mchoi@bell-fe05:**/scratch/bell/mchoi/project** $ qiime dada2 denoise-paired

> --i-demultiplexed-seqs demux.qza

> --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

mchoi@bell-fe05:**/scratch/bell/mchoi/project** $ qiime feature-table summarize \

> --i-table table.qza \

> --o-visualization table.qzv \

mchoi@bell-fe05:**/scratch/bell/mchoi/project** $ qiime feature-table tabulate-seqs \

> --i-data rep-seqs.qza \

> --o-visualization rep.seqs.qzv

mchoi@bell-fe05:**/scratch/bell/mchoi/project** $ qiime metadata tabulate \

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

> --o-visualization denoising-stats.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ 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

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity core-metrics-phylogenetic

> --i-phylogeny rooted-tree.qza

> --i-table table.qza

> --p-sampling-depth 14259

> --m-metadata-file metadata.tsv

> --output-dir core-metrics-results

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ 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\_group\_significance.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity alpha-group-significance

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

> --m-metadata-file metadata.tsv

> --o-visualization core-metrics-results/evenness\_group\_significance.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity beta-group-significance \

> --i-distance-matrix core-metrics-results/jaccard\_distance\_matrix.qza \

> --m-metadata-file metadata.tsv \

> --m-metadata-column treatment \

> --o-visualization core-metrics-results/jaccard\_treatment\_significance.qzv \

> --p-pairwise

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity beta-group-significance

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

> --m-metadata-file metadata.tsv

> --m-metadata-column treatment

> --o-visualization core-metrics-results/unweighted\_unifrac\_treatment\_significance.qzv

> --p-pairwise

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity beta-group-significance

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

> --m-metadata-file metadata.tsv

> --m-metadata-column sex

> --o-visualization core-metrics-results/unweighted\_unifrac\_sex\_significance.qzv

> --p-pairwise

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity beta-group-significance

> --i-distance-matrix core-metrics-results/jaccard\_distance\_matrix.qza > --m-metadata-file metadata.tsv

> --m-metadata-column sex

> --o-visualization core-metrics-results/jaccard\_sex\_significance.qzv > --p-pairwise

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime emperor plot

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

> --m-metadata-file metadata.tsv

> --p-custom-axes treatment\_numeric

> --o-visualization core-metrics-results/unweighted\_unifrac\_emperor\_treatment.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime emperor plot

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

> --m-metadata-file metadata.tsv

> --p-custom-axes treatment\_numeric

> --o-visualization core-metrics-results/bray\_curtis\_emperor\_treatment.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime diversity alpha-rarefaction

> --i-table table.qza

> --i-phylogeny rooted-tree.qza

> --p-max-depth 1000 \

> --m-metadata-file metadata.tsv

> --o-visualization alpha-rarefaction.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime sample-classifier classify-samples \

> --i-table table.qza \

> --m-metadata-file metadata.tsv \

> --m-metadata-column treatment \

> --p-optimize-feature-selection \

> --p-parameter-tuning \

> --p-estimator RandomForestClassifier \

> --p-n-estimators 20 \

> --p-random-state 123 \

> --output-dir classifier

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime metadata tabulate \

> --m-input-file classifier/predictions.qza \

> --o-visualization classifier/predictions.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime metadata tabulate \

> --m-input-file classifier/feature\_importance.qza \

> --o-visualization classifier/feature\_importance.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime feature-table filter-features \

> --i-table table.qza \

> --m-metadata-file classifier/feature\_importance.qza \

> --o-filtered-table classifier/important-feature-table.qza

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime sample-classifier heatmap \

> --i-table table.qza \

> --i-importance classifier/feature\_importance.qza \

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

> --m-sample-metadata-column treatment \

> --p-group-samples \

> --p-feature-count 30 \

> --o-filtered-table classifier/important-feature-table-top-30.qza \

> --o-heatmap classifier/important-feature-heatmap.qzv

mchoi@bell-fe00:**/scratch/bell/mchoi/project** $ qiime sample-classifier heatmap \

> --i-table table.qza \

> --i-importance classifier/feature\_importance.qza \

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

> --m-sample-metadata-column treatment \

> --m-feature-metadata-file taxonomy.qza \

> --m-feature-metadata-column Taxon \

> --p-group-samples \

> --p-feature-count 30 \

> --o-filtered-table classifier/important-feature-table-taxonomy-top-30.qza \

> --o-heatmap classifier/important-feature-heatmap-taxonomy.qzv