Qiime Commands

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Abstract

Commands for hands-on component for Qiime are found in guidelines.

Citation: Melissa Dsouza Qiime Commands. **protocols.io**
dx.doi.org/10.17504/protocols.io.fesbjee
Published: 26 Jul 2016

Guidelines

1. Checking mapping file format

$ validate_mapping_file.py -m map_file.txt -o mapping_file_output

2.1 Join paired end reads

$ join_paired_ends.py -f Undetermined_S0_L001_R1_001.fastq -
r Undetermined_S0_L001_R2_001.fastq -b Undetermined_S0_L001_I1_001.fastq -o reads

2.2 Depmultiplex & quality filter

$ split_libraries_fastq.py -i fastqjoin.join.fastq -b fastqjoin.join_barcodes.fastq -o split -m map_file.txt -q 29 --barcode_type 12 --store_demultiplexed_fastq

3.1 *De novo* OTU picking

$ pick_de_novo_otus.py -i subs_seqs_q.fasta -o uclust_otus/

3.2 Closed-reference OTU picking

$ pick_closed_reference_otus.py -i subs_seqs_q.fasta -r $PWD/gg_13_8_otus/rep_set/97_otus.fasta -t $PWD/gg_13_8_otus/taxonomy/97_otu_taxonomy.txt -o_ref_otus

3.3 Open-reference OTU picking

$ pick_open_reference_otus.py -i subs_seqs_q.fasta -r $PWD/gg_13_8_otus/rep_set/97_otus.fasta -o uclust_open_otu

BIOM files

$ biom summarize-table -i uclust_otus/otu_table_even10.biom
$ biom summarize-table -i uclust_otus/otu_table_even10.biom --qualitative

$ biom add-metadata -i $PWD/otu_table_even10.biom -o denovo_otu.biom --sample-metadata-fp map_file.txt --observation-metadata-fp $PWD/uclust_assigned_taxonomy/subs_seqs_q_rep_set_tax_assignments.txt --observation-header OTUID,taxonomy --sc-separated taxonomy

$ biom convert -i otu_table.biom -o otu_table.txt --table-type "otutable" --header-key taxonomy -b

More commands:

$ identify_chimeric_seqs.py -m ChimeraSlayer -i rep_set_aligned.fasta -a gold.fa -o chimeric_seqs.txt

$ core_diversity_analyses.py -i denovo_otu.biom -o core_diversity -e 10 -m map_file.txt -t ref_set.tre

1. Filter low sequence count samples from table (minimum sequence count: 7500)
$ filter_samples_from_otu_table.py -i denovo_otu.biom -o core_diversity7500/table_mc7500.biom -n 7500

2. Rarify the OTU table to 7500 sequences/sample
$ single_rarefaction.py -i core_diversity7500/table_mc7500.biom -o core_diversity7500s/table_even7500.biom -d 7500

3. Beta Diversity (weighted_unifrac)
$ beta_diversity.py -i core_diversity7500s/table_even7500.biom -o core_diversity7500/bdiv_even7500/ --metrics weighted_unifrac -t ref_set.tre

4. Principal coordinates (weighted_unifrac)
$principal_coordinates.py -i core_diversity7500/bdiv_even7500//weighted_unifrac_dm.txt -o core_diversity7500/bdiv_even7500//weighted_unifrac_pc.txt

5. Make emperor plots, weighted_unifrac)
$make_emperor.py -i core_diversity7500s/bdiv_even7500//weighted_unifrac_pc.txt -o core_diversity7500/bdiv_even7500//weighted_unifrac_emperor_pcoa_plot/ -m map_file.txt

6. Alpha rarefaction
$ multiple_rarefactions.py -i core_diversity7500/table_mc7500.biom -m 10 -x 7500 -s 749 -o core_diversity7500/arare_max7500//rarefaction/

7. Alpha diversity on rarefied OTU tables
$ alpha_diversity.py -i core_diversity7500/arare_max7500//rarefaction/ -o core_diversity7500_1105noblanks/arare_max7500//alpha_div/ -t ref_set.tre

8. Collate alpha
$ collate_alpha.py -i core_diversity7500/arare_max7500//alpha_div/ -o core_diversity7500_/arare_max7500//alpha_div_collated/

9. Rarefaction plot: All metrics
$ make_rarefaction_plots.py -i core_diversity7500/arare_max7500//
alpha_div_collated/ -m 150701_CAWSMF_1104.txt -
o core_diversity7500/arare_max7500//alpha_rarefaction_plots/

10. Summarize Taxonomy
$ summarize_taxa.py -i core_diversity7500s/taxa_plots/table_mc7500_sorted.biom -
o core_diversity7500/taxa_plots/

Protocol