising-stats.qza

qiime feature-table summarize \

--i-table table.qza \

--o-visualization table.qzv \

--m-sample-metadata-file sample\_info.tsv

qiime feature-table tabulate-seqs \

--i-data rep-seqs.qza \

--o-visualization rep-seqs.qzv

qiime metadata tabulate \

--m-input-file denoising-stats.qza \

--o-visualization denoising-stats.qzv

qiime feature-table summarize \

--i-table table.qza \

--o-visualization table.qzv \

--m-sample-metadata-file sample\_info.tsv

qiime feature-table tabulate-seqs \

--i-data rep-seqs.qza \

--o-visualization rep-seqs.qzv

qiime metadata tabulate \

--m-input-file denoising-stats.qza \

--o-visualization denoising-stats.qzv

qiime feature-table summarize \

--i-table table.qza \

--o-visualization table.qzv \

--m-sample-metadata-file sample\_info.tsv

qiime feature-table tabulate-seqs \

--i-data rep-seqs.qza \

--o-visualization rep-seqs.qzv

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

qiime diversity core-metrics-phylogenetic \

--i-phylogeny rooted-tree.qza \

--i-table table.qza \

--p-sampling-depth 1000 \

--m-metadata-file sample\_info.tsv \

--output-dir core-metrics-results

qiime diversity alpha-group-significance \

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

--m-metadata-file sample\_info.tsv \

--o-visualization core-metrics-results/faith-pd-group-significance.qzv

qiime diversity alpha-group-significance \

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

--m-metadata-file sample\_info.tsv \

--o-visualization core-metrics-results/evenness-group-significance.qzv

qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results/unweighted\_unifrac\_distance\_matrix.qza \

--m-metadata-file sample\_info.tsv \

--m-metadata-column treatment \

--o-visualization core-metrics-results/unweighted-unifrac-treatment-significance.qzv \

--p-pairwise

qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results/unweighted\_unifrac\_distance\_matrix.qza \

--m-metadata-file sample\_info.tsv \

--m-metadata-column sex \

--o-visualization core-metrics-results/unweighted-unifrac-sex-significance.qzv \

--p-pairwise

qiime emperor plot \

--i-pcoa core-metrics-results/unweighted\_unifrac\_pcoa\_results.qza \

--m-metadata-file sample\_info.tsv \--p-custom-axes treatment \

--o-visualization core-metrics-results/unweighted-unifrac-emperor-treatment.qzv

qiime emperor plot \

--i-pcoa core-metrics-results/bray\_curtis\_pcoa\_results.qza \

--m-metadata-file sample\_info.tsv \

--p-custom-axes treatment \

--o-visualization core-metrics-results/bray-curtis-emperor-treatment.qzv

qiime diversity alpha-rarefaction \

--i-table table.qza \

--i-phylogeny rooted-tree.qza \

--p-max-depth 1000 \

--m-metadata-file sample\_info.tsv \

--o-visualization alpha-rarefaction.qzv

qiime feature-classifier classify-sklearn \

--i-classifier classifier.qza \

--i-reads rep-seqs.qza \

--o-classification taxonomy.qza

qiime metadata tabulate \

--m-input-file taxonomy.qza \

--o-visualization taxonomy.qzv

qiime feature-classifier classify-sklearn \

--i-classifier silva-132-99-515-806-nb-classifier.qza \

--i-reads rep-seqs.qza \

--o-classification taxonomy.qza

qiime metadata tabulate \

--m-input-file taxonomy.qza \

--o-visualization taxonomy.qzv

qiime taxa barplot \

--i-table table.qza \

--i-taxonomy taxonomy.qza \

--m-metadata-file sample\_info.tsv \

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

qiime feature-table filter-samples \

--i-table table.qza \

--m-metadata-file sample\_info.tsv \

--p-where "[sex]='Female'" \

--o-filtered-table F\_SHM\_table.qza

qiime composition add-pseudocount \

--i-table F\_SHM\_table.qza \

--o-composition-table comp\_F\_SHM\_table.qza

qiime composition ancom \

--i-table comp\_F\_SHM\_table.qza \

--m-metadata-file sample\_info.tsv \

--m-metadata-column treatment \

--o-visualization ancom-subject.qzv

qiime taxa collapse \

--i-table F\_SHM\_table.qza \

--i-taxonomy taxonomy.qza \

--p-level 6 \

--o-collapsed-table F\_SHM\_table-l6.qza

qiime composition add-pseudocount \

--i-table F\_SHM\_table-l6.qza \

--o-composition-table comp\_F\_SHM\_table-l6.qza

qiime composition ancom \

--i-table comp\_F\_SHM\_table-l6.qza \

--m-metadata-file sample\_info.tsv \

--m-metadata-column treatment \