



--mode runall

--mode aln

Align to marker database (bowtie2)

Filter by alignment length (>80% read length)

Quality filter (MAPQ > 30)

Raw alignments (.bam)

--mode filter

Low-complexity filtering (Komplexity)

Duplicate read filtering (samtools)

Filtered alignments (.bam)

Count aligned reads, coverage, & percent sequence identity

Reads per marker (.txt)

Filter species & taxIDs by minimum observed markers & aligned reads (2+ markers, 4+ reads)

Summarize alignments per species (or taxID), no filtering

Reads per filtered species or taxID (.txt)

Relative abundance of species and higher taxonomic groups (.txt)

Reads per species or taxID (.txt)

Taxonomy tree of hits (.txt)