Single-end Reads (se.fast[a/q])
Paired-end Reads (pe1/2.fast[a/q])

Forward and Reverse Primers

sickle: Quality Trimming

Generate QC Plots

pandaseq: Overlap forward and reverse reads

uclust:
  * Dereplicate duplicate sequence
  * Annotate with cluster sizes
  * Sort by decreasing cluster sizes

uchime: Denovo chimera detection

Generate pipeline statistics

usearch:
  Match against reference database: min 95% Identity

Generate frequencies

Forward Database (F.fasta)
Reverse Database (R.fasta)

Generate QC plots

Generate frequencies

16S/18S Copy numbers (IDs.txt)

Generate pipeline statistics

usearch_aln_transition_prob.py:
  Generate transition matrices for a given Kmer size

collateResults.pl:
  Collate tables across multiple samples

gen_quantitative.py:
  Stats for quantitative comparison between even and uneven community