A QIIME workflow example chart
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file

script

visualization

Paired-end Illumina sequencing output

Paired-end reads of raw Illumina sequence
.fastq

join_paired_ends.py

Separate, quality-controlled fasta files of merged reads

Mapping file
.txt

Create this specific to your experiment

A "gold" database for alignment and chimera checking

Provided by greengenes, rdp, etc.

add_qiime_labels.py

Merged file of all seqs in all samples
combined_seqs.fna

pick_open_reference_otus.py

pick_otus.py

List of sequences per OTU ("OTU map")
seqs_otus.txt

pick_rep_set.py

List of one representative sequence of each OTU
rep_set.fna

align_seqs.py

Alignment of representative sequence of each OTU
rep_set_aligned.fna

assign_taxonomy.py

List of taxonomic assignments each OTU
rep_set_tax_assignments.txt

make_otu_table.py

"Biom" OTU table
otu_table.biom

make_phylogeny.py

Tree file
rep_phylo.tre

"Biom" OTU table
otu_table.biom

single_rarefaction.py

biom summarize_table

Subsampled "biom" OTU table
otu_table_even.biom

alpha_diversity.py

Summary of alpha diversity per community
alpha_diversity_even.txt

biom convert

Summarize_taxa_through_plots.py

"Classic" OTU table for R or other programs
otu_table_even.txt

Heatmap, other visualizations

Bar / area charts of composition

beta_diversity.py

Resemblance matrix (e.g., UniFrac)
unifrac.txt

principal_coordinates.py

Table of axis scores
PCoA.txt

make_2d_plots.py

PCoA ordination plots