NCBI Taxonomy
taxdump

Reference sequences
fasta

Samples Description
CSV

Forward reads
fastq

Reverse reads
fastq

inputs

illuminapairedend — micro-assembly of paired-end reads

ngsfilter — assignation of reads to samples

obiannotate — adding sequence length as a new attribute

obigrep — filtering of erroneous sequences (*e.g.* too short or too long sequences)

obiuniq — dereplication of sequences

obigrep — filtering of singleton sequences

obiclean — tag sequences for PCR/sequencing errors detection

obigrep — filtering of putative PCR/sequencing errors

ecotag — taxonomic assignation

tee — redirecting stdout to both file and stdin (Unix **tee** command)

obitab — conversion to table

obitaxonomy

Taxonomic database

Annotated sequences
fasta

Annotated sequences
CSV

outputs

further processing