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Appendix 3: Example configuration for QIIME.

1. *BIN_module.txt* file:

[Job Start]

Name pickotu

Memory 2G

Queue sci.q

CPU N

Major T

Order 1

Thread 1

Qsub False

Command BIN/pick_open_reference_otus.py -i Para_inputdir/all.fa -r DB_reference -o Para_outputdir -f

[Job End]

[Job Start]

Name biom2table

Memory 2G

Queue sci.q

CPU N

Major T

Order 2

Thread 1

Qsub False

Command BIN/biom convert--header-key taxonomy--to-tsv -i Para_outputdir/otu_table_mc2_w_tax_no_pynast_failures.biom -o Para_outputdir/otu_table.txt

[Job End]

[Job Start]

Name level

Memory 2G

Queue sci.q

CPU N

Major T

Order 3

Thread 1

Qsub False

Command BIN/summarize_taxa_through_plots.py -i Para_outputdir/otu_table_mc2_w_tax_no_pynast_failures.biom -o Para_outputdir/taxa_summaries

[Job End]

[Job Start]

Name alphadiversity

Memory 2G

Queue sci.q

CPU N

Major F

Order 3

Thread 1

Qsub False

Command BIN/parallel_alpha_diversity.py -i Para_outputdir/otu_table_mc2_w_tax_no_pynast_failures.biom -o alpha -m chao1,observed_species,shannon,simpson -t rep_set.tre

[Job End]

[Job Start]

Name betadiversity

Memory 2G

Queue sci.q

CPU N

Major F

Order 3

Thread 1

Qsub False

Command BIN/parallel_beta_diversity.py -i Para_outputdir/otu_table_mc2_w_tax_no_pynast_failures.biom -o beta -t rep_set.tre -m bray_curtis,weighted_unifrac, unweighted_unifrac

[Job End]

2. *pipeline_config.txt* file:

[Para]

Para_inputdir=/home/lusf/software/program/example

Para_outputdir=/home/lusf/software/CPLSTool/program/example/qiime_result

[DB]

DB_reference=/home/lusf/software/CPLSTool/program/example/97_otus.fasta.