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**

PANDAseq

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

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

Summarize_taxa_through_plots.py

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