#Importing data with the format PairedEndFasqManifestPhred33

$ qiime tools import \

--type 'SampleData[PairedEndSequencesWithQuality]' \

--input-path Manifest\_field \

--input-format PairedEndFastqManifestPhred33 \

--output-path qiime\_out/demux-paired-field.qza

#Importing data with the format PairedEndFasqManifestPhred33

$ qiime tools import \

--type 'SampleData[PairedEndSequencesWithQuality]' \

--input-path Manifest\_lab \

--input-format PairedEndFastqManifestPhred33 \

--output-path qiime\_out/demux-paired-lab.qza

qiime demux summarize \

--i-data qiime\_out/demux-paired-field.qza \

--o-visualization qiime\_out/demux-paired-field.qzv

qiime demux summarize \

--i-data qiime\_out/demux-paired-lab.qza \

--o-visualization qiime\_out/demux-paired-lab.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/\* /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab

qiime dada2 denoise-paired \

--i-demultiplexed-seqs qiime\_out/demux-paired-field.qza \

--p-trim-left-f 0 \

--p-trim-left-r 0 \

--p-trunc-len-f 300 \

--p-trunc-len-r 270 \

--o-table qiime\_out/table.field.qza \

--o-representative-sequences qiime\_out/rep-seqs.field.qza \

--o-denoising-stats qiime\_out/denoising-stats.field.qza

qiime dada2 denoise-paired \

--i-demultiplexed-seqs qiime\_out/demux-paired-lab.qza \

--p-trim-left-f 0 \

--p-trim-left-r 0 \

--p-trunc-len-f 300 \

--p-trunc-len-r 270 \

--o-table qiime\_out/table\_lab.qza \

--o-representative-sequences qiime\_out/rep-seqs\_lab.qza \

--o-denoising-stats qiime\_out/denoising-lab.qza

ml R/3.5.1

ml Qiime/2

$ qiime feature-table summarize \

--i-table qiime\_out/table\_lab.qza \

--o-visualization qiime\_out/table\_lab.qzv \

--m-sample-metadata-file ../Metadata.Lab

$ qiime feature-table tabulate-seqs \

--i-data qiime\_out/rep-seqs\_lab.qza \

--o-visualization qiime\_out/rep-seqs\_lab.qzv

$ qiime feature-table summarize \

--i-table qiime\_out/table\_field.qza \

--o-visualization qiime\_out/table\_field.qzv \

--m-sample-metadata-file ../Metadata.Field

$ qiime feature-table tabulate-seqs \

--i-data qiime\_out/rep-seqs\_field.qza \

--o-visualization qiime\_out/rep-seqs\_field.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/\* /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field

Lab

$ qiime metadata tabulate \

--m-input-file qiime\_out/denoising-lab.qza \

--o-visualization qiime\_out/denoising-lab.qzv

$ qiime feature-table summarize \

--i-table qiime\_out/table\_lab.qza \

--o-visualization qiime\_out/table\_lab.qzv \

--m-sample-metadata-file ../Metadata.Lab

$ qiime feature-table tabulate-seqs \

--i-data qiime\_out/rep-seqs\_lab.qza \

--o-visualization qiime\_out/rep-seqs\_lab.qzv

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

--i-sequences qiime\_out/rep-seqs\_lab.qza \

--o-alignment qiime\_out/aligned-rep-seqs-lab.qza \

--o-masked-alignment qiime\_out/masked-aligned-rep-seqs-lab.qza \

--o-tree qiime\_out/unrooted-tree-lab.qza \

--o-rooted-tree qiime\_out/rooted-tree-lab.qza

$ cd data/qiime\_out/

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/\* /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab

$ qiime diversity core-metrics-phylogenetic \

--i-phylogeny rooted-tree-lab.qza \

--i-table table\_lab.qza \

--p-sampling-depth 7848 \

--m-metadata-file ../../Metadata.Lab \

--output-dir core-metrics-results-lab

$ qiime diversity alpha-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

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

$ qiime diversity alpha-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

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

$ qiime diversity alpha-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

--o-visualization core-metrics-results-lab/shannon-group-significance-lab.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/core-metrics-results-lab/\*significance-lab.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab

$ qiime diversity beta-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

--m-metadata-column Strain\_Treatment \

--o-visualization core-metrics-results-lab/unweighted-unifrac-Strain\_Treatment-significance-lab.qzv \

--p-pairwise

$ qiime diversity beta-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

--m-metadata-column Strain\_Treatment \

--o-visualization core-metrics-results-lab/weighted-unifrac-Strain\_Treatment-significance.qzv \

--p-pairwise

$ qiime diversity beta-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

--m-metadata-column Strain\_Treatment \

--o-visualization core-metrics-results-lab/bray-curtis-Strain\_Treatment-significance.qzv \

--p-pairwise

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/core-metrics-results-lab/unweighted-unifrac-Strain\_Treatment-significance-lab.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab/core-metrics-results-lab

$ qiime diversity alpha-rarefaction \

--i-table table\_lab.qza\

--i-phylogeny rooted-tree-lab.qza \

--p-max-depth 24000\

--m-metadata-file ../../Metadata.Lab \

--o-visualization alpha-rarefaction-lab.qzv

scp -r [eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/alpha-rarefaction-lab.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab/](mailto:eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2_Real/data_lab/qiime_out/alpha-rarefaction-lab.qzv%20/Users/Julius/Desktop/hfb_1st_obj/chp1/lab/)

qiime feature-classifier classify-sklearn \

--i-classifier ../Silva\_132\_classifier.qza \

--i-reads rep-seqs\_lab.qza \

--o-classification taxonomy\_lab.qza

$ qiime metadata tabulate \

--m-input-file taxonomy\_lab.qza \

--o-visualization taxonomy\_lab.qzv

scp -r [eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/taxonomy\_lab.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab/](mailto:eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2_Real/data_lab/qiime_out/taxonomy_lab.qzv%20/Users/Julius/Desktop/hfb_1st_obj/chp1/lab/)

$ qiime taxa barplot \

--i-table table\_lab.qza \

--i-taxonomy taxonomy\_lab.qza \

--m-metadata-file ../../Metadata.Lab \

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

scp -r [eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/taxa-bar-plots-lab.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab/](mailto:eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2_Real/data_lab/qiime_out/taxa-bar-plots-lab.qzv%20/Users/Julius/Desktop/hfb_1st_obj/chp1/lab/)

$ qiime composition add-pseudocount \

--i-table table\_lab.qza \

--o-composition-table comp-table-lab.qza

$ qiime composition ancom \

--i-table comp-table-lab.qza \

--m-metadata-file ../../Metadata.Lab \

--m-metadata-column Strain\_Treatment \

--o-visualization ancom-Strain\_Treatment\_lab.qzv

scp -r [eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/ancom-Strain\_Treatment\_lab.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab/](mailto:eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2_Real/data_lab/qiime_out/ancom-Strain_Treatment_lab.qzv%20/Users/Julius/Desktop/hfb_1st_obj/chp1/lab/)

Field … need to do this step for lab

$ qiime metadata tabulate \

--m-input-file qiime\_out/denoising-stats.field.qza \

--o-visualization qiime\_out/denoising-stats.field.qzv

$ qiime feature-table summarize \

--i-table qiime\_out/table.field.qza \

--o-visualization qiime\_out/table.field.qzv \

--m-sample-metadata-file ../Metadata.Field

$ qiime feature-table tabulate-seqs \

--i-data qiime\_out/rep-seqs.field.qza \

--o-visualization qiime\_out/rep-seqs.field.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/\* /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field

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

--i-sequences qiime\_out/rep-seqs.field.qza \

--o-alignment qiime\_out/aligned-rep-seqs-field.qza \

--o-masked-alignment qiime\_out/masked-aligned-rep-seqs-field.qza \

--o-tree qiime\_out/unrooted-tree-field.qza \

--o-rooted-tree qiime\_out/rooted-tree-field.qza

$ cd data/qiime\_out/

qiime diversity core-metrics-phylogenetic \

--i-phylogeny rooted-tree-field.qza \

--i-table table.field.qza \

--p-sampling-depth 66 \

--m-metadata-file ../../Metadata.Field \

--output-dir core-metrics-results-fields-66

$ qiime diversity alpha-group-significance \

--i-alpha-diversity core-metrics-results-fields-66/faith\_pd\_vector.qza \

--m-metadata-file ../../Metadata.Field \

--o-visualization core-metrics-results-fields-66/faith-pd-group-significance-field.qzv

$ qiime diversity alpha-group-significance \

--i-alpha-diversity core-metrics-results-fields-66/evenness\_vector.qza \

--m-metadata-file ../../Metadata.Field \

--o-visualization core-metrics-results-fields-66/evenness-group-significance-field.qzv

$ qiime diversity alpha-group-significance \

--i-alpha-diversity core-metrics-results-fields-66/shannon\_vector.qza \

--m-metadata-file ../../Metadata.Field \

--o-visualization core-metrics-results-fields-66/shannon-group-significance-field.qzv

scp -r [eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/core-metrics-results-fields-66/\*significance-field.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field/**core-metrics-results-fields-66**](mailto:eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2_Real/data_field/qiime_out/core-metrics-results-fields-66/*significance-field.qzv%20/Users/Julius/Desktop/hfb_1st_obj/chp1/field/core-metrics-results-fields-66)

$ qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results-fields-66/unweighted\_unifrac\_distance\_matrix.qza \

--m-metadata-file ../../Metadata.Field \

--m-metadata-column Strain\_Treatment \

--o-visualization core-metrics-results-fields-66/unweighted-unifrac-Strain\_Treatment-significance-field.qzv \

--p-pairwise

$ qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results-fields-66/weighted\_unifrac\_distance\_matrix.qza \

--m-metadata-file ../../Metadata.Field \

--m-metadata-column Strain\_Treatment \

--o-visualization core-metrics-results-fields-66/weighted-unifrac-Strain\_Treatment-significance-field.qzv \

--p-pairwise

$ qiime diversity beta-group-significance \

--i-distance-matrix core-metrics-results-fields-66/bray\_curtis\_distance\_matrix.qza \

--m-metadata-file ../../Metadata.Field \

--m-metadata-column Strain\_Treatment \

--o-visualization core-metrics-results-fields-66/bray\_curtis-Strain\_Treatment-significance-field.qzv \

--p-pairwise

$ qiime diversity alpha-rarefaction \

--i-table table.field.qza\

--i-phylogeny rooted-tree-field.qza \

--p-max-depth 17300 \

--m-metadata-file ../../Metadata.Field \

--o-visualization alpha-rarefaction-field.qzv

scp -r [eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/alpha-rarefaction-field.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field/**core-metrics-results-fields-66**](mailto:eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2_Real/data_field/qiime_out/alpha-rarefaction-field.qzv%20/Users/Julius/Desktop/hfb_1st_obj/chp1/field/core-metrics-results-fields-66)

$ qiime feature-classifier classify-sklearn \

--i-classifier ../Silva\_132\_classifier.qza\

--i-reads rep-seqs.field.qza \

--o-classification taxonomy.field.qza

$ qiime metadata tabulate \

--m-input-file taxonomy.field.qza \

--o-visualization taxonomy.field.qzv

$ qiime taxa barplot \

--i-table table.field.qza \

--i-taxonomy taxonomy.field.qza \

--m-metadata-file ../../Metadata.Field \

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

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/taxa-bar-plots-field.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field

$ qiime composition add-pseudocount \

--i-table table.field.qza \

--o-composition-table comp-table-field.qza

$ qiime composition ancom \

--i-table comp-table-field.qza \

--m-metadata-file ../../Metadata.Field \

--m-metadata-column Strain\_Treatment \

--o-visualization ancom-Strain\_Treatment-field.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/ancom-Strain\_Treatment-field.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field

Exporting

qiime tools export **\**

--input-path bray\_curtis\_pcoa\_results.qza **\**

--output-path bray\_curtis\_pcoa\_results

Relative abundance

qiime feature-table relative-frequency \

--i-table table.field.qza \

--o-relative-frequency-table relative-frequency-table.field.qza

qiime tools export **\**

--input-path relative-frequency-table.field.qza **\**

--output-path core-metrics-results-fields-66/data2R/relative-frequency-table.field.qza

qiime taxa barplot \

--i-relative-frequency-table relative-frequency-table.field.qza \

--i-taxonomy taxonomy.field.qza \

--m-metadata-file ../../Metadata.Field \

--o-visualization relative-frequency-taxa-bar-plots-field.qzv

New rarefaction for field

$ qiime diversity alpha-rarefaction \

--i-table table.field.qza\

--i-phylogeny rooted-tree-field.qza \

--p-max-depth 200 \

--m-metadata-file ../../Metadata.Field \

--o-visualization alpha-rarefaction-field-200-sampling\_depht.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_field/qiime\_out/alpha-rarefaction-field-200-sampling\_depht.qzv /Users/Julius/Desktop/hfb\_1st\_obj/chp1/field

observed\_otus\_vector.qza

$ qiime diversity alpha-group-significance \

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

--m-metadata-file ../../Metadata.Lab \

--o-visualization core-metrics-results-lab/observed\_otus\_vector-group-significance-lab.qzv

scp -r eason2@snyder.rcac.purdue.edu:/scratch/snyder/e/eason2/Qiime2\_Real/data\_lab/qiime\_out/core-metrics-results-lab /Users/Julius/Desktop/hfb\_1st\_obj/chp1/lab/core-metrics-results-lab