16S rRNA analytic pipeline

Paired-end assembly of forward and reverse reads into contigs
[make.contigs]

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Contigs quality check
[filtering/trimming following mothur's MiSeq SOP]

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Reference-based & *de novo* chimera filtering
[identify_chimeric_seqs.py with usearch61]

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Annotation of all contigs
[classify.seqs with RDP classifier against RDP trainset 16]

Software used:
Mothur V.1.33.0 21
QIIME V.1.8 22
Custom R script

Extraction of contigs annotated as *Bifidobacterium* *Lactobacillus* *Streptococcus**
[get.lineage with taxon=Bifidobacterium-Lactobacillus-Streptococcus]

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Annotation of contigs at species and sub-species levels, based on signature sequences
[as described in Kieser et al. 2018]

Extraction of the other contigs
[remove.lineage with taxon=Bifidobacterium-Lactobacillus-Streptococcus]

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Contigs clustering into OTUs
[pick_otus.py with usearch_ref, optimal uclust and no chimera detection]

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Taxonomic assignment of OTUs
[parallel_assign_taxonomy_rdp.py with RDP Classifier against Greengenes 13.8]

Merger into final OTU table
[make_otu_table.py]